REMARKS

Claims 1, 6-11, 14-16, 18, 20, and 25-38 are pending in the application. No amendments have been made by the present response.

Interviews

Applicants wish to thank Examiner Yu for her courtesy and helpful comments in the telephone interviews with applicants' representative Jack Brennan conducted on October 15 and November 18, 2009. This issues raised during these interviews are addressed in detail below.

35 U.S.C. §102(b) (Anticipation)

At page 2 of the Advisory Action, the final rejection of claims 1, 9, 10, 11, 18, 20, and 28-38 as anticipated by Mastrangelo et al. (2000) Biotech. Bioeng. 67:544-54 ("Mastrangelo") was maintained.

Independent claim 1 is directed to a stable cell line comprising a Chinese Hamster Ovary (CHO) cell comprising an increased amount of Bcl-x_L protein, wherein the cell comprises a first expression vector encoding a secreted protein, and wherein the cell produces an increased amount of the secreted protein as compared to a cell that does not comprise an increased amount of the Bcl-x_L protein. Independent claim 18 is directed to a method of producing a polypeptide in a stable cell line comprising a CHO cell comprising an increased amount of Bcl-x_L protein.

In the telephone interviews with the Examiner on October 15 and November 18, 2009, applicants explained that Mastrangelo describes CHO- Bcl-x_L "stable transfectants" that do not contain an expression vector encoding a secreted protein, as is required by claim 1. Mastrangelo's subsequent alphaviral infection of the CHO- Bcl-x_L transfectants resulted in cells exhibiting clear variations over time in both viability and protein production. It is applicants' understanding that the Examiner no longer disputes applicants' assertion that alphavirus infection of Mastrangelo's CHO- Bcl-x_L stable transfectants results in a transient viral-based protein production system.

It is applicants' understanding that the Examiner's remaining issues concern whether claim 1 requires that the first expression vector be "stably" transfected (so as to distinguish it

from Mastrangelo's transient viral-based system) and whether such a stable transfectant is described in the working examples of the present application. These points are addressed in detail below.

First, the cell line of claim 1 is a stable cell line that produces an increased amount of a recombinant secreted protein as compared to a cell that does not comprise an increased amount of the Bcl-x_L protein. The fact that the claim requires the cell line to be "stable" necessarily means that any expression vector present in the cell line (including the "first expression vector" encoding the secreted protein) must necessarily be present in a stable/non-transient manner. For example, it would not be possible for the cell line to be "stable" if it were only transiently transfected with a vector that encodes the secreted protein. Transient production of a recombinant protein by a cell would clearly preclude that cell from being considered a "stable cell line" that produces the protein.

Second, the specification makes clear that the "100AB-37 cell line" (described in Example 4 on page 17 of the specification) is stably transfected with a vector encoding a secreted protein. The following quoted passages from the specification make this abundantly clear.

(i) "To further expand the application of Bcl-x_L, the next goal was to transfect an established CHO-DG44 cell line expressing a heterologous protein with the Bcl-x_L gene and examine the Bcl-x_L transfected cells for an increased production of the heterologous protein arising from expected prolonged viability." (Application at page 17, lines 1-5). This passage explicitly refers to an "established" CHO cell line expressing a heterologous protein (which protein is explained in subsequent passages to be the AQC2 antibody). The term "established" necessarily means that the cell line is stable. The person of ordinary skill in the art would understand that the cell line must be stable because there is no such thing as a "transient" established cell line. The specification makes clear that this established cell line expresses the heterologous protein and is used for Bcl-x_L transfection.

(ii) "The pBcl-x_L-zeo plasmid was used to transfect (by electroporation) the cell line 100AB-37, which is a DG44 CHO cell previously transfected with a nucleic acid molecule encoding the monoclonal antibody, AQC2. The 100AB-37 parent secretes the AQC2 monoclonal antibody with a specific productivity (s.p.) of 10 pg cell $^{-1}$ day^{-1}." (Application at page 17, lines 12-15). This passage explicitly refers to 100AB-37 as a "cell line" that has a

defined "specific productivity" of the AQC2 antibody. The person of ordinary skill in the art would understand these terms to necessarily mean that the cells are stably transfected with the nucleic acid molecule encoding the antibody. The skilled person would understand that the cell line must be a stable one because there is no such thing a "transient" cell line having a defined "specific productivity" associated with it. The reference to a specific productivity necessarily means that it is a stable feature of the cell line that is maintained in cell culture.

(iii) "Eight 100AB-37/ Bcl-x_L isolates expressing the highest titer were released from zeocin selection and <u>cultured further for stability</u> before examination for growth and titer (see below) in spinner flasks." (Application at page 17, lines 30-32). This passage explicitly states that the cells are stable, by stating that they were cultured further for "stability." This removes any doubt that the 100AB-37 cells following transfection with the pBcl-x_L-zeo plasmid were in fact "stable."

In addition to the foregoing, the present application refers to WO 02/083854 (copy enclosed as "Exhibit A") as describing the AQC2 antibody that is produced by the established cell line described on page 17 of the present application. (Application at page 10, line 30). WO 02/083854 describes in detail production of CHO cells expressing AQC2 and explicitly states that "[v]ectors were then designed for <u>stable expression</u> of huAQC2-c3 in CHO cells." (emphasis added; WO 02/083854 at page 75, lines 5-6). The skilled person having read the working example at page 17 of the present application in combination with WO 02/083854 would have clearly understood that the 100AB-37 cell line described in the application was stably transfected with a vector encoding the AQC2 antibody. The stable 100AB-37/ Bcl-x_L cell lines described in Example 4 that resulted from transfection of the established 100AB-37 cell line with a Bcl-x_L expression vector is a clear example of the stable cell line of claim 1.

In summary, the remarks above establish that (i) the term "stable" in claim 1 is a limitation that necessarily requires that the first expression vector be present in the cell in stable manner, and (ii) the 100AB-37/ Bcl-x_L cell line is clearly described in the application as an example of such a stable cell line. Because Mastrangelo fails to describe such a stable CHO cell line, the reference does not anticipate independent claims 1 or 18 or claims 9, 10, 11, 20, and 28-31 that depend directly or indirectly therefrom. Applicants request that the Examiner withdraw the rejection of the claims.

Claims 37 and 38

In addition to and independent of the remarks above as applied to independent claims 1 and 18, dependent claims 37 and 38 require that the expression vector that is contained within the cell and encodes the polypeptide produced by the cell at increased levels be a plasmid. The SFV-IL-12 vector used by Mastrangelo for IL-12 production is an alphavirus and clearly does not anticipate the plasmid-based system of dependent claims 37 and 38. For this additional reason, the rejection of these dependent claims as anticipated by Mastrangelo cannot stand.

35 U.S.C. §103(a) (Obviousness)

At page 3 of the final Office Action, claims 6, 7, 25, and 26 were finally rejected as unpatentable over Mastrangelo in view of Sinacore et al. (1996) Biotech. Bioeng. 52:518-28 ("Sinacore").

Sinacore was cited as disclosing a strain of CHO cells that is capable of growth in serum-free suspension culture. However, Sinacore provides nothing that supplements the deficiencies of Mastrangelo detailed above with respect to independent claims 1 and 18. Accordingly, once independent claims 1 and 18 are held allowable, dependent claims 6, 7, 25, and 26 should also be in condition for allowance.

At pages 3-4 of the final Office Action, claims 14-16 and 32-34 were finally rejected as unpatentable over Mastrangelo in view of Kim et al. (2000) Biotech. Bioeng. 71:184-93 ("Kim").

Kim was cited as disclosing the use of CHO cells to produce an antibody. However, Kim provides nothing that supplements the deficiencies of Mastrangelo detailed above with respect to independent claims 1 and 18. Accordingly, once independent claims 1 and 18 are held allowable, dependent claims 14-16 and 32-34 should also be in condition for allowance.

At page 4 of the final Office Action, claims 8 and 27 were finally rejected as unpatentable over Mastrangelo in view of Sinacore (as applied to claims 1, 7, 18, and 26) and further in view of Kim.

Kim was cited as disclosing the use of butyrate in recombinant CHO cell cultures to achieve high level expression of foreign proteins. However, Kim provides nothing that supplements the deficiencies of Mastrangelo detailed above with respect to independent claims 1 and 18. Accordingly, once independent claims 1 and 18 are held allowable, dependent claims 8 and 27 should also be in condition for allowance.

CONCLUSIONS

Applicants respectfully submit that all grounds for rejection have been overcome and that all claims are now in condition for allowance.

Please apply any charges or credits to Deposit Account No. 06-1050, referencing Attorney Docket No. 13751-0036US1.

Respectfully submitted,

Date: December 17, 2009

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EXHIBIT A

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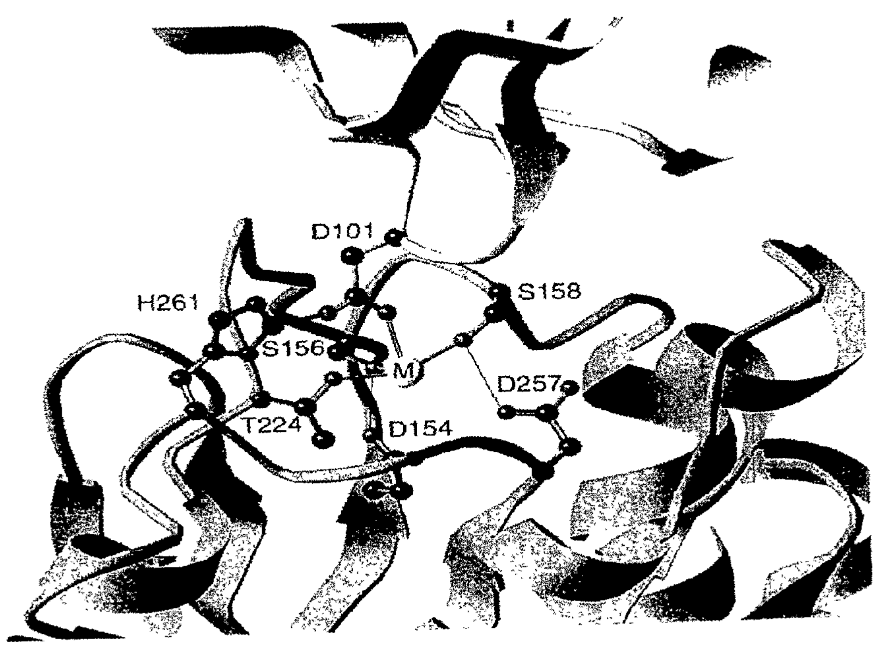
(54) Title: ANTIBODIES TO VLA-1



(57) Abstract: Antibodies that specifically bind to VLA-1 integrin and methods of using these antibodies to treat immunological disorders in a subject. Also included are crystal structures of complexes formed by VLA-1 antibodies and their ligands, and VLA-1 antagonists and agonists identified by using the structure coordinates of these structures.

WO 02/083854 A2

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ANTIBODIES TO VLA-1

FIELD OF THE INVENTION

This invention relates to antibodies to VLA-1 integrin and the use of these antibodies in treating inflammatory diseases and other immunological disorders. This invention also relates to the crystal structure of the complex between one such antibody and the α1-I domain of VLA-1, and to the use of this structural information for computational drug design.

BACKGROUND OF THE INVENTION

Integrins are a superfamily of cell surface receptors that mediate cell-cell and cell-matrix adhesion. These proteins are known to provide anchorage as well as signals for cellular growth, migration and differentiation during development and tissue repair. They have been implicated in immune and inflammatory processes.

Integrins are heterodimeric proteins composed of two noncovalently linked polypeptide chains, α and β. The amino terminus of each chain forms a globular head that contributes to interchain linking and to ligand binding. The globular heads are connected to the transmembrane segments by stalks. The cytoplasmic tails are usually less than 50 amino acid residues long. Integrin subfamilies were originally defined on the basis of which β subunit was used to form the heterodimers. The β1-containing integrins are also called VLA molecules, referring to "very late activation" antigens. VLA-1 to VLA-6 refer to β1 subfamily members containing α1 to α6 (i.e., CD49a to CD49f), respectively. For general

review, see *Cellular and Molecular Immunology*, eds. Abul K. Abbas et al., W.B. Saunders Company, Philadelphia, PA, 2000.

Collagen (both types I and IV) and laminin are known ligands of $\alpha 1\beta 1$ integrin (i.e., VLA-1). VLA-1 has been implicated in cell adhesion and migration on collagen (Keely et al., 1995, *J. Cell Sci.* 108:595-607; and Gotwals et al., 1996, *J. Clin. Invest.* 97:2469-2477); in promoting contraction and reorganization of collagen matrices, a critical component of wound healing (Gotwals et al., *supra*; and Chiro, 1991, *Cell* 67:403-410); and in regulating the expression of genes involved in extracellular matrix remodeling (Riikonen et al., 1995, *J. Biol. Chem.* 270:1-5; and Langholz et al., 1995, *J. Cell Biol.* 131:1903-1915). Thus, improper regulation of VLA-1 may result in certain pathological conditions such as fibrosis.

Moreover, it has been suggested that VLA-1 may play a role in T cell /monocyte-driven diseases. Anti-VLA-1 antibodies block T-cell dependent cytokine expression (Miyake et al., 1993, *J. Exp. Med.* 177:863-868). Expression of VLA-1 is increased in persistently activated, 2 to 4 week old cultured T cells (Hemler et al., 1985, *Eur. J. Immunol.* 15:502-508). VLA-1 is also expressed on a high percentage of T cells isolated from the synovium of patients with rheumatoid arthritis (Hemler et al., 1986, *J. Clin. Invest.* 78:692-702).

Several crystal structures of integrin α subunits have been determined, including the structures of the $\alpha 2$-I domain of $\alpha 2\beta 1$ (PDB accession code 1aox; Emsley et al., 1997, *J. Biol. Chem.* 272:28512-28517); the $\alpha 1$-I domain of rat $\alpha 1\beta 1$ (PDB accession number 1ck4; Nolte et al., 1999, *FEBS Lett.* 452:379-385; WO 00/20459); the $\alpha 1$ subunit of human $\alpha 1\beta 1$ (PDB accession code 1qc5; Rich et al., 1999, *J. Biol. Chem.* 274:24906-24913); the αL-I and αM-I domains; and vWF-A3 (Lee et al., 1995, *Cell* 80:631-635; Lee et al., 1995, *Structure* 3:1333-1340; Qu et al., 1995, *Proc. Natl. Acad. Sci. USA* 92:10277-10281; Qu et al., 1996, *Structure* 4:931-942). The $\alpha 2\beta 1$ structure revealed a helix (i.e., the C-helix) that created a trench or groove on one face of the protein at the metal-ion binding site (Emsley et al., *supra*). The crystal structure of the $\alpha 2$-I domain complexed to a short collagen-based triple helical peptide revealed that the collagen-based peptide was bound to that trench, where the $\alpha 2$-I amino acids that made intermolecular or metal contacts included

Asp151, Asn154, Tyr157, Gln215, Asp219, Leu220, Thr221, Asp254, Glu256, His258, Tyr285, Leu286, Asn289, Leu291, Asn295, and Lys298 (PDB accession code 1dzi; Emsley et al., 2000, *Cell* 101:47-56; WO 01/73444). The amino acid numbering immediately above is based on PDB accession code 1dzi and herein referred to as "crystal numbering." The crystal structures of the rat and human α1-I domains revealed a similar trench.

SUMMARY OF THE INVENTION

The present invention provides anti-VLA-1 antibodies and methods of using these antibodies to treat a variety of inflammatory and immunological disorders.

Specifically, the invention embraces an antibody that specifically binds to VLA-1 (e.g., human VLA-1). This antibody contains light chain complementarity determining regions ("CDR"s) defined by amino acid residues 24 to 33, 49 to 55, and 88 to 96 of SEQ ID NO:1, and/or heavy chain complementarity determining regions defined by amino acid residues 31 to 35, 50 to 65, and 98 to 107 of SEQ ID NO:2. These CDRs may contain mutations (e.g., deletions, insertions and/or substitutions) in the non-antigen-contacting portions, as determined from the crystal structure disclosed herein, without affecting the VLA-1-binding activity of the antibody. Exemplary mutations are S24N, G92S and D101A in the light chain CDRs, and G55S in the heavy chain CDR2. In one embodiment, the antibody of this invention contains a light chain variable domain sequence of SEQ ID NO:1 and/or a heavy chain variable domain sequence of SEQ ID NO:2.

In a related embodiment, the antibody of this invention contains the same heavy and light chain polypeptide sequences as an antibody produced by hybridoma mAQC2, deposited on April 18, 2001 at the American Type Culture Collection ("ATCC"), 10801 University Boulevard, Manassas, VA 20110-2209 and having ATCC accession number PTA3273. (All ATCC deposits recited herein were made under the Budapest Treaty). This antibody can be produced by, for example, hybridoma mAQC2, or cells containing nucleic acid sequences isolated from that hybridoma that encode the heavy and light chains of the mAQC2 monoclonal antibody.

In another embodiment, the antibody is a humanized antibody comprising at least one (e.g., 2, 3, 4, or 5) of the following residues in its light chain: Q1, L4, P46, W47 and Y71; or at least one (e.g., 2, 3, 4, 5, 6 or 7) of the following residues in its heavy chain: D1, V12, S28, F29, A49, T93, R94 (Kabat numbering convention). For instance, the antibody comprises Q1, L4 and Y71 in the light chain; and/or (i) F29, A49, T93 and R94, or (ii) A49 and T93, in the heavy chain.

The humanized antibody of this invention may contain a light chain variable domain sequence defined by amino acid residues 1 to 106 of SEQ ID NO:3, and/or a heavy chain variable domain sequence defined by amino acid residues 1 to 118 of SEQ ID NO:4. The humanized antibody may comprise the same heavy and/or light chain polypeptide sequences as an antibody produced by cell line hAQC2 (ATCC accession number PTA3275; deposited on April 18, 2001).

In another embodiment, the humanized antibody of this invention may contain a mutation (e.g., deletion, substitution or addition) at one or more (e.g., 2, 3, 4, 5, 6, 7 or 8) of certain positions in the heavy chain such that an effector function of the antibody (e.g., the ability of the antibody to bind to a Fc receptor or a complement factor) is altered without affecting the antibody's ability to bind to VLA-1 (U.S. Patent 5,648,260). These heavy chain positions include, without limitation, residues 234, 235, 236, 237, 297, 318, 320 and 322 (EU numbering system). The humanized antibody can, for instance, contain the mutations L234A (i.e., replacing leucine at position 234 of an unmodified antibody with alanine) and L235A (EU numbering system) in its heavy chain. In one related embodiment, the antibody comprises the same heavy chain polypeptide sequence as an antibody produced by cell line hsAQC2 (ATCC accession number PTA3356; deposited on May 4, 2001).

In yet another embodiment, the humanized antibody of this invention may contain a mutation (e.g., deletion or substitution) at an amino acid residue that is a site for glycosylation, such that the glycosylation site is eliminated. Such an antibody may be clinically beneficial for having reduced effector functions or other undesired functions while retaining its VLA-1 binding affinity. Mutations of glycosylation sites can also be beneficial for process development (e.g., protein expression and purification). For instance, the heavy chain of the antibody may

contain the mutation N297Q (EU numbering system) such that the heavy chain can no longer be glycosylated at this site. In one related embodiment, the humanized antibody may comprise the same heavy chain polypeptide sequence as an antibody produced by cell line haAQC2 (ATCC accession number PTA3274; deposited on April 18, 2001).

In still other embodiments, the heavy and/or light chains of the antibody of this invention contain mutations that increase affinity for binding to VLA-1 and thereby increase potency for treating VLA-1-mediated disorders.

Embraced in this invention are also a composition containing an antibody of the invention and a pharmaceutically acceptable carrier; an isolated nucleic acid containing a coding sequence for SEQ ID NO:1; an isolated nucleic acid containing a coding sequence for SEQ ID NO:2; an isolated nucleic acid containing a coding sequence for the light chain of an antibody produced by hybridoma mAQC2; an isolated nucleic acid containing a coding sequence for the heavy chain of an antibody produced by hybridoma mAQC2; an isolated nucleic acid containing a coding sequence for the light chain of an antibody produced by cell line hAQC2; an isolated nucleic acid containing a coding sequence for the heavy chain of an antibody produced by cell line hAQC2; an isolated nucleic acid containing a coding sequence for the heavy chain of an antibody produced by cell line haAQC2; an isolated nucleic acid containing a coding sequence for the heavy chain of an antibody produced by cell line hsAQC2; an isolated nucleic acid containing a coding sequence for residues 1 to 106 of SEQ ID NO:3; an isolated nucleic acid containing a coding sequence for residues 1 to 118 of SEQ ID NO:4; cells of hybridoma mAQC2; cells from cell line hAQC2; cells from cell line haAQC2; and cells from cell line hsAQC2.

The present invention also provides a method of treating a subject with an immunological disorder mediated by VLA-1, including administering to the subject an effective amount of an antibody of this invention. For instance, this method is used to treat a human subject to palliate, ameliorate, stabilize, reverse, prevent, slow or delay progression of the disorder. Alternatively, this method is used prophylactically to treat a human subject at risk for developing this immunological disorder so as to

prevent or delay the onset of the disorder. An "effective amount" of the composition can be administered in one or more dosages.

VLA-1 mediated immunological disorders include, but are not limited to, disorders in which the VLA-1 activity level is elevated in one or more tissues as compared to a normal subject. Examples of such disorders are skin related conditions (e.g., psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle cells), fibrosis (e.g., kidney or lung fibrosis), allergic rhinitis, respiratory distress syndrome, asthma, bronchitis, tendinitis, bursitis, fever, migraine headaches, gastrointestinal conditions (e.g., inflammatory bowel disease, Crohn's disease, gastritis, irritable bowel syndrome, colitis and colorectal cancer), vascular diseases (e.g., atherosclerosis), periarteritis nodosa, thyroiditis, aplastic anemia, Hodgkin's Disease, rheumatic fever, osteoarthritis, autoimmune diseases (e.g., type I diabetes, myasthenia gravis, rheumatoid arthritis, systemic lupus erythematosus, and multiple sclerosis), sarcoidosis, nephrotic syndrome, renal failure, Bechet's Syndrome, polymyositis, gingivitis, hypersensitivity (e.g., delayed type hypersentivity or immediate hypersensitivity), graft and transplant rejections, graft versus host disease (GVHD), conjunctivitis, swelling occurring after injury, myocardial ischemia, and endotoxin shock syndrome.

The present invention also provides a method of determining the level of VLA-1 in a tissue (e.g., tissue specimen and body fluid) comprising contacting the tissue (e.g., *in vivo* or *in vitro*) with the antibody of the invention, and then detecting the binding of the antibody to the tissue, thereby determining the level of VLA-1 in the tissue.

As used herein, the antibody of this invention can be, for instance, a murine antibody, a humanized antibody, or a chimeric antibody. It can be a whole antibody (i.e., with two full length light chains and two full length heavy chains) of any isotype and subtypes (e.g., IgM, IgD, IgG_1, IgG_2, IgG_3, IgG_4, IgE, IgA_1 and IgA_2; with either kappa or lambda light chain). Alternatively, the antibody of this invention refers to an antigen-binding fragment (e.g., Fab, $F(ab')_2$, and single chain Fv) of a whole antibody.

The present invention further provides crystallizable compositions and crystals of complexes formed by a rat-human chimeric α1-I domain (mutant RΔH) and a hAQC2 Fab fragment, and methods for using such compositions and crystals. This invention also provides the structure coordinates and binding sites of the chimeric domain and the hAQC2 Fab fragment. The atomic coordinates derived from the crystal structure described herein provide a structural basis for the biological activities of hAQC2 as well as a basis for rational design of VLA-1 agonists or antagonists with predicted biological activities (e.g., small molecule compounds or antibodies such as hAQC2 variants).

The crystal structure disclosed herein is the first crystal structure of an α1-I domain of an α1β1 integrin/ Fab complex. This structure shows the residues critical for Fab binding by α1-I domain. In addition, the Fab binds in the putative collagen-binding site and inhibits collagen binding. Amino acid residues found in the binding site on the α1-I domain include Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Glu218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294 (crystal numbering). Residues on the Fab fragment found to bind to the α1-I domain include light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101 (crystal numbering).

This invention also provides a computer for producing a three-dimensional representation of a molecular complex, where the molecular complex is defined by the set of structure coordinates of a complex of a chimeric I domain of an α1β1 integrin RΔH and humanized antibody hAQC2, according to Fig. 19; or a homologue of the molecular complex, the homologue having a root mean square deviation from the backbone atoms of the amino acids of not more than 0.65 Å. The computer includes a machine-readable data storage medium including a data storage material encoded with machine-readable data, where the data contains at least a portion of the structure coordinates of the complex according to Fig. 19; a working memory for storing instructions for processing the machine-readable data; a central-processing unit coupled to the working memory and to the machine-readable data storage medium for processing the machine readable data into the three-dimensional

representations; and a display coupled to the central-processing unit for displaying the three-dimensional representation.

This invention further provides a computer for producing a three-dimensional representation of a molecule or molecular complex including a binding site defined by structure coordinates of hAQC2 amino acids including at least seven (e.g., 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101 (crystal numbering), according to Fig. 19; or a homologue of the molecule or molecular complex, where the homologue includes a binding site that has a root mean square deviation from the backbone atoms of the hAQC2 amino acids of not more than 1.10 Å. This invention also provides a computer for producing a three-dimensional representation of: a binding site defined by structure coordinates of hAQC2 amino acids including at least seven (e.g., 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101 (crystal numbering), according to Fig. 19; a binding site of a homologue that has a root mean square deviation from the backbone atoms of the hAQC2 amino acids of not more than 1.10 Å.

This invention also provides a method for identifying an inhibitor of an I domain of an integrin including the steps of using structure coordinates of hAQC2 amino acids including at least seven (e.g., 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16) of light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101 (crystal numbering), according to Fig. 19 or ± a root mean square deviation from the backbone atoms of the hAQC2 amino acids not more than 1.10 Å, to generate a three-dimensional structure of a binding site; employing the three-dimensional structure to design or select a potential antagonist; synthesizing the potential antagonist; and contacting the potential antagonist with hAQC2 to determine the ability of the potential antagonist to interact with hAQC2, where the ability of the potential antagonist to interact with hAQC2 indicates that the potential antagonist is

an inhibitor of the I domain. This invention further provides an inhibitor of I domain of integrin identified by this method.

This invention also provides a computer for producing a three-dimensional representation of a molecule or molecular complex including: a binding site defined by structure coordinates of I domain amino acid residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294 (crystal numbering), according to Fig. 19; or a homologue of the molecule or molecular complex, where the homologue includes a second binding site that has a root mean square deviation from the backbone atoms of the I domain amino acids not more than 0.65 Å. This invention also provides a computer for producing a three-dimensional representation of: a first binding site defined by structure coordinates of I domain amino acids residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294 (crystal numbering), according to Fig. 19; or a binding site of a homologue that has a root mean square deviation from the backbone atoms of the I domain amino acids not more than 0.65 Å.

This invention also provides a computer for producing a three-dimensional representation of a molecule or molecular complex including: a binding site defined by structure coordinates of I domain amino acids including at least three of residues Glu192, Gln218, Arg219, Gly220, and Gly221 (crystal numbering), according to Fig. 19; or a homologue of the molecule or molecular complex, where the homologue includes a second binding site that has a root mean square deviation from the backbone atoms of the I domain amino acids not more than 1.0 Å. The invention further provides a computer for producing a three-dimensional representation of a binding site defined by structure coordinates of I domain amino acids including at least three of residues Glu192, Gln218, Arg219, Gly220, and Gly221 (crystal numbering), according to Fig. 19; or a binding site of a homologue that has a root mean square deviation from the backbone atoms of the I domain amino acids not more than 1.0 Å.

This invention further provides methods for using these three-dimensional representations to design chemical entities that associate with the chimeric domain or the hAQC2 Fab fragment, or portions thereof; and act as potential inhibitors of the chimeric domain or the hAQC2 Fab fragment, or portions thereof. This invention also relates to compositions including chemical entities, such as inhibitors and variants of the chimeric domain or variants of the hAQC2 Fab fragment, where such chemical entities and variants are rationally designed by means of the structure coordinates of the chimeric domain or the hAQC2 Fab fragment, or binding sites. The invention further relates to use of the above-identified chemical entities to treat or prevent conditions associated with inappropriate or abnormal $\alpha 1\beta 1$ activity in a subject.

This invention further provides a method for identifying an inhibitor of an I domain of an integrin including the steps of using the structure coordinates of I domain amino acids residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294 (crystal numbering), according to Fig. 19, to generate a three-dimensional structure of a binding site; employing the three-dimensional structure to design or select a potential antagonist; synthesizing the potential antagonist; and contacting the potential antagonist with I domain to determine the ability of the potential antagonist to interact with I domain, where the ability of the potential antagonist to interact with the I domain indicates that the potential antagonist is an inhibitor of the I domain.

This invention also provides a method for identifying an inhibitor of an I domain of an integrin including the steps of using the structure coordinates of at least three of I domain amino acids including residues Glu192, Gln218, Arg219, Gly220, and Gly221 (crystal numbering), according to Fig. 19, or ± a root mean square deviation from the backbone atoms of the I domain amino acids not more than 0.65 Å, to generate a three-dimensional structure of a binding site; employing the three-dimensional structure to design or select a potential antagonist; synthesizing the potential antagonist; and contacting the potential antagonist with I domain to determine the ability of the potential antagonist to interact with I domain of integrin,

where the ability of the potential antagonist to interact with the I domain indicates that the potential antagonist is an inhibitor of the I domain. This invention also provides an inhibitor of I domain of integrin identified by this method.

Other features and advantages of the invention will be apparent from the following detailed description, and from the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. *Collagen-binding integrins $\alpha 1\beta 1$ and $\alpha 2\beta 1$ on activated leukocytes.* (A). Flow cytometric analysis of $\alpha 1$ and $\alpha 2\beta 1$ integrin expression on IL-2-activated splenocytes (d 11). Cells were labeled with either anti-$\alpha 1$ mAb, anti-$\alpha 2$ mAb, or non-binding control mAb (grey lines), and followed by FITC-anti-hamster immunoglobulin. (B) Effect of anti-$\alpha 1$ and anti-$\alpha 2$ mAbs on leukocyte adhesion to collagen. 10^5 IL-2 activated splenocytes were treated with indicated mAbs for 15 min before plating onto either type IV or type I collagen-coated wells for 1 h at 37°C. Adhesion was calculated as illustrated in Example 1, and expressed as % adhesion relative to control mAb-treated cells. Adhesion assays were done in triplicate, and at least three independent experiments were performed. One representative experiment is shown.

Figure 2. *Effect of anti-integrin mAbs on the effector phase of delayed-type hypersensitivity.* SRBC-sensitized mice were injected i.p. with the indicated mAbs 1 h prior to SRBC challenge. Footpad thickness was measured 20 h after antigen challenge, and results shown as % increase in footpad thickness ± SEM as illustrated in Example 2. These data represent a summary of eight experiments with n = 79 (PBS), 68 (control hamster Ig), 68 (anti-$\alpha 1$), 29 (anti-$\alpha 2$), 18 (anti-$\alpha 1$ + anti-$\alpha 2$), 45 (anti-$\alpha 4$), 18 (anti-$\alpha 5$), 20 (anti-$\alpha 6$), and 10 (anti-$\beta 1$). The mAbs used were: Ha4/8 (control hamster Ig group 2), Ha31/8 (anti-$\alpha 1$), Ha1/29 (anti-$\alpha 2$), PS/2 (anti-$\alpha 4$), 5H10-27 (anti-$\alpha 5$), GoH3 (anti-$\alpha 6$), and HMβ1-1 (anti-$\beta 1$).

Figure 3. *Effect of anti-integrin mAbs on the effector phase of contact hypersensitivity.* FITC-sensitized mice were injected i.p. with the indicated mAbs 4 h prior to FITC challenge. Ear thickness was measured at baseline and 24 h later, and results shown as % increase in ear thickness ± SEM as illustrated in Example 3.

These data represent a summary of nine experiments with n = 74 (PBS), 60 (control hamster Ig), 26 (anti-ICAM-1), 44 (anti-α1), 44 (anti-α2), 38 (anti-α1 + anti-α2), 36 (anti-α4), 16 (anti-α5), 26 (anti-α4 + anti-α5), 24 (anti-α6), and 22 (anti-β1). The hamster mAbs used were: Ha4/8 (control hamster Ig group 2), Ha31/8 (anti-α1), Ha1/29 (anti-α2), HMβ1-1 (anti-β1), 3E2 (anti-ICAM-1); the rat mAbs used were: R35-95 and R35-38 (control rat IgG2a and rat IgG2b, respectively), PS/2 (anti-α4), 5H10-27 (anti-α5), GoH3 (anti-α6).

Figure 4. *Contact hypersensitivity responses in α1-deficient mice compared to wild-type mice.* FITC-sensitized mice were injected i.p. with indicated mAbs 4 h prior to FITC challenge. Ear thickness was measured at baseline and 24 h later, and results shown as % increase in ear thickness ± SEM as illustrated in Example 4. Groups of four to five mice per condition were used, and all experiments were performed a minimum of three times. One representative experiment is shown.

Figure 5. *Effect of anti-α1 and anti-α2 mAbs on croton oil-induced non-specific inflammation.* Mice were injected i.p. with indicated mAbs 4 h prior to ear painting with croton oil. Ear thickness was measured at baseline and 24 h later, and results shown as % increase in ear thickness ± SEM as illustrated in Example 5. Groups of four to five mice per condition were used, and all experiments were performed a minimum of three times. One representative experiment is shown.

Figure 6. *Effect of anti-α1 and α2 mAbs in collagen mAb-induced arthritis.* Mice were injected i.p. with anti-collagen mAbs at d 0, followed by LPS on day 3. Mice were injected i.p. with indicated mAbs every 3rd day starting on d 0. Clinical arthritis was apparent 2-3 d following LPS injection and continued for several weeks. Each limb was evaluated on a 0 to 4 scale every 3rd day as illustrated in Example 6 and results are expressed as the mean arthritic score between d 9 and d 15 (± SEM) of all four limbs. These data represent a summary of four experiments with each experiment consisting of groups of three to four mice per condition.

Figure 7. *Effect of anti-α1 and α2 mAbs in collagen mAb-induced arthritis.* A. Preventative treatment of mice with either anti-α1 or anti-α2 mAb decreases arthritic score. Mice were treated with anti-collagen mAbs at d 0, followed by LPS on d 3. Arthritis was apparent by d 6 and continued for several weeks. Mice

were treated with the indicated mAbs every 3rd day starting on d 0. Each limb was evaluated and scored on a 0 to 4 scale every 3rd day. Results are expressed as the mean arthritic score between d 9 and d 15 (± SEM) of all four limbs (maximum score of 16). Groups of 4 mice per condition were used; the average of 12 experiments is shown. B. $\alpha 1$-deficient mice have a reduced arthritic score comparable to anti-$\alpha 1$ mAb-treated wild-type mice. Experimental details and scoring are as outlined above. Groups of 4 mice per condition were used; the average of 2 experiments is shown.

Figure 8. Development of arthritis is delayed in the absence of lymphocytes and inhibition of arthritis by anti-$\alpha 1$ mAb occurs in the absence of lymphocytes. Wild-type B6,129 or RAG-1-deficient B6,129 mice were treated with anti-collagen mAbs at day 0, followed by LPS on day 3. Arthritis was apparent by day 6 and continued for several weeks. Mice were treated with the indicated mAbs every 3rd day starting on day 0. Each limb was evaluated and scored on a 0 to 4 scale every 3rd day. Results are expressed as the mean arthritic score per limb (maximum score of 4). Groups of 4 mice per condition were used.

Figure 9. Dose response of anti-$\alpha 1$ mAb inhibition of arthritis. Wild-type Balb/c mice were treated with anti-collagen mAbs at day 0, followed by LPS on day 3. Arthritis was apparent by day 6 and continued for several weeks. Mice were treated i.p. with the indicated dose of either Ha4/8 (isotype control) or Ha31/8 (anti-$\alpha 1$) mAbs every 3rd day starting on day 0. Each limb was evaluated and scored on a 0 to 4 scale every 3rd day. Results are expressed as the mean arthritic score per limb (maximum score of 4). Groups of 4 mice per condition were used.

Figure 10. Therapeutic treatment with anti-$\alpha 1$ mAb can decrease arthritic score. Wild-type Balb/c mice were treated with anti-collagen mAbs at day 0, followed by LPS on day 3. Arthritis was apparent by day 6 and continued for several weeks. Mice were treated i.p. with mAbs (250 μg) or Ig fusion protein (200 μg) every 3rd day starting on day 4. Mice received either mAb (Ha4/8 isotype control or Ha31/8 anti-$\alpha 1$), Ig fusion protein (Isotype control Ig or TNF-R55-Ig) or a combination of both (250 ug Ha31/8 and 200 ug TNF-R55-Ig). Each limb was evaluated and scored on a 0 to 4 scale every 3rd day. Results are expressed as the mean arthritic score per limb (maximum score of 4). Groups of 4 mice per condition were used.

Figure 11. *Location of the Epitope for the anti-$\alpha 1$ I domain Blocking mAbs.* A. Amino acid sequence of the rat (top; SEQ ID NO:63) and human (below; SEQ ID NO:64) α1-I domain. The residues that comprise the MIDAS (metal ion dependent adhesion site) motif are shown in bold. The human amino acids that replaced the corresponding rat residues (RΔH) are shown below the rat sequence in the boxed region. For clarity, residue numbering in the text refers to this figure, , unless otherwise designated, e.g., as crystal numbering. B. Increasing concentrations of mAb AJH10 (ATCC No. PTA-3580; deposited under the Budapest Treaty with the American Type Culture Collection, Manassas, VA, USA on August 2, 2001) were bound to plates coated with 30 μg/ml human (circles), rat (triangles) or RΔH (squares) α1-I domain. Data shown is representative of three experiments.

Figure 12. Amino acid sequence of the human α1-I domain (SEQ ID NO:64).

Figure 13. *Identification of a blocking mAb to the $\alpha 1$-I domain.* A. Increasing concentration of mAbs AEF3 (triangles) or AJH10 (circles) were bound to plates coated with 30 μg/ml α1- I domain. B. The α1-I domain was treated with increasing concentrations of mAb AJH10 (diamonds) or mAb BGC5 (squares) and bound collagen IV (2 μg/ml) coated plates. C. K562-α1 cell were treated with increasing concentration of mAbs AEF3(triangles) or AJH10 (circles) and bound to collagen IV (5 μg/ml) coated plates. 45-50% of cells added to each well adhered to collagen IV. Data shown is representative of three independent experiments.

Figure 14. *Species Cross-reactivity of the blocking mAbs* analyzed by fluorescence activated cell sorter (FACS). Rabbit vascular smooth muscle cells were incubated with either mAb AJH10 (bottom) or murine IgG control (top) and analyzed by fluorescence activated cell sorter (FACS).

Figure 15. *The $\alpha 1$-I domain binds collagen.* A. Increasing concentrations of the human α1-I domain were bound to plates previously coated with 1 μg/ml collagen I (squares) or collagen IV (circles). Values shown have been corrected for background binding to BSA. B. 2 μg/ml human α1-I domain was mixed with increasing concentration of an anti- human α1 integrin antibody 5E8D9 (squares) or an anti- human α2- integrin antibody A2IIE10 (circles), and then bound

to plates previously coated with 1 μg/ml collagen IV. C. Plates were coated with 1 μg/ml collagen IV or 3% BSA. α1-I domain (2 μg/ml) was subsequenctly bound to coated plates plates in the presence of 1 mM Mn^{2+}, 1 mM Mg^{2+}, or 5 mM EDTA. Data shown is representative of three independent experiments.

Figure 16. *Characterization of Humanized AQC2 Forms*. mAQC2 (triangles), chAQC2 (circles), hAQC2 (inverted triangles) and hAQC2' (squares) were evaluated.

A. Inhibition of VLA-1 binding to type IV collagen.

B. Inhibition of α1-I domain binding to type IV collagen.

C. Binding to immobilized α1-I domain.

D. Competition with biotinylated mAQC2 for binding to immobilized α1-I domain.

Figure 17. *Characterization of Humanized AQC2 Forms* by FACS.

Figure 18. *Characterization of Humanized AQC2 Forms* by FACS.

Figure 19. *Atomic structure coordinates for the α1-I domain/Fab complex*, as derived by X-ray crystallography from crystals of that complex in Protein Data Bank (PDB) format. The coordinates of the two complexes in the asymmetric unit are listed as follows.

Complex 1: molecule A = I domain of integrin
molecule H = heavy chain of hAQC2 Fab
molecule L = light chain of hAQC2 Fab
molecule M = Mn^{+2}

Complex 2: molecule B = I domain of integrin
molecule X = heavy chain of hAQC2 Fab
molecule Y = light chain of hAQC2 Fab
molecule M = Mn^{+2}

Figure 20. *I domain-Fab complex*. A. Ribbon diagram of the I domain-Fab complex. The I domain is colored green and the antibody heavy and light chain yellow and blue, respectively. The Mn^{+2} ion is the white colored sphere. B. Close-up of the MIDAS (Metal-Ion-Dependent-Adhesion-Site) site showing the coordination of the metal ion (white sphere) by Asp101 (crystal numbering). The

protein backbones are shown as ribbons and the side chains in the ball-and-stick representation. The blue cylinders represent interactions between the metal ion and protein atoms. The thin lines represent H-bonds. Fig. 20 was made with the software program RIBBONS (Carson, 1991, *J. Appl. Cryst.* 24:958-961).

Figure 21. *A diagram of a system used to carry out the instructions encoded by the storage medium of Figs. 22 and 23.*

Figure 22. *A cross section of a magnetic storage medium.*

Figure 23. *A cross section of an optically-readable data storage medium.*

DETAILED DESCRIPTION OF THE INVENTION

It is a discovery of the present invention that an antibody to an integrin (e.g., VLA-1) and fragment thereof, particularly, an α1-integrin subunit, can block the interaction of pro-inflammatory leukocytes with components of the extracellular matrix including, but not limited to collagens, laminin and fibronectin. This discovery illustrates the importance of adhesion molecules of the integrin family, particularly α1β1, in the peripheral tissue environment during conditions related to inflammation. It also extends the role of integrins family and fragments thereof in inflammation beyond leukocyte attachment and extravasation at the endothelial interface by highlighting the importance of the matrix-rich peripheral tissue environment to immune responses and it reveals peripheral tissues as a new point of intervention for adhesion based therapies.

I. Anti-Integrin Antibodies

The methods of the present invention contemplate the use of antibodies to integrins where the integrins contemplated include molecules which comprise a β chain, including but not limited to β1, β2, β3, β4, β5, β6, β7, β8, non-covalently bound to an α chain, including but not limited to α1, α2, α3, α4, α5, α6, α7, α8, α9, α10, αV, αL, αM, αX, αD, αE, αIIb. Examples of the various integrins contemplated for use in the invention include, but are not limited to:

α1β1, α2β1, α3β1, α4β1, α5β1, α6β1, α7β1, α8β1, α9β1, α10β1, αVβ1, αLβ1, αMβ1, αXβ1, αDβ1, αIIbβ1, αEβ1;

α1β2, α2β2, α3β2, α4β2, α5β2, α6β2, α7β2, α8β2, α9β2, α10β2, αVβ2, αLβ2, αMβ2, αXβ2, αDβ2, αIIbβ2, αEβ2;

α1β3, α2β3, α3β3, α4β3, α5β3, α6β3, α7β3, α8β3, α9β3, α10β3, αVβ3, αLβ3, αMβ3, αXβ3, αDβ3, αIIbβ3, αEβ3;

α1β4, α2β4, α3β4, α4β4, α5β4, α6β4, α7β4, α8β4, α9β4, α10β4, αVβ4, αLβ4, αMβ4, αXβ4 αDβ4, αIIbβ4, αEβ4;

α1β5, α2β5, α3β5, α4β5, α5β5, α6β5, α7β5, α8β5, α9β5, α10β5, αVβ5, αLβ5, αMβ5, αXβ5, αDβ5, αIIbβ5, αEβ5;

α1β6, α2β6, α3β6, α4β6, α5β6, α6β6, α7β6, α8β6, α9β6, α10β6, αVβ6, αLβ6, αMβ6, αXβ6, αDβ6, αIIbβ6, αEβ6;

α1β7, α2β7, α3β7, α4β7, α5β7, α6β7, α7β7, α8β7, α9β7, α10β7, αVβ7, αLβ7, αMβ7, αXβ7, αDβ7, αIIbβ7, αEβ7;

α1β8, α2β8, α3β8, α4β8, α5β8, α6β8, α7β8, α8β8, α9β8, α10β8, αVβ8, αLβ8, αMβ8, αXβ8, αDβ8, αIIbβ8, αEβ8;

The methods of the present invention also contemplate the use of antibodies to integrin fragments including for example antibodies to a β chain alone, including but not limited to β1, β2, β3, β4, β5, β6, β7, β8, as well as an α chain alone, including but not limited to α1, α2, α3, α4, α5, α6, α7, α8, α9, α10, αV, αL, αM, αX, αD, αE, αIIb. In addition, the methods of the present invention further contemplate the use of antibodies to integrin fragments including for example

antibodies to the I domain of the α chain, including but not limited to the I domain from α1β1 (Briesewitz et al., 1993, *J. Biol. Chem.* 268:2989); α2β1 (Takada and Hemler, 1989, *J Cell Biol* 109:397), αLβ2 (Larson et al., 1989, *J Cell Biol* 108:703), αMβ2 (Corbi et al., 1988, *J Biol Chem* 263:12403), αXβ2 (Corbi et al., 1987, *EMBO J* 6:4023), αDβ2 (Grayson et al., 1988, *J Exp Med* 188:2187), αEβ7 (Shaw et al., 1994, *J Biol Chem* 269:6016). In one embodiment, the α1-I domain antigenic determinant includes an amino acid sequence of at least 6 contiguous amino acids, wherein the contiguous sequence is found within the sequence of Fig. 12. In a related embodiment, the contiguous sequence is Val-Gln-Arg-Gly-Gly-Arg.

Methods for producing integrins for use in the present invention are known to those of skill in the art (see, e.g., Springer et al., 1990, *Nature* 346:425-434).

Embodiments of the present invention further include anti-integrin polyclonal and monoclonal antibodies. Embodiments of the present invention include a monoclonal antibody such an anti-α1monoclonal antibody. Antibodies for treatment, in particular for human treatment, include human antibodies, humanized antibodies, chimeric antibodies, and antigen-binding fragments of whole antibodies such as Fab, Fab', F(ab')2 and F(v) antibody fragments. Some antibodies of this invention may also include proteins containing one or more immunoglobulin light chains and/or heavy chains, such as monomers and homo-or hetero-multimers (e.g., dimers or trimers) of these chains, where these chains are optionally disulfide-bonded or otherwise cross-linked. These antibodies may be capable of binding to one or more antigens (e.g., α1, α2, α6 or alpha-I domain containing integrin subunits).

An α1β1function blocking antibody as used herein refers to an antibody that binds to the α1-I domain, for example, residues 92-97 of Fig. 12, and blocks α1β1function as tested, for example, by their ability to inhibit K562-α1 dependent adhesion to Collagen IV (see Example 15).

The following describes the various methods of making the antibodies of this invention. Methods that are known in the art but not specifically described herein are also within the scope of this invention. For instance, antibodies of this invention can also be identified using phage-displayed antibody libraries, such as those described in Smith, 1985, *Science* 228:1315-7; U.S. Patents 5,565,332,

5,733,743, 6,291,650, and 6,303,313. Additional antibodies of this invention can be made by coupling the heavy chains identified herein with a noncognate light chain, e.g., a light chain identified by phage display technology.

II. Non-Human Hybridoma Antibodies

The monoclonal antibodies of this invention can be generated by well known hybridoma technology. For instance, β_1 -/- animals (e.g., mice, rats or rabbits) can be immunized with purified or crude $\alpha_1\beta_1$ preparations, cells transfected with cDNA constructs encoding α_1, β_1 or both antigens, cells that constitutively express $\alpha_1\beta_1$, and the like. The antigen can be delivered as purified protein, protein expressed on cells, protein fragment or peptide thereof, or as naked DNA or viral vectors encoding the protein, protein fragment, or peptide. Sera of the immunized animals are then tested for the presence of anti-$\alpha_1\beta_1$ antibodies. B cells are isolated from animals that test positive, and hybridomas are made with these B cells.

Antibodies secreted by the hybridomas are screened for their ability to bind specifically to VLA-1 (e.g., binding to α_1-transfected cells and not to untransfected parent cells) and for any other desired features, e.g., having the desired CDR consensus sequences, inhibiting (or not inhibiting in the case of nonblockers) the binding between collagen and VLA-1.

Hybridoma cells that test positive in the screening assays are cultured in a nutrient medium under conditions that allow the cells to secrete the monoclonal antibodies into the culture medium. The conditioned hybridoma culture supernatant is then collected and antibodies contained in the supernatant are purified. Alternatively, the desired antibody may be produced by injecting the hybridoma cells into the peritoneal cavity of an unimmunized animal (e.g., a mouse). The hybridoma cells proliferate in the peritoneal cavity, secreting the antibody which accumulates as ascites fluid. The antibody may then be harvested by withdrawing the ascites fluid from the peritoneal cavity with a syringe.

The monoclonal antibodies can also be generated by isolating the antibody-coding cDNAs from the desired hybridomas, transfecting mammalian host cells (e.g., CHO or NSO cells) with the cDNAs, culturing the transfected host cells, and recovering the antibody from the culture medium.

III. Chimeric Antibodies

The monoclonal antibodies of this invention can also be generated by engineering a cognate hybridoma (e.g., murine, rat or rabbit) antibody. For instance, a cognate antibody can be altered by recombinant DNA technology such that part or all of the hinge and/or constant regions of the heavy and/or light chains are replaced with the corresponding components of an antibody from another species (e.g., human). Generally, the variable domains of the engineered antibody remain identical or substantially so to the variable domains of the cognate antibody. Such an engineered antibody is called a chimeric antibody and is less antigenic than the cognate antibody when administered to an individual of the species from which the hinge and/or constant region is derived (e.g., a human). Methods of making chimeric antibodies are well known in the art. Human constant regions include those derived from IgG1 and IgG4.

IV. Fully Human Antibodies

The monoclonal antibodies of this invention also include fully human antibodies. They may be prepared using *in vitro*-primed human splenocytes, as described by Boerner et al., 1991, *J. Immunol.* 147:86-95, or using phage-displayed antibody libraries, as described in, e.g., U.S. Patent 6,300,064.

Alternatively, fully human antibodies may be prepared by repertoire cloning as described by Persson et al., 1991 , *Proc. Nat. Acad. Sci. USA* 88: 2432-2436; and Huang and Stollar, 1991, *J. Immunol. Methods* 141: 227-236. In addition, U.S. Patent 5,798,230 (Aug. 25, 1998) describes preparation of human monoclonal antibodies from human B cells, wherein human antibody-producing B cells are immortalized by infection with an Epstein-Barr virus, or a derivative thereof, that expresses Epstein-Barr virus nuclear antigen 2 (EBNA2), a protein required for immortalization. The EBNA2 function is subsequently shut off, resulting in an increase in antibody production.

Some other methods for producing fully human antibodies involve the use of non-human animals that have inactivated endogenous Ig loci and are transgenic for un-rearranged human antibody heavy chain and light chain genes. Such transgenic animals can be immunized with $\alpha_1\beta_1$ and hybridomas are then made from B cells

derived therefrom. These methods are described in, e.g., the various GenPharm/Medarex (Palo Alto, CA) publications/patents concerning transgenic mice containing human Ig miniloci (e.g., Lonberg U.S. Patent 5,789,650); the various Abgenix (Fremont, CA) publications/patents with respect to XENOMICE (e.g., Kucherlapati U.S. Patents 6,075,181, 6,150,584 and 6,162,963; Green et al., 1994, *Nature Genetics* 7:13-21; and Mendez et al., 1997, *Nature Genetics* 15(2):146-56); and the various Kirin (Japan) publications/patents concerning "transomic" mice (e.g., EP 843 961, and Tomizuka et al., 1997, *Nature Genetics* 16:133-1443).

V. Humanized Antibodies

The monoclonal antibodies of this invention also include humanized versions of cognate anti-$\alpha_1\beta_1$ antibodies derived from other species. A humanized antibody is an antibody produced by recombinant DNA technology, in which some or all of the amino acids of a human immunoglobulin light or heavy chain that are not required for antigen binding (e.g., the constant regions and the framework regions of the variable domains) are used to substitute for the corresponding amino acids from the light or heavy chain of the cognate, nonhuman antibody. By way of example, a humanized version of a murine antibody to a given antigen has on both of its heavy and light chains (1) constant regions of a human antibody; (2) framework regions from the variable domains of a human antibody; and (3) CDRs from the murine antibody. When necessary, one or more residues in the human framework regions can be changed to residues at the corresponding positions in the murine antibody so as to preserve the binding affinity of the humanized antibody to the antigen. This change is sometimes called "back mutation." Humanized antibodies generally are less likely to elicit an immune response in humans as compared to chimeric human antibodies because the former contain considerably fewer non-human components.

The methods for making humanized antibodies are described in, e.g., Winter EP 239 400; Jones et al., 1986, *Nature* 321:522-525; Riechmann et al., 1988, *Nature* 332:323-327 (1988); Verhoeyen et al., 1988, *Science* 239:1534-1536; Queen et al., 1989, *Proc. Nat. Acad. Sci.* USA 86:10029; U.S. Patent 6,180,370; and Orlandi et al., 1989, *Proc. Natl. Acad. Sci.* USA 86:3833. Generally, the transplantation of murine (or other non-human) CDRs onto a human antibody is achieved as follows.

The cDNAs encoding heavy and light chain variable domains are isolated from a hybridoma. The DNA sequences of the variable domains, including the CDRs, are determined by sequencing. The DNAs encoding the CDRs are transferred to the corresponding regions of a human antibody heavy or light chain variable domain coding sequence by site directed mutagenesis. Then human constant region gene segments of a desired isotype (e.g, $\gamma 1$ for CH and k for CL) are added. The humanized heavy and light chain genes are co-expressed in mammalian host cells (e.g., CHO or NSO cells) to produce soluble humanized antibody. To facilitate large scale production of antibodies, it is often desirable to produce such humanized antibodies in bioreactors containing the antibody-expressing cells, or to produce transgenic mammals (e.g., goats, cows, or sheep) that express the antibody in milk (see, e.g., U.S. Patent 5,827,690).

At times, direct transfer of CDRs to a human framework leads to a loss of antigen-binding affinity of the resultant antibody. This is because in some cognate antibodies, certain amino acids within the framework regions interact with the CDRs and thus influence the overall antigen binding affinity of the antibody. In such cases, it would be critical to introduce "back mutations" (*supra*) in the framework regions of the acceptor antibody in order to retain the antigen-binding activity of the cognate antibody.

The general approach of making back mutations is known in the art. For instance, Queen et al. (*supra*), Co et al., 1991, *Proc. Nat. Acad. Sci.* USA 88:2869-2873, and WO 90/07861 (Protein Design Labs Inc.) describe an approach that involves two key steps. First, the human V framework regions are chosen by computer analysis for optimal protein sequence homology to the V region framework of the cognate murine antibody. Then, the tertiary structure of the murine V region is modeled by computer in order to visualize framework amino acid residues that are likely to interact with the murine CDRs, and these murine amino acid residues are then superimposed on the homologous human framework.

Under this two-step approach, there are several criteria for designing humanized antibodies. The first criterion is to use as the human acceptor the framework from a particular human immunoglobulin that is usually homologous to

the non-human donor immunoglobulin, or to use a consensus framework from many human antibodies. The second criterion is to use the donor amino acid rather than the acceptor if the human acceptor residue is unusual and the donor residue is typical for human sequences at a specific residue of the framework. The third criterion is to use the donor framework amino acid residue rather than the acceptor at positions immediately adjacent to the CDRs.

One may also use a different approach as described in, e.g., Tempest, 1991, *Biotechnology* 9: 266-271. Under this approach, the V region frameworks derived from NEWM and REI heavy and light chains, respectively, are used for CDR-grafting without radical introduction of mouse residues. An advantage of using this approach is that the three-dimensional structures of NEWM and REI variable regions are known from X-ray crystallography and thus specific interactions between CDRs and V region framework residues can be readily modeled.

VI. Other Moieties

The monoclonal antibodies of this invention may further include other moieties to effect the desired functions. For instance, the antibodies may include a toxin moiety (e.g., tetanus toxoid or ricin) or a radionuclide (e.g., ^{111}In or ^{90}Y) for killing of cells targeted by the antibodies (see, e.g., U.S. Patent 6,307,026). The antibodies may include a moiety (e.g., biotin, fluorescent moieties, radioactive moieties, histidine tag or other peptide tags) for easy isolation or detection. The antibodies may also include a moiety that can prolong their serum half life, for example, a polyethylene glycol (PEG) moiety, and a member of the immunoglobulin super family or fragment thereof (e.g., a portion of human IgG1 heavy chain constant region such as the hinge, CH2 and CH3 regions).

VII. Crystallizable Compositions and Crystals

This invention also provides a crystallizable composition containing a complex of: (1) a rat-human chimeric α1-I domain (e.g., mutant RΔH), or a portion thereof (e.g., a polypeptide including 135 to 336 amino acids of the rat-human chimeric α1-I domain); and (2) a Fab fragment of hAQC2, or a portion thereof (e.g., a polypeptide including 3 to 213 amino acids of the light chain and/or a polypeptide including 3 to 219 amino acids of the heavy chain). An exemplary complex is shown

in Fig. 20. The RΔH α1-I domain can include, e.g., amino acid residues 145 to 336 (crystal numbering) (SEQ ID NO:59, *infra*) of the rat α1 subunit. The hAQC2 Fab fragments may include light chain amino acid residues 1 to 106 (e.g., 1-213) of SEQ ID NO:3 and heavy chain amino acid residues 1 to 118 (e.g., 1-219) of SEQ ID NO:4. The hAQC2 Fab fragments may be obtained by papain digestion of the whole antibody or made by recombinant methods. The Fab fragments include at least an antigen-binding portion of the variable domains of the light chain and/or the heavy chains of hAQC2.

```
145  TQLDIV
151  IVLDGSNSIY PWESVIAFLN DLLKRMDIGP KQTQVGIVQY
191  GENVTHEFNL NKYSSTEEVL VAANKIVQRG GRQTMTALGI
231  DTARKEAFTE ARGARRGVKK VMVIVTDGES HDNYRLKQVI
271  QDCEDENIQR FSIAILGHYN RGNLSTEKFV EEIKSIASEP
311  TEKHFFNVSD ELALVTIVKA LGERIF
```

(SEQ ID NO:59)

Some crystallizable compositions and crystals of this invention may contain a molecule or molecular complex that is homologous to the α1-I domain and/or the hAQC2 Fab fragment by amino acid sequence or by three-dimensional structure. Examples of homologues include, but are not limited to: the α1-I domain and/or the hAQC2 Fab fragment with mutations, such as conservative substitutions, additions, deletions or a combination thereof. "Conservative substitutions" refer to replacement residues that are physically similar in size, shape, hydrophobicity, charge, and/or chemical properties to the corresponding reference residues. Methods for identifying a "corresponding" amino acid are known in the art and are based upon sequence, structural alignment, its functional position or a combination thereof as compared to the crystal structure solved in the present invention. For example, corresponding amino acids may be identified by superimposing the backbone atoms of the amino acids in the α1-I domain/hAQC2 complex and a α1-I domain and/or hAQC2 homologue using well known software applications, such as QUANTA (Molecular Simulations, Inc., San Diego, CA ©1998,2000). The corresponding

amino acids may also be identified using sequence alignment programs such as the "bestfit" program available from the Genetics Computer Group, which uses the local homology algorithm described by Smith and Waterman in *Adv. Appl. Math.* 2:482 (1981).

Crystallizable compositions of this invention may further include one or more components that promote crystallization and/or is compatible with crystallization conditions. Such components may include, but are not limited to, buffer, salts, precipitating agents and other reagents. One component can be 30% weight/volume Polyethylene Glycol 1500 (PEG1500).

The instant invention also provides methods of making crystals from crystallizable compositions including a complex of α1-I domain and an antigen-binding portion of hAQC2 (e.g., Fab, Fab' or other fragments, *supra*). Various techniques of crystallization can be used in the claimed invention, including, but not limited to, vapor-diffusion, dialysis, microbatch, batch, and liquid-liquid diffusion. Vapor diffusion methods include, but are not limited too, sitting-drop, hanging-drop and sandwich-drop techniques. Vapor-diffusion methods can use techniques to control the rate of crystallization, such as the addition of oils on the drops or reservoir solution. Crystallization methods can include mixing a reservoir solution containing precipitating agent with an aqueous solution of a complex of α1-I domain and an antigen-binding portion of hAQC2 to produce a crystallizable composition. The mixture or crystallizable composition may then be crystallized using the various above-listed techniques. The crystallizable composition of this invention may be an aqueous solution of a complex of α1-I domain and an antigen-binding portion of hAQC2 containing the complex at a concentration of about 1 to 50 mg per mL, such as a concentration of about 5 to 15 mg per mL (e.g., 11 mg per mL).

VIII. Crystal Structures and Structure Coordinates

This invention further provides the three-dimensional structure of a crystal including a complex of mutant RΔH, and a hAQC2 Fab fragment at 2.8 Å resolution (Example 24, *infra*). The three-dimensional structures of other related crystals may also be determined using techniques described herein and those known in the art. The three-dimensional structure of this complex is defined by a set of

structure coordinates set forth in Fig. 19. These structure coordinates are Cartesian atomic coordinates derived from mathematical equations related to the patterns obtained from diffraction of a monochromatic beam of X-rays by the atoms or scattering centers of the crystalline complex of the α1-I domain and the hAQC2 Fab fragment. Diffraction data are first used to calculate an electron density map of the repeating unit of the crystal. The electron density map is then used to establish the positions of individual atoms of the complex.

This invention provides a molecule or a molecular complex defined by all or part of the structure coordinates of all amino acids set forth in Fig. 19, as well as a homologue of the molecule or molecular complex, where the homologue has a root mean square deviation from the backbone atoms of these amino acids between 0.00 Å and 0.65 Å, such as between 0.00 Å and 0.60 Å (e.g., between 0.00 Å and 0.50 Å). The term "root mean square deviation" or "r.m.s. deviation" means the square root of the arithmetic mean of the squares of the deviations from the mean. It is a way to express the deviation or variation from a trend or object. For purposes of this invention, the "root mean square deviation" or "r.m.s. positional deviation" defines the variation in the backbone of a protein from the relevant portion of the backbone of the polypeptide as defined by the structure coordinates described herein.

A molecule or a molecular complex of this invention may also include a binding site defined by structure coordinates of at least seven amino acids of the hAQC2 Fab fragment selected from the group including of light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101 (crystal numbering) according to Fig. 19; or a homologue of the molecule or molecular complex, where the homologue includes a binding site that has a root mean square deviation from the backbone atoms of one or more of these amino acids between 0.00 Å and 1.10 Å, such as between 0.00 Å and 1.00 Å (e.g., between 0.00 Å and 0.50 Å). The term "binding site" as used herein, refers to a region of a molecule or molecular complex that, as a result of its shape and charge, favorably associates with another chemical entity. The term "site" includes, but is not limited to, trench, cleft, channel or pocket. For instance, binding sites on the α1-I domain may include a collagen-binding site

(Emsley et al., 1997, *supra*), an antibody-binding site, and an allosteric (or IDAS) binding site (Huth et al., 2000, *Proc. Natl. Acad. Sci. U.S.A.* 97:5231-5236). The term “chemical entity” includes, but is not limited to, any molecule, molecular complex, compound or fragment thereof. The term "associate with" refers to an association or binding in a condition of proximity between a chemical entity, or portions thereof, and a binding pocket or binding site on a protein. The association may be non-covalent -- where the juxtaposition is energetically favored by hydrogen bonding or van der Waals or electrostatic interactions -- or it may be covalent.

A molecule or molecular complex of this invention can include a binding site defined by structure coordinates of α1-I domain amino acids selected from the group consisting of residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294 (crystal numbering), according to Fig. 19, or a homologue of the molecule or molecular complex, where the homologue includes a binding site that has a root mean square deviation from the backbone atoms of the α1-I domain amino acids between 0.00 Å and 0.92 Å.

A molecule or molecular complex of this invention also may include a binding site defined by structure coordinates of α1-I domain amino acids selected from the group consisting of residues Glu192, Gln218, Arg219, Gly220, and Gly221 (crystal numbering), according to Fig. 19; or a homologue of the molecule or molecular complex, where the homologue includes a binding site that has a root mean square deviation from the backbone atoms of the α1-I domain amino acids between 0.00 Å and 0.30 Å.

Those of skill in the art will understand that a set of structure coordinates for a polypeptide is a relative set of points that define a shape in three dimensions. Thus, it is possible that an entirely different set of coordinates that define a similar or identical shape could be generated using mathematical manipulations of the structure coordinates in Fig. 19. For example, the structure coordinates could be manipulated by crystallographic permutations of the structure coordinates, fractionalization of the structure coordinates, integer additions or subtractions to sets of the structure coordinates, inversion of the structure coordinates, or any combination

thereof. Moreover, slight variations in the individual coordinates will have little effect on overall shape.

Alternatively, modification in the crystal structure due to mutations, such as additions, substitutions, and/or deletions of amino acids, or other changes in any of the polypeptide components (e.g., a hAQC2 Fab fragment or a α1-I domain) that make up the crystal can also account for variations in structure coordinates. If such variations are within an acceptable standard error as compared to the original coordinates, the resulting three-dimensional shape is considered to be the same as that of the unmodified crystal.

It is therefore necessary to determine whether an entity is sufficiently similar to all or parts of the structure described herein as to be considered the same. Such analyses may be carried out using current software applications, such as QUANTA (Accelrys, Inc. and Molecular Simulations, Inc., San Diego, CA ©1998,2000) and O (Jones et al., 1991, *Acta Cryst.* A47:110-119), and accompanying User Guides. The Molecular Similarity application of QUANTA and the LSQ application of O permit comparisons between different structures, different conformations of the same structure, and different parts of the same structure. The general procedure used in both applications is to input the structures to be compared, define the equivalent atomic positions in these structures, perform a fitting operation, and analyze the results.

When each structure is input into the application, it is given a name. and identified as the fixed structure or a moving structures. Atom equivalency is usually defined by equivalent atoms such as protein backbone atoms (N, Cα, C and O) for all conserved residues between the two structures being compared. The moving structure is translated and rotated to obtain an optimum or least-squares fit with the fixed structure. The root mean square difference of the fit over the specified pairs of equivalent atom is reported by both programs in angstroms.

For the purpose of this invention, any molecular complex that has a root mean square deviation of conserved residue backbone atoms (N, Cα, C, 0) between 0.00 Å and 1.50 Å, such as between 0.00 Å and 1.00 Å (e.g., between 0.00 Å and 0.50 Å), when superimposed on the relevant backbone atoms described by

structure coordinates listed in Fig. 19 are considered identical.

IX. Determining Other Crystal Structures

The structure coordinates set forth in Fig. 19 can also be used to aid in obtaining structural information about another crystallized molecular entity, such as another hAQC2 containing amino acid substitutions in one of its CDRs. This may be achieved by any well-known techniques, including molecular replacement, an especially useful method for determining the structures of mutants and homologues of α1-I domain/Fab.

The structure coordinates set forth in Fig. 19 can also be used for determining at least a portion of the three-dimensional structure of molecular entities that contain at least some structural features similar to at least a portion of the α1-I domain or the hAQC2 Fab. Therefore, another embodiment of this invention provides a method of utilizing molecular replacement to obtain structural information about a crystallized molecule or molecular complex with unknown structure including the steps of: (a) generating an X-ray diffraction pattern from the crystallized molecule or molecular complex; and (b) applying at least a portion of the structure coordinates set forth in Fig. 19 to the X-ray diffraction pattern to generate a three-dimensional electron density map of the molecule or molecular complex with unknown structure.

By using molecular replacement, all or part of the structure coordinates set forth in Fig. 19 can be used to determine the unknown structure of a crystallized molecular entity more rapidly and efficiently than attempting to determine such information *ab initio*. Molecular replacement provides an accurate estimation of the phases for an unknown structure. Phases are a factor in equations used to solve crystal structures that cannot be determined directly. Obtaining accurate values for the phases, by methods other than molecular replacement, can often be a time-consuming process that involves iterative cycles of approximations and refinements and greatly hinders the solution of crystal structures. However, when the crystal structure of a protein containing at least a homologous portion has been solved, the phases from the known structure can often provide a satisfactory estimate of the phases for the unknown structure.

Thus, molecular replacement involves generating a preliminary model

of a molecule or molecular complex whose structure coordinates are unknown, by orienting and positioning the relevant portion of the complex according to Fig. 19 within the unit cell of the crystal of the unknown molecule or molecular complex, so as best to account for the observed X-ray diffraction pattern of the crystal of the molecule or molecular complex whose structure is unknown. Phases can then be calculated from this model and combined with the observed X-ray diffraction pattern amplitudes to generate an electron density map of the structure whose coordinates are unknown. This, in turn, can be subjected to any well-known model building and structure refinement techniques to provide a final, accurate structure of the unknown crystallized molecule or molecular complex (Lattman, 1985, *Meth. Enzymol.* 115:55-77; Rossmann, ed., "The Molecular Replacement Method", Int. Sci. Rev. Ser., No. 13, Gordon & Breach, New York, 1972). The structure of any portion of any crystallized molecule or molecular complex that is sufficiently homologous to any portion of the α1-I domain and/or the hAQC2 Fab fragment (according to Fig. 19) can be solved by this method.

X. Computer and Storage Medium

To use the structure coordinates of this invention, e.g., those set forth in Fig. 19, it is usually necessary to convert the coordinates into a three-dimensional representation or shape. Commercially available graphical software programs including, but not limited to, O (Jones et al., 1991, *Acta Cryst.* A47:110-119) and INSIGHTII (© Accelrys, Inc. and Molecular Simulations, Inc., San Diego, CA) are capable of generating three-dimensional representations of molecules or molecular complexes, or portions thereof, from a set of structure coordinates.

In accordance with the present invention, the structure coordinates of the molecular entities of this invention are stored in a storage medium readable by machine (e.g., a computer). Using a computer and appropriate software, such data may be used for a variety of purposes, such as drug discovery and X-ray crystallographic analysis of other protein crystals.

Accordingly, a machine-readable data storage medium may include a data storage material encoded with machine-readable data including at least a portion of the structure coordinates set forth in Fig. 19. The computer may further include

instructions to produce three-dimensional representations of the molecular complexes of $\alpha 1$-I domain and the hAQC2 Fab fragment by processing the machine-readable data of this invention. The computer of this invention may also include a display, a graphical interface for displaying, or an input device for moving and manipulating the three-dimensional graphical representation of the structure coordinates.

This invention also provides a computer for determining at least a portion of the structure coordinates corresponding to X-ray diffraction data obtained from a molecular complex of $\alpha 1\beta 1$ integrin and the Fab fragment of hAQC2 antibody, where the computer includes a machine-readable data storage medium including a data storage material encoded with machine-readable data, where the data includes at least a portion of the structure coordinates of the molecular complex of $\alpha 1$-I domain and the hAQC2 Fab fragment according to Fig. 19, or X-ray diffraction data obtained from the crystalline molecular complex. The computer further includes instructions for performing a Fourier transform of the machine readable coordinate data, and instructions for processing this machine readable diffraction data into structure coordinates. This computer may further include: a working memory for storing instructions for processing the machine-readable data; a central-processing unit coupled to the working memory and to the machine-readable data; and optionally a graphical interface or display coupled to the central-processing unit for displaying the three-dimensional graphical representation of the structure coordinates of the molecule or molecular complex.

This invention further provides a computer for producing a three-dimensional representation of: a molecule or a molecular complex defined by at least a portion or all of the structure coordinates of all the $\alpha 1$-I domain and the hAQC2 Fab fragment amino acids set forth in Fig. 19, or a homologue of the molecule or molecular complex, where the homologue has a root mean square deviation from the backbone atoms of the amino acids of between 0.00 Å than 1.50 Å, such as between 0.00 Å and 1.00 Å, (e.g., between 0.00 Å and 0.50 Å). Further in this invention the computer includes: a machine-readable data storage medium including a data storage material encoded with machine-readable data, where the data includes at least a portion or all of the structure coordinates of all of the $\alpha 1$-I domain and the Fab

hAQC2 fragment amino acids set forth in Fig. 19.

A computer of this invention may also produce a three-dimensional representation of a molecule or molecular complex including a binding site. The binding site may be defined by structure coordinates of at least seven amino acids of: the hAQC2 Fab fragment selected from the group including light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101 (crystal numbering) according to Fig. 19; or a homologue of the molecule or molecular complex, where the homologue includes a binding site that has a root mean square deviation from the backbone atoms of the at least one amino acid of the hAQC2 Fab fragment of between 0.00 Å and 1.10 Å, such as between 0.00 Å and 1.00 Å, (e.g., between 0.00 Å and 0.50 Å). Further, the computer of this invention includes: a machine-readable data storage medium including a data storage material encoded with machine-readable data, where the data includes the structure coordinates of at least seven amino acids of the hAQC2 Fab fragment selected from the group consisting of light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101 (crystal numbering) according to Fig. 19.

This invention also provides a computer for producing a three-dimensional representation of: a molecule or molecular complex including a binding site defined by structure coordinates I domain amino acids selected from the group consisting of residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294 (crystal numbering), according to Fig. 19; or a homologue of the molecule or molecular complex, where the homologue includes a binding site that has a root mean square deviation from the backbone atoms of the I domain amino acids between 0.00 Å and 0.92 Å. Further in this invention, the computer includes: a machine-readable data storage medium including a data storage material encoded with machine-readable data, where the data includes the structure coordinates of I domain amino acids selected from the group consisting of residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221,

Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294 (crystal numbering), according to Fig. 19.

This invention also provides a computer for producing a three-dimensional representation of a molecule or molecular complex including a binding site defined by structure coordinates of I domain amino acids selected from the group consisting of residues Glu192, Gln218, Arg219, Gly220, and Gly221 (crystal numbering), according to Fig. 19; or a homologue of the molecule or molecular complex, where the homologue includes a binding site that has a root mean square deviation from the backbone atoms of I domain amino acids between 0.00 Å and 0.30 Å. Further in this invention the computer includes: a machine-readable data storage medium including a data storage material encoded with machine-readable data, where the data includes the structure coordinates I domain amino acids selected from the group consisting of residues Glu192, Gln218, Arg219, Gly220, and Gly221 (crystal numbering), according to Fig. 19.

Fig. 21 demonstrates one such embodiment. System 10 includes a computer 11 including a central-processing unit ("CPU") 20, a working memory 22 which may be, e.g., RAM (random-access memory) or "core" memory, mass storage memory 24 (such as one or more disk or tape drives or CD-ROM or DVD-ROM drives), one or more cathode-ray tube ("CRT") display terminals 26, one or more keyboards 28, one or more input lines 30, and one or more output lines 40, all of which are interconnected by a conventional bidirectional system bus 50.

Input hardware 36, coupled to computer 11 by input lines 30, may be implemented in a variety of ways. Machine-readable data of this invention may be inputted via the use of a modem or modems 32 connected by a telephone line or dedicated data line 34. Alternatively or additionally, the input hardware 36 may include CD-ROM or DVD-ROM drives or tape or disk drives 24. In conjunction with display terminal 26, keyboard 28 may also be used as an input device.

Output hardware 46, coupled to computer 11 by output lines 40, may similarly be implemented by conventional devices. By way of example, output hardware 46 may include CRT display terminal 26 for displaying a graphical representation of a binding site of this invention using a program such as QUANTA as

described herein. Output hardware might also include a printer 42, so that hard copy output may be produced, or a disk drive 24, to store system output for later use.

In operation, CPU 20 coordinates the use of the various input and output devices 36, 46, coordinates data accesses from mass storage 24 and accesses to and from working memory 22, and determines the sequence of data processing steps. A number of programs may be used to process the machine-readable data of this invention. Such programs are discussed in reference to the computational methods of drug discovery as described herein. Specific references to components of the hardware system 10 are included as appropriate throughout the following description of the data storage medium.

Fig. 22 shows a cross-section of a magnetic data storage medium 100 which can be encoded with machine-readable data that can be carried out by a system such as system 10 of Fig. 21. Medium 100 can be a conventional floppy diskette or hard disk, having a suitable substrate 101, which may be conventional, and a suitable coating 102, which may be conventional, on one or both sides, containing magnetic domains (not visible) whose polarity or orientation can be altered magnetically. Medium 100 may also have an opening (not shown) for receiving the spindle of a disk drive or other data storage device 24.

The magnetic domains of coating 102 of medium 100 are polarized or oriented so as to encode in manner which may be conventional, machine readable data such as that described herein, for execution by a system such as system 10 of Fig. 21.

Fig. 23 shows a cross-section of an optically-readable data storage medium 110 which also can be encoded with such machine-readable data, or a set of instructions, which can be carried out by a system such as system 10 of Fig. 21. Medium 110 can be a conventional compact disk or DVD disk read only memory (CD-ROM or DVD-ROM) or a rewritable medium, such as a magneto-optical disk which is optically readable and magneto-optically writable. Medium 100 has a suitable substrate 111, which may be conventional, and a suitable coating 112, which may be conventional, usually of one side of substrate 111.

In the case of CD-ROM, as is well known, coating 112 is reflective and is impressed with a plurality of pits 113 to encode the machine-readable data. The

arrangement of pits is read by reflecting laser light off the surface of coating 112. A protective coating 114, which is substantially transparent, is provided on top of coating 112.

In the case of a magneto-optical disk, as is well known, coating 112 has no pits 113, but has a plurality of magnetic domains whose polarity or orientation can be changed magnetically when heated above a certain temperature, as by a laser (not shown). The orientation of the domains can be read by measuring the polarization of laser light reflected from coating 112. The arrangement of the domains encodes the data as described above.

XI. Rational Drug Design

The present invention permits the use of structure-based and rational drug design techniques to design, select, and synthesize or isolate chemical entities, such as inhibitors of the α1-I domain and to improve known inhibitors of this domain. These inhibitors may be capable of blocking the collagen-binding site of VLA-1. This invention also permits the use of structure-based and rational drug design techniques to design variants that may act as inhibitors of collagen binding.

The three-dimensional representation of this invention can be used experimentally or computationally to design potential inhibitors, other chemical entities, variants of the Fab fragment or combinations of chemical entities that may bind to and effect the biological functions of the hAQC2 Fab fragment or the chimeric α1-I domain of the current invention.

One skilled in the art can use one of several methods to screen chemical entities for their ability to associate with the complex of the hAQC2 Fab fragment or the chimeric α1-I domain of the current invention and more particularly with a binding site of either the I domain or the Fab fragment. This process may begin by visual inspection of, for example, the binding site for either the I domain or the Fab fragment on the computer screen, based on the coordinates of the complex in Fig. 19. Selected chemical entities may then be positioned in a variety of orientations, or docked, within an individual binding site of either the I domain or the Fab fragment. Docking may be accomplished using software such as QUANTA, followed by energy minimization and molecular dynamics with standard molecular mechanics forcefields,

such as CHARMM (Molecular Simulations, Inc., Burlington, MA ©1994) and AMBER (P.A. Kollman, University of California at San Francisco, ©1994).

Specialized computer programs may also assist in the process of selecting chemical entities. These include, *inter alia*:

1. GRID (Goodford, P.J., 1985, *J. Med. Chem.* 28:849-857). GRID is available from Oxford University, Oxford, UK.

2. MCSS (Miranker, A. and M. Karplus, 1991, *Proteins: Structure, Function and Genetics* 11:29-34). MCSS is available from Molecular Simulations, Burlington, MA.

3. AUTODOCK (Goodsell, D.S. and A.J. Olsen, 1990, *Proteins: Structure, Function, and Genetics* 8:195-202). AUTODOCK is available from Scripps Research Institute, La Jolla, CA.

4. DOCK (Kuntz, I.D. et al., 1982, *J. Mol. Biol.* 161:269-288). DOCK is available from University of California, San Francisco, CA.

Once suitable chemical entities have been selected, they can be assembled into a single compound. Assembly may proceed by visual inspection of the relationship of the entities to each other on the three-dimensional image displayed on a computer screen in relation to the structure coordinates of the complex of hAQC2 Fab fragment and the chimeric α1-I domain. This is followed by manual model building using software such as Quanta or Sybyl.

The above-described evaluation process for chemical entities may be performed in a similar fashion for compounds or for variants that may bind the α1-I domain.

Useful programs to aid one of skill in the art in connecting the individual chemical entities include:

1. CAVEAT (Bartlett, P.A. et al, "CAVEAT: A Program to Facilitate the Structure-Derived Design of Biologically Active Molecules". In "Molecular Recognition in Chemical and Biological Problems", Special Pub., 1989, Royal Chem. Soc., 78:182-196). CAVEAT is available from the University of California, Berkeley, CA.

2. 3D Database systems such as MACCS-3D (MDL Information Systems, San Leandro, CA). This area is reviewed in Martin, Y.C., 1992, *J. Med. Chem.* 35:2145-2154.

3. HOOK (available from Molecular Simulations, Burlington, MA).

Instead of proceeding to build an inhibitor or binding compound in a step-wise fashion one chemical entity at a time, as described above, binding compounds may be designed as a whole or "de novo" using either an empty binding site (such as a binding site of the α1-I domain or the hAQC2 Fab fragment) or optionally including some portion(s) of a known α1-I domain or the hAQC2 Fab fragment binding compound. These methods include:

1. LUDI (Bohm, H.-J., 1992, *J. Comp. Aid. Molec. Design* 6:61-78). LUDI is available from Biosym Technologies, San Diego, CA.

2. LEGEND (Nishibata, Y. and A. Itai, 1991, *Tetrahedron* 47:8985). LEGEND is available from Molecular Simulations, Burlington, MA.

3. LeapFrog (available from Tripos Associates, St. Louis, MO).

Other molecular modeling techniques may also be employed in accordance with this invention. See, e.g., Cohen, N.C. et al., 1990, *J. Med. Chem.* 33:883-894. See also Navia, M.A. and M.A. Murcko, 1992, *Curr. Opin. Struct. Biol.* 2:202-210.

Once an entity has been designed or selected by the above methods, the efficiency with which that entity may bind to the α1-I domain or the hAQC2 Fab fragment can be tested and optimized by computational evaluation. For example, a compound that has been designed or selected to function as a α1-I domain binding compound can traverse a volume not overlapping that occupied by the binding site when it is bound to the chimeric α1-I domain. An effective α1-I domain binding compound can demonstrate a relatively small difference in energy between its bound and free states (i.e., a small deformation energy of binding). Thus, the most efficient α1-I domain binding compound should be designed with a deformation energy of binding of not greater than about 10 kcal/mole, e.g., not greater than 7 kcal/mole. α1-I domain binding compounds may interact with the α1-I domain in more than one conformation that is similar in overall binding energy. In those cases, the deformation energy of binding is taken to be the difference between the energy of the free compound and the average energy of the conformations observed when the compound binds to the protein.

A compound designed or selected as binding to α1-I domain may be further computationally optimized so that in its bound state it would lack repulsive electrostatic interaction with the target protein. Such non-complementary (e.g., electrostatic) interactions include repulsive charge-charge, dipole-dipole and charge-dipole interactions. Specifically, the sum of all electrostatic interactions between the compound and the protein when the compound is bound to α1-I domain, should make a neutral or favorable contribution to the enthalpy of binding.

Specific computer software is available in the art to evaluate compound deformation energy and electrostatic interaction. Examples of programs designed for such uses include: Gaussian 92, revision C (M.J. Frisch, Gaussian, Inc., Pittsburgh, PA ©1992); AMBER, version 4.0 (P.A. Kollman, University of California at San Francisco, ©1994); QUANTA/CHARMM (Molecular Simulations, Inc., Burlington, MA ©1994); and Insight II/Discover (Biosysm Technologies Inc., San Diego, CA ©1994). These programs may be implemented, for instance, using a Silicon Graphics workstation. Other hardware systems and software packages will be known to those skilled in the art.

One other useful drug design technique enabled by this invention is iterative drug design. Iterative drug design is a method for optimizing associations between a protein and a compound (that compound includes an antibody) by determining and evaluating the three-dimensional structures of successive sets of protein/compound complexes. In iterative drug design, a series of crystals of a protein complexed with entities that bind the protein are obtained and then the three-dimensional structure of each molecular complex is solved. Such an approach provides insight into the associations between the proteins and other entities of each complex. This is accomplished by selecting chemical entities with inhibitory activity, obtaining crystals of these new complexes, solving the three-dimensional structure of the complexes, and comparing the associations between the new complexes and the previously solved complex. Associations within a complex can be optimized by observing how changes in the components of the complex affect associations.

In some cases, iterative drug design is carried out by forming successive complexes and then crystallizing each new complex. Alternatively, a

pre-formed protein crystal is soaked in the presence of another chemical entity, thereby forming a complex and obviating the need to crystallize each individual complex.

XII. Pharmaceutical Compositions

The pharmaceutical compositions of this invention contains one or more VLA-1 antagonists of the present invention (e.g., anti-VLA-1 antibodies and the small molecular VLA-1 antagonists identified by the above-described rational drug design methods), or pharmaceutically acceptable derivatives thereof. The compositions may further contain a pharmaceutically acceptable carrier, such as an adjuvant, a vehicle, a buffer, and a stabilizer.

The pharmaceutical compositions of this invention may be given orally, topically, intravenously, subcutaneously, intraperitoneally, intramuscularly, intramedullarily, intraarterially, intra-articularly, intra-synovially, intrasternally, intrathecally, intrahepatically, intraspinally, intracranially as desired, or just locally at sites of inflammation or tumor growth. The pharmaceutical compositions of this invention may also be administered by inhalation through the use of, e.g., a nebulizer, a dry powder inhaler or a metered dose inhaler, or by implantation of an infusion pump or a biocompatible sustained release implant into the subject.

The pharmaceutical compositions may be in the form of a sterile injectable preparation, for example a sterile injectable aqueous or oleaginous suspension. This suspension may be formulated according to techniques known in the art using suitable dispersing, wetting, and suspending agents. If given orally, the pharmaceutical compositions can be administered in form of capsules, tablets, aqueous suspensions or solutions. For topical applications, the pharmaceutical compositions may be formulated in a suitable ointment.

The dosage and dose rate of the VLA-1 antagonists of this invention effective to produce the desired effects will depend on a variety of factors, such as the nature of the disease to be treated, the size of the subject, the goal of the treatment, the specific pharmaceutical composition used, and the judgment of the treating physician. Dosage levels of between about 0.001 and about 100 mg/kg body weight per day, for example between about 0.1 and about 50 mg/kg body weight per day, of the active

ingredient compound are useful. For instance, an antibody of the invention will be administered at a dose ranging between about 0.01 mg/kg body weight/day and about 20 mg/kg body weight/day, e.g., ranging between about 0.1 mg/kg body weight/day and about 10 mg/kg body weight/day, and at intervals of every one to fourteen days. In another embodiment, the antibody is administered at a dose of about 0.3 to 1 mg/kg body weight when administered intraperitoneally. In yet another embodiment, the antibody is administered at a dose of about 5 to 12.5 mg/kg body weight when administered intravenously. In one embodiment, an antibody composition is administered in an amount effective to provide a plasma level of antibody of at least 1 mg/ml.

XIII. Diseased Conditions And Animal Models

The VLA-1 antagonists of the invention are useful in the treatment, including prevention, of $\alpha_1\beta_1$-mediated diseases such as those enumerated above. The treatments of this invention are effective on both human and animal subjects afflicted with these conditions. Animal subjects to which the invention is applicable extend to both domestic animals and livestock, raised either as pets or for commercial purposes. Examples are dogs, cats, cattle, horses, sheep, hogs and goats.

The efficacy of the VLA-1 antagonists of the invention can be tested in various animal models. For instance, useful psoriasis and arthritis models include those described in WO 00/72881. Kidney fibrosis models include those described in WO 99/61040, the Alport's syndrome kidney model described in Cosgrove et al., 2000, *Am. J. Path.* 157:1649-1659, and the SNF1 mouse model of lupus nephritis described in Kalled et al., 2001, *Lupus* 10:9-22. Vascular fibrosis models for restenosis include a rat carotid balloon injury model described in Smith et al., 1999, *Circ. Res.* 84:1212-1222. Lung fibrosis models for idiopathic pulmonary fibrosis and scleroderma-associated pulmonary fibrosis include a bleomycin-induced pulmonary fibrosis model described in Wang et al., 1999, *Thorax* 54:805-812. Liver cirrhosis models for hepatitis C- or alcohol-induced cirrhosis include the bile duct ligation model described in George et al., 1999, *Proc. Natl. Acad. Sci. USA* 96:12719-12724 and the CCL4-induced liver fibrosis model described in Shi et al., 1997, *Proc. Natl. Acad. Sci. USA* 94:10663-10668.

The efficacy of the treatments of this invention may be measured by a number of available diagnostic tools, including physical examination, blood tests, proteinuria measurements, creatinine levels and creatinine clearance, pulmonary function tests, chest X-rays, bronchoscopy, bronchoalveolar lavage, lung biopsy, plasma blood urea nitrogen (BUN) levels, observation and scoring of scarring or fibrotic lesions, deposition of extracellular matrix such as collagen, smooth muscle actin and fibronectin, kidney function tests, ultrasound, magnetic resonance imaging (MRI), and CT scan.

XIV. Diagnostic Methods

The antibodies of this invention can be used to diagnose diseased conditions associated with altered $\alpha_1\beta_1$ expression levels. A tissue sample from a subject, such as a tissue biopsy, body fluid sample or lavage (e.g., alveolar lavage), can be tested in an antigen capture assay, ELISA, immunohistochemistry assay, and the like using the antibodies. A tissue sample from a normal individual is used as control.

Practice of the present invention will employ, unless indicated otherwise, conventional techniques of cell biology, cell culture, molecular biology, microbiology, recombinant DNA, protein chemistry, and immunology, which are within the skill of the art. Such techniques are described in the literature. See, for example, *Molecular Cloning: A Laboratory Manual*, 2nd edition (Sambrook et al., Eds.), 1989; *Oligonucleotide Synthesis*, (M.J. Gait, Ed.), 1984; U.S. Patent 4,683,195 to Mullis et al.; *Nucleic Acid Hybridization*, (B.D. Hames and S.J. Higgins), 1984; *Transcription and Translation*, (B.D. Hames and S.J. Higgins), 1984; *Culture of Animal Cells* (R.I. Freshney, Ed.), 1987; *Immobilized Cells and Enzymes*, IRL Press, 1986; *A Practical Guide to Molecular Cloning* (B. Perbal), 1984; *Methods in Enzymology*, Volumes 154 and 155 (Wu et al., Eds.), Academic Press, New York; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos, Eds.), 1987; *Immunochemical Methods in Cell and Molecular Biology* (Mayer and Walker, Eds.), 1987; *Handbook of Experiment Immunology*, Volumes I-IV (D.M. Weir and C.C. Blackwell, Eds.), 1986; *Manipulating the Mouse Embryo*, 1986.

Unless otherwise defined, all technical and scientific terms used herein

have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Exemplary methods and materials are described below, although methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present invention. All publications and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. The materials, methods, and examples are illustrative only and not intended to be limiting. Throughout this specification and claims, the word "comprise," or variations such as "comprises" or "comprising" will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

The following Examples are provided to illustrate the present invention, and should not be construed as limiting thereof.

EXAMPLES

Chemical reagents

Fluorescein isothiocyanate (FITC) was purchased from Sigma Chemical Co. (St. Louis, MO). Croton oil was purchased from ICN Biochemicals (Aurora, OH). Whole sheep blood in Alsevers solution was obtained from East Acres Biologicals (Southbridge, MA). Type I rat tail collagen and type IV mouse collagen were purchased from Collaborative Research Inc. (Bedford, MA) and Gibco (Gaithersburg, MD), respectively.

Balb/c female mice of 6-8 weeks of age were purchased from Taconic (Germantown, NY) and the $\alpha1\beta1$ integrin-deficient mice on a Balb/c background were as previously described (3).

Example 1

Monoclonal Antibodies. Function-blocking mAbs to murine antigens were prepared in an azide-free and low endotoxin format: Ha31/8 (hamster anti-CD49a; integrin $\alpha1$) (Mendrick et al. 1995. *Lab. Invest.* 72:367-375), Ha1/29 (hamster anti-CD49b; integrin $\alpha2$)($\beta1$) (Mendrick et al. 1995. *Lab. Invest.* 72:367-375; Mendrick, D.L. and D.M. Kelly 1993 *Lab. Invest.* 69:690-702), hamster group II

control mAb Ha4/8 (hamster anti-KLH)(Mendrick, D.L. and D.M. Kelly 1993 *Lab. Invest.* 69:690-702), and PS/2 (rat anti-CD49d; integrin α4β1 chain) (Miyake et al. 1991 *J. Exp. Med.* 173:599-607). In addition, the following function-blocking mAbs to murine antigens were purchased as no-azide/low endotoxin preparations from Pharmingen (San Diego, CA): HMβ1-1 (hamster anti-CD29; integrin β1chain) (Noto et al. 1995 *Int. Immunol.* 7:835-842), Ha2/5 (hamster anti-CD29; integrin β1chain)(Mendrick, D.L. and D.M. Kelly 1993 *Lab. Invest.* 69:690-702), 3E2 (hamster anti-CD54, ICAM-1)(Scheynius et al.1993 J. Immunol. 150:655-663), 5H10-27 (rat anti-CD49e; integrin α5)(Kinashi, T., and T.A. Springer. 1994. *Blood Cells*. 20:25-44), GoH3 (rat anti-CD49f; integrin α6)(Sonnenberg et al. 1987 *J. Biol. Chem.* 262:10376-10383), and the rat isotype control mAbs R35-95 (rat IgG2a) and R35-38 (rat IgG2b).

Adhesion Assay. Splenocytes from Balb/c mice were cultured with 20 ng/ml IL-2 for 7-12 d. Adhesion of cells to type I and type IV collagen was as previously described (Gotwals et al. 1996 *J. Clin. Invest.* 97:2469-2477). Briefly, 96-well Maxisorp plates (Nunc, Napierville, IL) were coated with either 10 μg/ml type IV or 5 μg/ml type I collagen and non-specific sites blocked with 1% BSA. IL-2 activated splenocytes were labeled with 2 μM BCECF [2',7'-bis(carboxyethyl)-5(6) carboxyl fluorescein penta acetoxymethylester](Molecular Probes, Eugene, OR) and incubated with 10 μg/ml of indicated mAbs for 15 min. 10^5 cells in 0.25% BSA in RPMI were then added to coated wells and incubated for 60 min at 37°C. Unbound cells were removed by washing three times with 0.25% BSA in RPMI. Adhesion was quantified using a CytoFluor 2350 fluorescent plate reader (Millipore, Bedford, MA). The ratio of bound cells to input cells was measured and percent adhesion relative to control mAb-treated cells (normalized to 100%) calculated. Background values due to cell adhesion on wells coated with BSA alone were subtracted.

Expression and functional blockade of α1β1 and α2β1 on activated leukocytes. Given the key role leukocytes play in inflammation, we decided to test whether anti-α1 and anti-α2 mAbs were capable of blocking leukocyte adhesion to collagens. In order to obtain leukocytes expressing high levels of both α1 and α2, murine T cells were stimulated *in vitro* with IL-2 for 7-12 d. These cells expressed

high levels of both $\alpha1$ and $\alpha2$ (Fig. 1A), and bound well to both collagen type IV and type I-coated surfaces (Fig. 1B). Adhesion to type IV collagen was partially inhibited by anti-$\alpha1$ mAb alone and was not inhibited by anti-$\alpha2$ mAb alone. In contrast, adhesion to type I collagen was completely inhibited by anti-$\alpha2$ mAb and anti-$\alpha1$ mAb alone showed only partial inhibition. Both anti-$\beta1$ mAb and the combination of anti-$\alpha1$ and anti-$\alpha2$ mAbs completely inhibited adhesion to types I and IV collagen. Having demonstrated that the $\alpha1\beta1$ and $\alpha2\beta1$ integrins are expressed on activated T cells and that anti-$\alpha1$ and $\alpha2$ mAbs are able to functionally block leukocyte adhesion to collagens, we used these mAbs to investigate the *in vivo* role of these integrins in animal models of inflammatory disorders.

Example 2

Inhibition of DTH responses by anti-integrin mAbs. SRBC-induced delayed type hypersensitivity (DTH) responses were adapted from a previously published protocol (Hurtrel et al., 1992, *Cell. Immunol.* 142:252-263). Briefly, mice were immunized s.c. in the back with 2 x 10^7 SRBC in 100 ul PBS on d 0. The mice were challenged on d 5 by injecting 1 x 10^8 SRBC in 25 ul PBS s.c into the right hind footpad. Footpad thickness was measured with an engineer's caliper (Mitutoyo/MTI, Paramus, NJ) 20 h after antigen challenge, and the degree of footpad swelling calculated. Results are reported as the mean percent increase footpad thickness ± SEM and calculated as % increase = [1- (Right footpad thickness 20 h after antigen challenge/Uninjected left footpad thickness 20 h after antigen challenge)] x 100. To block the effector phase of the SRBC-induced DTH response, therapeutic or control mAb (100 ug), which were prepared according to the methods described in Example 1, was given i.p. 1 h prior to antigen challenge on d 5.

SRBC-induced DTH is a well characterized *in vivo* model of inflammation, and in particular psoriasis, that has been used to demonstrate the importance of a variety of cytokines and adhesion molecules in inflammation (Tedder et al., 1995, *J. Exp. Med.* 181:2259-2264, Terashita et al., 1996, *J. Immunol.* 156:4638-4643). SRBC-sensitized mice received anti-integrin mAbs 1 h prior to footpad antigen challenge and inflammation was assessed 20 h later as measured by increased footpad thickness. PBS and control hamster Ig-treated mice showed a 60-

70% increase in footpad thickness 20 h after antigen challenge (Fig. 2). Compared to control hamster Ig treatment, anti-α1 or anti-α2 mAbs resulted in a 68% and 60% inhibition in footpad thickness, respectively. The combination of anti-α1 and α2 mAbs resulted in 71% inhibition, demonstrating little additive effect over anti-α1 or anti-α2 mAbs alone. Treatment with other anti-integrin mAbs was also effective at inhibiting DTH effector response. The degree of inhibition seen with the various mAb treatments was 49% (anti-α4), 23% (anti-α5), and 57% (anti-α6). Lastly, mAb blockade of the common β1 integrin subunit (mAb HMBI-1) inhibited the effector DTH response by 67%.

Example 3

Inhibition of CHS effector responses by anti-integrin mAbs. Contact hypersensitivity (CHS) to FITC was assayed as previously described (Gaspari et al., 1991, *In* Current Protocols in Immunology. J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, and W. Strober, editors. John Wiley & Sons, New York. Section 4.2:1). Briefly, mice were sensitized by painting 100 ul 0.5% FITC in 1:1 acetone/dibutylphthalate onto the shaved back on d 0. 10 d later, animals were challenged by applying 5 ul 0.5% FITC onto both sides of each ear. Ear swelling response was determined by ear thickness measured with an engineer's caliper (Mitutoyo/MTI, Paramus, NJ) at the time of antigen challenge (d 10) and 24 h later, and the results reported as mean percent increase in baseline ear thickness ± SEM. Increase in ear thickness was calculated as % increase = [1- (Ear thickness 24 h after antigen challenge/Ear thickness at the time of antigen challenge)] x 100. To block the effector phase of the CHS response, therapeutic or control mAb (250 ug) was given i.p. 4 h prior to antigen challenge on d 10. Mice that were antigen-sensitized and ear challenged with vehicle only (vehicle control) or mice that were ear challenged without prior sensitization (irritant control) served as negative controls (never exceeded 2% increase in ear thickness).

Given that CHS is mechanistically distinct from DTH and involves different effector cells, we investigated what effect anti-integrin mAbs had on the effector phase of the CHS response. Mice were hapten-sensitized using FITC applied to their shaved backs, followed 10 d later with FITC challenge to the ear resulting in

an inflammatory response the next day. FITC-sensitized mice demonstrated a 60-70% increase in thickness 24 h after antigen challenge (Fig. 3). Consistent with published results (Scheynius et al., *J. Immunol.* 150:655-663), anti-ICAM-1 mAb treatment resulted in 51% inhibition of ear swelling. Compared to control hamster mAb, treatment of mice with anti-$\alpha 1$ or anti-$\alpha 2$ mAb 4 h prior to antigen challenge resulted in 37% and 57% inhibition in ear swelling, respectively (Fig. 3). The combination of anti-$\alpha 1$ and anti-$\alpha 2$ mAbs resulted in slightly greater inhibition of ear swelling (65%). Treatment with other mAbs to $\beta 1$ integrins revealed that while anti-$\alpha 4$ and anti-$\alpha 5$ mAbs resulted in no inhibition of FITC-induced CHS effector response when compared to control rat mAb, treatment with anti-$\alpha 6$ mAb resulted in an 86% inhibition of effector responses. Lastly, mAb blockade of the common $\beta 1$ integrin subunit inhibited CHS effector responses by 74%. Similar CHS results were obtained using different strains of mice (C57/BL6, 129/Sv) and a different sensitizing agent (oxazolone) (data not shown). Similar to the results seen in the SRBC-induced DTH model, histologic analysis of inflammed ears revealed that both edema formation and leukocytic infiltration were inhibited by anti-$\alpha 1$ and anti-$\alpha 2$ mAb treatment.

Consistent with the finding that $\alpha 1\beta 1$ and $\alpha 2\beta 1$ can be expressed on IL-2-activated splenocytes, analysis of lymph nodes from antigen-sensitized mice (FITC or oxazolone) revealed $\alpha 1\beta 1$ and $\alpha 2\beta 1$ to be expressed exclusively on CD44^{hi} LFA-1^{hi} activated CD4+ and CD8+ T cells (data not shown). Treatment of mice with anti-$\alpha 1$ and anti-$\alpha 2$ mAbs did not result in deletion of these cells, as the numbers of activated T cells in both spleen and lymph nodes seen in response to antigen sensitization in the CHS model was unaffected. In addition, effector cells were not functionally deleted as prolonged treatment of antigen-sensitized mice with anti-$\alpha 1$ and anti-$\alpha 2$ mAbs (d 10-16) did not affect the inflammatory response of mice challenged with antigen at d 20 (data not shown).

Example 4

CHS effector responses are decreased in $\alpha 1\beta 1$-deficient mice. To exclude the possibility that the inhibitory role of $\alpha 1\beta 1$ in the effector response of FITC-mediated CHS was mAb-mediated, experiments were carried out in wild-type and $\alpha 1\beta 1$-integrin deficient mice (Fig. 4). MAb inhibition of the effector phase in

wild-type mice was consistent with previous results, with 56% inhibition in ear thickness seen with anti-$\alpha1$, 56% with anti-$\alpha2$, and 62% with a combination of anti-$\alpha1$ and anti-$\alpha2$. The effector phase of CHS was significantly reduced in untreated $\alpha1\beta1$-deficient mice as compared to untreated wild-type mice (30% vs 71% increase in ear thickness, respectively). As expected, the level of ear swelling in untreated $\alpha1\beta1$-deficient mice was equivalent to the level of ear swelling seen in anti-$\alpha1$ mAb-treated wild-type mice. Lastly, mAb blockade of $\alpha2\beta1$ in the $\alpha1\beta1$-deficient mice resulted in only slightly increased inhibition of ear swelling, consistent with the results seen in wild-type mice treated with a combination of anti-$\alpha1$ and anti-$\alpha2$ mAbs.

Example 5

To further exclude the possibility that the inhibitory effect of the anti-integrin mAbs seen in both the DTH and CHS models of inflammation is caused by a general anti-inflammatory effect mediated by the anti-$\alpha1$ and anti-$\alpha2$ mAbs, the effect of these mAbs on irritant dermatitis was studied.

To assess irritant dermatitis, mice were painted with 5 ul of 0.8% croton oil in acetone on both sides of each ear. Therapeutic or control antibodies were given 4 h prior to the application of the irritant. Ear swelling was measured 24 h later as described above and compared to ear thickness prior to croton oil application. Results are reported as mean percent increase in baseline ear thickness ± SEM as described above. Mice painted with acetone only (vehicle control) served as a negative control.

24 h later, ears of mice treated with croton oil showed a significant increase in ear thickness (48%), when compared to mice receiving vehicle only (acetone). Toxic ear swelling caused by croton oil was not significantly affected in mice pretreated with anti-$\alpha1$ or anti-$\alpha2$ mAbs when compared to either PBS or control mAb-treated animals (Fig. 5). Histologic examination of the croton oil-treated ears revealed no differences in numbers or types of infiltrating cells or edema formation in mice treated with anti-$\alpha1$ or anti-$\alpha2$ mAbs, as compared to control mAb-treated mice or PBS-treated mice (data not shown).

Example 6

Inhibition of arthritis by $\alpha 1\beta 1$ and $\alpha 2\beta 1$. As $\alpha 1\beta 1$ is well expressed on infiltrating cells in the synovium of arthritis patients, we decided to examine whether anti-α1 or anti-α2 mAbs would be inhibitory in an accelerated model of arthritis previously described (Terato et al., 1992, *J. Immunol.* 148:2103-2108; Terato et al., 1995, *Autoimmunity* 22:137-147).

Arthrogen-CIA Antibody kits were purchased from Stratagene (La Jolla, CA) and arthritis induced using a well established protocol (Terato et al., 1992, *J. Immunol.* 148:2103-2108; Terato et al., 1995, *Autoimmunity* 22:137-147). Briefly, arthritis was induced through i.p. injection of a cocktail of 4 anti-collagen type II mAbs (1 mg each) on d 0, followed by i.p. injection of 50 ug LPS on d 3. Over the course of the next 3-4 d, the mice developed swollen wrists, ankles and digits. Therapeutic or control mAb (250 ug) was administered i.p. 4 h prior to injection of the anti-collagen mAbs on d 0, and again 4 h prior to LPS administration on d 3, and then continuing every 3rd day for the length of the experiment. Beginning on d 3, mice were evaluated for the development of arthritis. Severity of arthritis in each limb was scored using a four point system. 0=normal; 1=mild redness, slight swelling of ankle or wrist; 2=moderate swelling of ankle or wrist; 3=severe swelling including some digits, ankle, and foot; 4=maximally inflamed.

Severe arthritis in Balb/c mice developed within 72 h after LPS injection and persisted for more than 3 weeks. Neither injection of anti-collagen mAbs alone nor LPS alone induced arthritis. Mice receiving control mAb treatment displayed equally severe arthritis as than seen in PBS-treated mice (Fig. 6). In contrast, treatment with anti-α1 mAb alone resulted in a marked reduction (78%) in arthritis, lasting the duration of the experiment. Treatment with anti-α2 mAb alone also had a beneficial effect, resulting in a 32% decrease in the arthritic score as compared to control mAb-treated mice. The combination of anti-α1 and anti-α2 mAbs resulted in a similar degree of inhibition as seen with anti-α1 mAb alone.

Example 7

Histological analysis of effect of anti-α1 and anti-α2 mAb treatment on the inflammatory cellular infiltrate. Further histological analysis of the SRBC-induced DTH response confirmed the ability of anti-α1 and anti-α2 mAb treatment to modulate the elicited inflammatory response. An unchallenged footpad from an SRBC-sensitized mouse showed virtually no inflammatory cellular infiltrate when compared to an SRBC-challenged footpad from the same mouse. Treatment of SRBC-sensitized mice with anti-α1 and anti-α2 mAbs either alone or combined greatly reduced the number of these infiltrating cells found in SRBC-challenged footpads when compared to control mAb-treated mice. Closer examination of the infiltrating cells revealed most cells to be composed of neutrophils, with some monocytes and lymphocytes present, and confirmed that anti-α1 and anti-α2 mAb treatment greatly decreased the numbers of these cells.

Example 8

Immunohistochemical demonstration of α1-expressing cells in the inflammatory cellular infiltrate. Immunohistochemistry was performed to more precisely determine the nature of the infiltrating cells and whether they express collagen-binding integrins. Infiltrating cells from an inflamed footpad of an untreated mouse were examined for expression of α1β1 integrin and cell lineage markers. α1β1 integrin was found to be expressed on many infiltrating leukocytes. Dual immunohistochemistry was utilized to identify the nature of the infiltrating cells and the distribution of α1β1 expression. Using cell lineage markers, the infiltrate was found to be composed largely of granulocyte/monocytes (Mac-1+), with many of these cells being neutrophils (Gr1+), along with a smaller number of T lymphocytes (CD3+). Expression of α1 β1 integrin was found among all three subsets of cells, with α1 expressed on a subset of Mac-1+ granulocyte/monocytes, a subset of Gr1+ neutrophils, and on the majority of infiltrating CD3+ T lymphocytes. Detailed immunohistochemical analysis revealed that although anti-α1 and anti-α2 mAb treatment reduced the numbers of infiltrating cells, no change in the cellular composition of the infiltrate was seen (data not shown). Immunohistochemistry

staining with a FITC anti-hamster mAb confirmed the ability of the anti-α1 and anti-α2 mAb to localize to the inflamed footpad (data not shown).

Example 9

Inhibition of arthritis by mAbs to α1β1 and α2β1 and in α1-deficient mice. As α1β1 is well expressed on infiltrating cells in the synovium of arthritis patients, we decided to examine whether anti-α1 or anti-α2 mAbs would be inhibitory in an accelerated model of arthritis previously described (Terato et al., 1992, *J. Immunol* 148:2103-2108; Terato et al., 1995, *Autoimmunity* 22:137-147). This model involves injection of a cocktail of anti-collagen type II mAbs into mice, followed later by LPS administration, resulting in the development of arthritis over the next 3-7 d. Mice were given mAb every 3rd day starting at d 0, and scored for the development of arthritis every 3rd day. Severe arthritis developed in all mice within 72 h after LPS injection and persisted for more than 3 weeks. Neither injection of anti-collagen mAbs alone nor LPS alone induced arthritis. Mice receiving control mAb treatment displayed equally severe arthritis as than seen in PBS-treated mice (Fig. 7). In contrast, treatment with anti-α1 mAb alone resulted in a marked reduction (79% and higher) in arthritis, lasting the duration of the experiment. Treatment with anti-α2 mAb alone also had a beneficial effect, resulting in a 37% decrease in the arthritic score as compared to control mAb-treated mice. The combination of anti-α1 and anti-α2 mAbs resulted in a similar degree of inhibition as seen with anti-α1 mAb alone. Reduction of arthritic score with anti-α1 mAb treatment was seen in all mice and compares favorably with several other mAb-based treatments for arthritis such as soluble TNF receptor Ig fusion protein (Mori et al., 1996, *J. Immunol.* 157:3178-3182), anti-Mac-1 (Taylor et al., 1996, *Immunology.* 88:315-321), anti-α4 (Seiffge, 1996, *J. Rheumatol.* 23:2086-2091), and anti-ICAM-1 (Kakimoto et al., 1992, *Cell Immunol.* 142:326-337). In agreement with mAb-based data showing an important role for α1β1 in arthritis, untreated α1-deficient mice showed significant reduction in arthritic score when compared to wild-type mice.

Example 10

Effect of anti-α1 mAb treatment on the immunopathology of arthritic joints. Joints from wild-type arthritic mice (day 8) receiving either control mAb or anti-α1 mAb treatment were compared visually and histologically to joints from a normal untreated mouse. Visually, joints from control mAb-treated mice demonstrated redness and swelling of the entire foot including digits, while anti-α1 mAb-treated mice showed little if any signs of inflammation in either joints or digits. Histologic examination showed severe changes in control mAb-treated arthritic joints, with extensive infiltration of the subsynovial tissue with inflammatory cells, adherence of cells to the joint surface, and marked cartilage destruction as evidenced by proteoglycan loss. Consistent with previous reports (Terato et al., 1992, *J. Immunol* 148:2103-2108; Terato et al., 1995, *Autoimmunity* 22:137-147), the majority of the infiltrating cells in this model are neutrophils. Anti-α1 mAb treatment of mice dramatically reduced the amount of inflammatory infiltrate and the degree of cartilage destruction.

Example 11

Development of arthritis is delayed in the absence of lymphocytes and inhibition of arthritis by anti-α1 mAb occurs in the absence of lymphocytes. To determine what cell types might be important in the collagen mAb-induced arthritis model we compared the ability of wild-type B6-129 mice and RAG-1-deficient B6-129 mice to develop arthritis (Fig. 8). Genetic deletion of the RAG-1 (recombination activating gene-1) gene results in a complete loss of mature T and B lymphocytes (Mombaerts et al., 1992, *Cell* 68:869-877). Both the wild-type and RAG-1-deficient mice developed arthritis, though the kinetics of induction in the RAG-1-deficient mice is significantly slower (Fig. 8). These results suggest that while lymphocytes are involved in this model of arthritis, they are not required for the development and progression of the disease. Published reports examining the effect of the RAG-1-deficient mice in other models of arthritis also found that loss of T and B lymphocytes delayed the onset of arthritis (Plows et al., 1999, *J. Immunol.* 162:1018-1023). Treatment of either wild-type or RAG-1-deficient mice with anti-α1 mAb completely inhibited arthritis (Fig. 8). These results demonstrate that the effectiveness of anti-α1

mAb in this model is not dependent on the presence of lymphocytes, and that as suggested by previous experiments (Fig. 7), the efficacy of anti-α1 mAb in preventing disease may be through its action on other α1-expressing cells, such as macrophages and neutrophils.

Example 12

Dose response of anti-α1 mAb inhibition of arthritis. Given the striking effects of anti-α1 mAb treatment on preventing arthritis, we extended these studies to include a dose response analysis (Fig. 9). Different doses of mAb were admininstered i.p. every 3rd day starting at day 0. In agreement with earlier data, a 250 ug dose of anti-α1 mAb resulted in near complete prevention of arthritis. A lower dose of 100 ug of anti-α1 mAb was partially effective at preventing arthritis in this model, while lower doses did not have any discernable effect on arthritic score (Fig. 9).

Example 13

Therapeutic treatment with anti-α1 mAb can decrease arthritic score. Given the effectiveness of anti-α1 mAb in preventing arthritis, we attempted to treat mice that are on their way to develop disease. Arthritis was induced in mice by injection of a cocktail of anti-collagen type II mAbs on day 0, followed by LPS administration on day 3. Mice were then treated with either anti-α1 mAb or a soluble TNF receptor Ig fusion protein starting on day 4. Progression of arthritis was completely blocked in mice receiving anti-α1 mAb starting at day 4, when compared to mice receiving control hamster mAb starting at day 4 (Fig. 10). The degree of inhibition seen with therapeutic administration of anti-α1 mAb was complete and was equal to that seen with preventative treatment of anti-α1 mAb (started at day 0) (Fig. 10). In comparison, treatment with TNF receptor Ig fusion protein from day 4 onwards resulted in only a 60-70% inhibition in arthritic score when compared to control Ig fusion protein (Fig. 10). Combined treatment of anti-α1 mAb and TNF receptor Ig fusion together was effective at completely inhibiting arthritic score, which is not surprising given the complete effectiveness of anti-α1 mAb treatment alone in suppressing arthritis. In summary, these results indicate that therapeutic treatment

with anti-α1 mAb is effective at inhibiting arthritic score, and compares favorably to therapeutic treatment with a TNF antagonist.

Example 14

Cloning and mutagenesis of the α1-I domain. Human and rat α1β1 integrin I domain sequences were amplified from full length cDNAs (Kern, et al., 1994, *J. Biol. Chem.* 269, 22811-22816; Ignatius et al., 1990, *J. Cell Biol.* 111, 709-720) by the polymerase chain reaction (PCR) (PCR CORE Kit; Boehringer Mannheim, GmbH Germany), using either human specific primers,
5'-CAGGATCCGTCAGCCCCACATTTCAA-3' [forward] (SEQ ID NO:7), and
5'-TCCTCGAGGGCTTGCAGGGCAAATAT-3' [reverse] (SEQ ID NO:8),
or rat specific primers,
5'-CAGGATCCGTCAGTCCTACATTTCAA-3' [forward] (SEQ ID NO:9), and
5'-TCCTCGAGCGCTTCCAAAGCGAATAT-3' [reverse] (SEQ ID NO:10).

The resulting PCR amplified products were purified, ligated into pGEX4t-i (Pharmacia), and transformed into competent DH5α cells (Life Technologies). Ampicillin resistant colonies were screened for the expression of the ~45 kDa glutathione S-transferase-I domain fusion protein. The sequences from inserts of plasmid DNA of clones that were selected for further characterization were confirmed by DNA sequencing.

A rat/human chimeric α1-I domain (RΔH) was generated (MORPH Mutagenesis kit; 5 prime – 3 prime), exchanging the rat residues G92, R93, Q94, and L97 (Fig. 11) for the corresponding human residues, V, Q, R, and R, respectively. Clones harboring the RΔH I domain were identified by the loss of a diagnostic Stu 1 restriction enzyme site, and the inserts confirmed by DNA sequencing. The amino acid sequence of the human α1-I domain is shown in Fig. 12.

Example 15

Generation of mAbs specific to the α1-I domain. Monoclonal antibodies have proved to be very useful probes in studying the relationship between structure and function of integrin subunits. For example, mAbs were used extensively to study regions of the β1 subunit associated with an activated conformation (Qu, A., and Leahy, D. J. (1996) *Structure* 4, 931-942). Thus, to identify potential probes for

conformational changes of the α1-I domain, we generated a panel of mAbs to the human α1-I domain.

Generation of anti-α1 I domain Monoclonal Antibodies. Female Robertsonian mice (Jackson Labs) were immunized intraperitoneally (i.p.) with 25 μg of purified human α1β1 (Edwards et al., 1995, *J. Biol. Chem.* 270, 12635-12640; Gotwals et al., 1999, *Biochemistry* 38:8280-8) emulsified with complete Fruend's adjuvant (LifeTechnologies). They were boosted three times i.p. with 25 μg of α1β1 emulsified with incomplete Freunds's adjuvant (LifeTechnologies). The mouse with the highest anti-α1-I domain titer was boosted i.p. with 100 μg of α1β1 three days prior to fusion, and intravenously with 50 μg of α1β1 one day prior to fusion. Spleen cells were fused with FL653 myeloma cells at a 1:6 ratio and were plated at 100,000 and 33,000 per well into 96 well tissue culture plates.

Supernatants were assessed for binding to the α1β1 integrin by single color FACS. Prior to FACS analysis, supernatants were incubated with untransfected K562 cells to eliminate IgG that bound solely to the β subunit. Subsequently, 3-5 X 10^4 K562 cells transfected with the α1 integrin subunit (K562-α1) suspended in FACS buffer (1% fetal calf serum (FCS) in PBS containing 0.5% NaN_3) were incubated with supernatant for 45 minutes at 4° C, washed and incubated with anti-mouse IgG conjugated to phycoerythrin. After washing twice with FACS buffer, cells were analyzed in a Becton Dickinson Flow Cytometer.

Supernantants from the resulting hybridomas were screened for binding to the α1-I domain. Briefly, 50 μl of 30 μg/ml human α1-I domain-GST fusion in PBS was coated onto wells of a 96 –well plate (Nunc) overnight at 4° C. The plates were washed with PBS, blocked with 1% BSA in PBS and the hybridoma supernatant was incubated with the I domain at room temperature for 1 hour. After extensive washing with PBS containing 0.03% Tween 20, alkaline phosphatase linked anti-mouse IgG (Jackson ImmunoResearch) was added for an additional hour. After a final wash, 1 mg/ml *p*-nitrophenylphosphate (*p*NPP) in 0.1 M glycine, 1 mM $ZnCl_2$, and 1 mM $MgCl_2$ was added for 30 minutes at room temperature, and the plates were read at O.D. 405.

Selected supernatants were tested for their ability to inhibit K562-α1 dependent adhesion to Collagen IV. K562-α1 cells were labeled with 2 mM 2',7' (bis-2-carboxyethyl-5 and 6) carboxyfluorescein penta acetoxymethylester (BCECF; Molecular Probes) in DMEM containing 0.25% BSA at 37° C for 30 minutes. Labeled cells were washed with binding buffer (10 mM Hepes, pH 7.4; 0.9% NaCl; and 2% glucose) and resuspended in binding buffer plus 5 mM $MgCl_2$ at a final concentration of 1 X 10^6 cells/ml. 50 μl of supernatant was incubated with an equal volume of 2 X 10^5 K562-α1 cells in wells of a 96 well plate. The plate was then centrifuged and the supernatants removed. Cells were resuspended in binding buffer and transferred to wells of a collagen-coated plate and incubated for 1 hour at 37° C. Following incubation, the non-adherent cells were removed by washing three times with binding buffer. Attached cells were analyzed on a Cytofluor (Millipore).

We initially identified 19 hybridomas, the supernatants of which bound to human leukemia K562 cells expressing the α1β1 integrin (K562-α1) and to the α1-I domain. The immunoglobulins were purified from each of these hybridomas and tested for the ability to block either K562-α1 or α1- I domain binding to collagen IV. The mAbs fall into two classes: those that block and those that do not block α1β1 function. For example, while the mAbs produced by clones AEF3, BGC5, AQC2 and AJH10 bind the α1-I domain (Fig. 13A, data not shown for BGC5), only mAbs AJH10 and AQC2 inhibit α1-I domain-dependent (Fig. 13B; Fig. 16B) or K562-α1 (Fig. 13C; Fig. 16C) adhesion to collagen IV.

Sequencing of the Complementarity Determining Regions. To establish the clonal origin of this panel of mAbs, we amplified by PCR and sequenced the CDRs from 12 of the 19 antibodies (data not shown).

2 μg of mRNA, isolated from 10^7 hybridomas (FastTrack mRNA isolation kit , Invitrogen), was reverse transcribed (Ready-To-Go You Prime First Strand Kit, Pharmacia Biotech) using 25 pM each of the following primers: heavy chain VH1FOR-2 (Michishita et al., 1993, *Cell* 72:857-867); light chain, VK4FOR, which defines four separate oligos (Kern et al., 1994, *J. Biol. Chem.* 269:22811-22816). For each hybridoma, heavy and light chains were amplified in four separate PCR reactions using various combination of the following oligos: 1) Heavy chain:

VH1FR1K (Kamata et al., 1995, *J. of Biol. Chem.* 270:12531-12535), VH1BACK, VH1BACK (Baldwin et al.(1998) *Structure* 6, 923-935), $V_H$fr1a, $V_H$fr1b, $V_H$fr1e, $V_H$fr1f, $V_H$fr1g (Ignatius et al. (1990) *J. Cell Biol.* 111, 709-720), or VH1FOR-2 (Michishita, M., Videm, V., and Arnaout, M. A. (1993) *Cell* 72, 857-867); 2) Light chain: VK1BACK (Baldwin et al. (1998) *Structure* 6, 923-935), VK4FOR, VK2BACK oligos (Kern et al. (1994) *J. Biol. Chem.* 269, 22811-22816), or $V_K$fr1a, $V_H$fr1c, $V_H$fr1e, $V_H$fr1f (Ignatius et al. (1990) *J. Cell Biol.* 111, 709-720). Products were amplified (5 min at 95° C, 50 cycles of 1 min at 94° C, 2 min at 55° C, 2 min at 72° C, and a final cycle of 10 min at 72° C), gel purified (QIAquick, Qiagen), and sequenced directly using various of the listed oligos on an ABI 377 Sequencer.

Sequences from clones producing function-blocking mAbs were nearly identical across all the complementarity-determining regions (CDRs) and the intervening framework regions suggesting that these hybridomas are clonally related.

Example 16

Immunoblotting and FACS Analysis. Sequences of the variable regions of the non-blocking antibodies were markedly different from the clonally related family of sequences found for the blocking antibodies. As the blocking antibodies appear to originate from a single clone, we chose two (AJH10 and AQC2) to characterize further.

Immunoblotting The smooth muscle cell layer dissected from sheep aorta, and K562-α1 cells were extracted with 1% Triton X-100 in 50 mM Hepes, pH 7.5, 150 mM NaCl, 10 mM phenylmethylsulfonyl flouride (PMSF), 20 μg/ml aprotinin, 10 μg/ml leupeptin, 10 mM ethylenediaminetetraacetic acid (EDTA). Samples were subjected to 4-20% gradient SDS-PAGE, and electroblotted onto nitrocellulose membranes. The blots were blocked with 5% dry milk in TBS; washed in TBS containing 0.03% Tween-20, and incubated with antibodies in blocking buffer containing 0.05% NaN_3 for 2 hours. Blots were then washed as before, incubated with horseradish peroxidase conjugated anti-mouse IgG for one hour, washed again and then treated with ECL reagent (Amersham). Blots were then exposed to film (Kodak) for 30 to 60 seconds, and developed.

Immunoblotting and FACS analysis (Fig. 14) demonstrate that AJH10 reacts with human, rabbit, and sheep, but not rat $\alpha 1\beta 1$ integrin suggesting that the blocking mAbs bind to an evolutionarily conserved, linear epitope. The non-blocking mAbs were neither efficient at immunoblotting nor did they react with species other than human.

Example 17

Binding of the $\alpha 1$- I domain to collagen is divalent cation-dependent

A. Purification of the $\alpha 1$- I domains.

The $\alpha 1$-I domains were expressed in *E. coli* as GST (glutathione-S-transferase) fusion proteins containing a thrombin cleavage site at the junction of the sequences. The clarified supernatant from cells lysed in PBS was loaded onto a glutathione Sepharose 4B column (Pharmacia) which was washed extensively with PBS. The $\alpha 1$-I domain-GST fusion protein was eluted with 50 mM Tris-HCl, pH 8.0, 5 mM glutathione (reduced). For denaturation studies, the I domain was cleaved with thrombin in 50 mM Tris, pH 7.5, and purified from the GST fusion partner. DTT was added to 2 mM and the sample was loaded on a glutathione Sepharose 4B column. The flow-through and wash fractions were pooled and loaded onto a Q Sepharose FF column (Pharmacia). The $\alpha 1$-I domain was eluted with 50 mM Tris HCl, pH 7.5, 10 mM 2-mercaptoethanol, 75 mM NaCl. The purified I domain displayed its predicted mass (Lee et al. (1995) *Structure* 3, 1333-1340, 871 Da) by electrospray ionization-mass spectrometry (ESI-MS), migrated as a single band by SDS-PAGE, and the protein eluted as a single peak of appropriate size by size exclusion chromotography on a Superose 6 FPLC column (Pharmacia).

B. Functional Analysis

96 well plates were coated overnight at 4° C with 1 μg/ml collagen IV (Sigma) or collagen Type I (Collaborative Biomedical), washed with Triton buffer (0.1% Triton X-100; 1 mM $MnCl_2$; 25 mM Tris-HCl; 150 mM NaCl), and blocked with 3% bovine serum albumin (BSA) in 25 mM Tris-HCl; 150 mM NaCl (TBS). Serial dilutions of the $\alpha 1$- I domain-GST fusion protein in TBS containing 1 mM $MnCl_2$ and 3% BSA were incubated on the coated plates at room temperature for 1 hour, and washed in Triton buffer. Bound $\alpha 1$- I domain was detected with serial

additions of 10 μg/ml biotinylated anti-GST polyclonal antibody (Pharmacia); ExtrAvidin-horseradish peroxidase (Sigma) diluted 1:3000 in TBS containing 1 mM $MnCl_2$ and 3% BSA, and 1-Step ABTS (2,2'-Azine-di[3-ethylbenzthiazoline sulfonate]; Pierce). Plates were read at O.D. 405 on a microplate reader (Molecular Devices).

Results.

The human and rat (95% identity to human) α1-I domains were expressed in *E. coli* as GST-fusion proteins and purified over glutathione sepharose. Both proteins were examined for binding to collagen I and IV using a variation of an ELISA-based assay previously described (Qu, A., and Leahy, D. J. (1995) *Proc. Natl. Acad. Sci. USA* 92, 10277-10281). The human α1-I domain binds collagen IV with better efficiency than collagen I (Fig. 15A). An antibody specific to the α1-I domain, but not an antibody specific to the α2-I domain (Fig. 15B) abrogated binding to both ligands (data for collagen I is not shown). Both Mn^{2+} and Mg^{2+} stimulated binding, and EDTA reduced binding to background levels (Fig. 15C). No measurable differences in ligand binding were detected between the human and rat α1-I domains suggesting that the sequence differences between species are not functionally relevant (data not shown). Thus, the α1-I domain, specifically, require cation for efficient ligand binding.

Example 18

A Cation-Dependent Epitope Resides near the MIDAS motif. We exploited the observation that AJH10 recognizes the human, but not the rat α1-I domain sequences to map the epitope for the α1β1 function-blocking mAbs. The human and rat sequences differ by only 12 amino acids, 4 of which lie in a stretch of 6 amino acids (aa 92-97, Fig. 11A) adjacent to the critical threonine (Fig. 11A, aa 98) within the MIDAS motif. To test the hypothesis that the 6 amino acid residues, Val-Gln-Arg-Gly-Gly-Arg, comprise the epitope for the blocking mAbs, we constructed a chimeric I domain (RΔH), exchanging the rat residues G92, R93, Q94, and L97 for the corresponding human residues, V, Q, R, and R, respectively. AJH10, along with all the function-blocking mAbs, recognizes the chimeric I domain (RΔH; Fig. 11B).

To orient these residues with respect to the MIDAS domain in the

tertiary structure of the α1- I domain, we modeled the α1-I domain using the coordinates of the crystal structure of the α2 I domain.

A homology model of the human α1 I –domain was built using the X-ray crystal structure of the human α2 I-domain (Ward et al. (1989) *Nature* 341, 544-546). The model was built using the homology modeling module of Insight II (version 2.3.5; Biosym Technologies). The program CHARMM (Clackson et al. (1991) *Nature* 352, 624-628) was used with the all-hydrogen parameter set 22 with a distant dependent dielectric constant of two times the atom separation distance. We first did 1000 steps of steepest descent minimization with mass-weighted harmonic positional constraints of 1kcal/(mol Å^2) on all atoms of the α1-I domain. This minimization was followed by another 1000 steps of steepest descent and 5000 steps of Adopted-Basis Newton Raphson with constraints of 0.1 kcal/(mol Å^2) on the C-α atoms of the α1-I domain to avoid significant deviations from the α2-I domain X-ray crystal structure.

The α1β1 and α2β1 integrin sequences exhibit 51% identity with no insertions or deletions, suggesting that the overall structure of the two I domains will be similar. The metal coordination site is predicted to be the same in the α1-I domain as in the α2-I domain, and the residues that comprise the epitope for the blocking mAbs lie on a loop between helix α3 and helix α4 which contains the threonine within the MIDAS motif critical for cation binding. The α1-I domain model predicts that the amide nitrogen of Q92 (Fig. 11A) hydrogen bonds with the carbonyl group of I33, the residue adjacent to S32. Thus, the loop that contains the epitope may play a functional role in stabilizing the MIDAS region.

Example 19

Monoclonal antibody AQC2 (i.e., mAQC2; "m" for murine) (Example 15, *supra*) is an IgG$_1$, kappa antibody. To identify the nucleotide sequences encoding the heavy and light chains of this antibody, total cellular RNA from AQC2 murine hybridoma cells was obtained by using a QIAGEN RNEASY midi kit in accordance with the manufacturer's instructions. Then cDNAs encoding the variable regions of the heavy and light chains were cloned by RT-PCR from total cellular RNA using a GIBCO BRL SUPERSCRIPT Preamplification System for First Strand cDNA

Synthesis following the manufacturer's recommended protocol. Random hexamers were used for priming.

The heavy chain variable domain of mAQC2 was amplified by PCR from the first strand cDNA with the primers: 5' TGA GGA GAC GGT GAC CGT GGC CCT TGG CCC C 3' (SEQ ID NO:11) and 5' AGG TSM ARC TGC AGS AGT CWG G 3' (S=C/G, M=A/C, R=A/G, and W=A/T) (SEQ ID NO:12). The PCR was subjected to 30 cycles using Clontech's Advantage Taq polymerase: denature 30 sec at 94°C, anneal 1 min at 50°C, and elongate 1.5 min at 68°C. The mAQC2 light chain with its signal sequence was amplified by PCR using the primers: 5' ACT AGT CGA CAT GGA TTT WCA GGT GCA GAT TWT CAG CTT C 3' (W=A/T) (SEQ ID NO:13) and 5' ACT GGA TGG TGG GAA GAT GGA 3' (SEQ ID NO:14). The PCR was subjected to 30 cycles using Stratagene's cloned Pfu polymerase: denature 1 min at 94°C, anneal 1 min at 50°C, and elongate 2 min at 72°C. The PCR products for the heavy and light chains were gel-purified using a QIAGEN QIAQUICK gel extraction kit following the manufacturer's recommended protocol.

Purified heavy chain product was subcloned into Invitrogen's pCR2.1-TOPO TA vector using its TOPO TA cloning kit. Purified light chain was subcloned into Invitrogen's pCRbluntIITOPO vector using its Zero blunt TOPO cloning kit following the manufacturer's recommended protocol. Inserts from multiple independent subclones were sequenced. With the exception of degenerate positions within the PCR primers, the insert sequences of the independent subclones were identical.

The polypeptide sequences of mAQC2 were deduced from their coding sequences. The N-terminal amino acid sequence for the mature light chain predicted by the cDNA sequence from the PCR product amplified with a signal sequence exactly matched the N-terminal sequence of purified mAQC2 light chain derived from Edman degradation (DVKVVESGG; SEQ ID NO:15). BLAST analyses of the variable domain sequences confirmed their immunoglobulin identity.

The polypeptide sequence of the light chain variable domain of mAQC2 is shown below:

1	QIVLTQFPAL	MSASPGEKVT	MTC**SASSSVN**	**HMF**WYQQKPK	
41	SSPKPWIY**LT**	**SNLAS**GVPAR	FSGSGSGTSY	SLTISSMEAE	
81	DAATYYC**QQW**	**SGNPWT**FGGG	TKLEIK	106	

(SEQ ID NO:1)

The CDRs are shown in boldface. The CDRs are defined according to Kabat et al., Sequences of Proteins of Immunological Interest, 5th Edition, The United States Department of Health and Human Services, The United States Government Printing Office, 1991. Using the Kabat numbering system, SEQ ID NO:1 is represented as follows, where a dash denotes the absence of an amino acid:

1	QIVLTQFPAL	MSASPGEKVT	MTC**SASS-SV**	**NHMF**WYQQKP	
41	KSSPKPWIY**L**	**TSNLAS**GVPA	RFSGSGSGTS	YSLTISSMEA	
81	EDAATYYC**QQ**	**WSGNPWT**FGG	GTKLEIK	107	

The polypeptide sequence of the heavy chain variable domain of mAQC2 is:

1	DVKVVESGGG	LVKPGGSLKL	ACAASGFSFS	**RYTMS**WVRQI
41	PEKRLEWVA**T**	**ISGGGHTYYL**	**DSVKG**RFTIS	RDNAKNTLYL
81	QMSSLRSEDT	AMYYCTR**GFG**	**DGGYFDV**WGQ	GTTVTVSS

(SEQ ID NO:2)

The CDRs are shown in boldface. Using the Kabat numbering system, SEQ ID NO:2 is represented as follows, where positions numbers are consecutive numerals unless otherwise indicated:

1	DVKVVESGGG	LVKPGGSLKL	ACAASGFSFS	**RYTMS**WVRQI
41	PEKRLEWVA**T**	**ISGGGHTYYL**	**DSVKG**RFTIS	RDNAKNTLYL
81	QM			
82a-c	SSL			
83	RSEDTAMY	YCTR**GFGDGG**		

100a-b	**YF**		
101	**DVWGQGTTVT**	VSS	113

As used herein, residue position numbers of variable domains are designated in accordance with the Kabat numbering system unless otherwise indicated.

Example 20

This example describes the generation of a murine-human chimeric antibody, chAQC2.

The cDNAs encoding the variable regions of the mAQC2 heavy and light chains were used to construct chAQC2 expression vectors, in which the mAQC2 variable regions were linked to human IgG_1 and kappa constant regions.

The heavy chain chimera was constructed as follows. A 0.33 kb PstI-BstEII fragment from the mAQC2 heavy chain plasmid pAND083 was subcloned into the phosphatased 2.82 kb PstI-BstEII vector fragment from the 5a8 heavy chain plasmid pLCB7, so as to add a murine heavy chain signal-encoding sequence and a murine splice donor site to the cDNA of the mAQC2 heavy chain variable region. 5a8 is a molecularly cloned CD4-specific mAb (see, e.g., Boon et al., 2002, *Toxicology* 172:191-203). In the mature heavy chain encoded by the resultant plasmid (pAND092), the N-terminus differed by five residues from the N-terminus (DVKVVE; SEQ ID NO:16) of the cognate mAQC2 heavy chain.

To correct the heavy chain N-terminus, pAND092 was subjected to unique site elimination (USE) mutagenesis using an USE mutagenesis kit (Amersham Pharmacia Biotech) following the manufacturer's recommended protocol. The Q1D, Q3K, L4V, Q5V, Q6E substitutions were encoded by the mutagenic primer 5' GCA CCA GGT GCC CAC TCC GAC GTC AAG GTG GTG GAG TCA GGG GGA GGC TTA GTG 3' (SEQ ID NO:17). Mutated plasmid clones were identified by their new AatII and HinfI sites and eliminated PstI site. The heavy chain coding sequence was then confirmed by DNA sequencing. The correctly mutated plasmid was called pAND094. The 0.43 kb NotI-HindIII fragment from pAND094 and the 1.21 kb HindIII-NotI fragment from the plasmid pEAG964 (containing a coding sequence for

a human IgG_1 constant region) were subcloned into the NotI site of pCH269, a plasmid derived from the pCEP4 EBV expression vector (Invitrogen). The resultant plasmid was named pAND099.

The light chain chimera was generated as follows. A 0.46 kb EcoRI fragment from the mAQC2 light chain variable domain plasmid pAND081 was subcloned into the phosphatased 2.7 kb vector fragment of the pUC-derived pNN09 cloning vector, to add a 5' NotI site. The resulting plasmid, pAND091, was subjected to mutagenesis using the Amersham USE kit (*supra*) to introduce a BglII site at the 3' end of the coding sequence. The mutagenic primer had the sequence 5' GGA GGC ACC AAG CTG GAG ATC TAA CGG GCT GAT GCT GC 3' (SEQ ID NO:18). The correctly mutated plasmid was identified by its BglII and BstYI site changes. The light chain coding sequence in the resultant plasmid pAND093 was confirmed by DNA sequencing. Then the 0.44 kb NotI-BglII light chain variable domain fragment from pAND093 and the 0.68 kb BclI-NotI fragment from the plasmid pEAG963 (containing a coding sequence for a human kappa light chain constant domain) were subcloned into the NotI site of pCH269 (*supra*), producing plasmid pAND102. To create an unblocked kappa light chain (Q1E), pAND093 was subjected to USE mutagenesis with the mutagenic primer 5' CAT AAT GTC CAG GGG AGA AAT TGT TCT CAC CCA G 3' (SEQ ID NO:19), to introduce an XmnI site. The mutated plasmid was identified by screening for an XmnI site change. The light chain sequence in the resultant plasmid pAND097 was confirmed by DNA sequencing. The 0.44 kb NotI-BglII light chain variable domain fragment from pAND097 and the 0.68 kb BclI-NotI fragment from the plasmid pEAG963 (containing a human kappa light chain constant domain) were subcloned into the NotI site of pCH269, producing plasmid pAND098.

To generate chAQC2 antibodies, expression vectors (chAQC2 heavy chain vector pAND099 + chAQC2 light chain vector pAND102, and chAQC2 heavy chain vector pAND099 + chAQC2 unblocked light chain vector pAND098) were co-transfected into 293-EBNA cells. The transfectants were tested for antibody secretion and specificity. The controls were cells transfected with the corresponding vectors without an insert or with DNA constructs encoding ch5c8 (a molecularly

cloned CD154-specific mAb described in, e.g., Elster et al., 2001, *Transplantation* 72:1473-1478) or chCBE11 (a molecularly cloned LTβR-specific mAb described in, e.g., Browning et al., 1996, *J. Biol. Chem.* 271:24934-24938).

Then transfectants with the desired antibody secretion were lysed, and protein A immunoprecipitation was performed on the lysates and conditioned medium. Western blot analysis of the precipitates performed with anti-human heavy and light chain antibodies indicated that chAQC2-transfected cells synthesized and efficiently secreted heavy and light chains at levels similar to ch5c8-transfected and chCBE11-transfected cells. Further, huVLA-1-expressing K562α1 cells were stained with the conditioned medium from the transfected cells, and FACS analysis was performed on the stained cells. The results indicated that the chAQC2 antibody produced staining patterns similar to those of mAQC2, while conditioned media from mock-transfected and ch5c8-transfected cells failed to stain K562α1 cells. Chimeric AQC2 produced from scaled-up transient transfection was purified and shown to bind to VLA-1 by FACS titration. Chimeric AQC2 with either a wildtype or a genetically unblocked light chain bound to VLA-1. See also Figs. 16A-D (discussed below).

Example 21

This example describes a method of humanizing the mAQC2 monoclonal antibody.

Analysis of the mAQC2 variable domains. The variable domains in the light and heavy chains of mAQC2 were compared with the consensus sequences for mouse and human subgroups (Kabat et al, *supra*) using the software program FASTA. The light chain variable domain was found to be a member of mouse subgroup VI with 89% identity in a 109 amino acid overlap. This domain also corresponded to human subgroup I with 72% identity in a 113 amino acid overlap. The heavy chain variable domain was found to be a member of mouse subgroup IIId with 86% identity in a 129 amino acid overlap. This heavy chain variable domain also corresponded to human subgroup III with 79% identity in a 130 amino acid overlap.

The CDRs were categorized into canonical classes according to Chothia et al., *Nature* 342, pp. 877-883 (1989). The key residues defining each

canonical class determine to a large extent the structural conformation of the CDR loop, and thus should be retained in the reshaped antibody. The L1 loop of mAQC2 fell into canonical class 1 (10 residue loop), L2 into class 1 (7 residue loop) and L3 into class 1 (9 residue loop). The H1 loop fell into class 1 (5 residue loop) and the H2 loop into class 1 (16 residue loop) residues. The H3 loop did not seem to belong to any canonical class. The canonical residues important for these classes were all included in the humanized antibodies.

Unusual framework residues in mAQC2 were determined by analyzing all mouse and human variable chain sequences in the September 1999 version of the Kabat database. It was believed that mAQC2-specific differences might indicate somatic mutations that enhance binding affinity if these differences were close to the binding site. Unusual mAQC2 residues further away from the binding site and unusual human framework residues were removed in case they would create immunogenic epitopes in the humanized antibody. Unusual framework residues found in mAQC2 were 7(F), 10(L), and 41(K) in the light chain; and 4(V), 21(A), and 40(I) in the heavy chain. None of these unusual mouse framework residues were retained the humanized antibodies.

Modeling the structure of the variable regions. The light and heavy chains of mAQC2 were aligned against a nonredundant database to determine which structural frames to use to construct three-dimensional models of the mAQC2 light and heavy chains. Using FASTA, the light chain was found to have 82% sequence identity to monoclonal murine antibody ab57 (1CLOL), whereas the heavy chain was found to have 76% sequence identity to murine 6d9 Fab fragment (1HYY). Using the molecular modeling software package SYBYL (Tripos Inc.), the approximate three-dimensional structures of the mAQC2 light and heavy chains were built using the light chain of ab57 and the heavy chain of 6d9, respectively. The structural integrity of the models was assessed at the console and was found to be reasonable.

Design of the reshaped variable regions. Two approaches were used to choose human acceptor frameworks to "accept" mAQC2's CDRs. The first approach was by homology matching and the other by using consensus human Ig sequences. Under the homology approach, the Kabat database, the nonredundant

database from NCBI, ENTREZ (The National Institutes of Health), and the Incyte database were searched using the software programs FASTA and BLAST. The choice of human acceptor frameworks was made based on sequence identity between mAQC2 frameworks and human frameworks (excluding frameworks from previously humanized antibodies) and the source of the antibody.

The frameworks from an immunoglobulin variable region gene having a GENBANK accession number of gi:587330 (human kappa subgroup I Vκ-lc147) were eventually chosen for the light chain of the humanized antibody (Welschof et al., *J. Immunol. Meth.* 179:203-14 (1995)). The frameworks from Amulc11 (Kabat ID 044469; human subgroup III) were chosen for the heavy chain of the humanized antibody (Huang et al., *J. Immunol.* 151:5290-300 (1993)).

Back mutations of the human frameworks. Strategies for determining which back mutations to make are available on the Humanization bY Design web sites under mirrored urls: http://mathbio.nimr.mrc.ac.uk/jsaldan and http://www.cryst.bbk.ac.uk/~ubcg07s. Previous experiments have shown that it is important to retain canonical residues, interface packing residues and unusual murine residues that are close to the binding site. In addition, residues in the "Vernier Zone," which forms a platform on which the CDRs rest (Foote et al., *J. Mol. Biol.* 224, p. 487 (1992)) and those close to CDR H3 should be considered.

Four reshaped versions were designed for each of the variable light and heavy chains, as shown in Table 1. Two of the four versions for each chain were designed by homology matching (designated huAQC2-h1 and -h2) and the other two versions by consensus matching (huAQC2-c1 and -c2). It should be noted that the sequences for huAQC-h1 heavy chain and huAQC-c1 heavy chain are identical.

Table 1. Sequences of mAQC2, huAQC2, and human frameworks

LIGHT CHAIN

	FR1
Vk-1cl47	D--M--S-SSL---V-DR--I--*
huAQC2-h2	------S-SSL---V-DR--I--
huAQC2-h1	------S-SSL---V-DR--I--
mAQC2	QIVLTQFPALMSASPGEKVTMTC
huAQC2-c1	--Q---S-SSL---V-DR--I--
huAQC2-c2	--Q---S-SSL---V-DR--I--

	CDR1	FR2
Vk-1cl47	R--Q-ISYLN	------GKA--LL--
huAQC2-h2	----------	------GKA--LL--
huAQC2-h1	----------	------GKA------
mAQC2	SASSSVNHMF	WYQQKPKSSPKPWIY
huAQC2-c1	----------	------GKA------
huAQC2-c2	----------	------GKA--LL--

	CDR2	FR3
Vk-1cl47	AA-S-Q-	---S---------DFT-----LQP--F-----
huAQC2-h2	-------	---S---------D-T-----LQP--F-----
huAQC2-h1	-------	---S---------D-T-----LQP--F-----
mAQC2	LTSNLAS	GVPARFSGSGSGTSYSLTISSMEAEDAATYYC
huAQC2-c1	-------	---S---------D-T-----LQP--F-----
huAQC2-c2	-------	---S---------D-T-----LQP--F-----

	CDR3	FR4	Framework changes
Vk-1cl47	--SYST-L-	------V---	25
huAQC2-h2	---------	------V---	21
huAQC2-h1	---------	------V---	19
mAQC2	QQWSGNPWT	FGGGTKLEIK**	0
huAQC2-c1	---------	--Q---V---	21
huAQC2-c2	---------	--Q---V---	23

HEAVY CHAIN:

	FR1	CDR1
AMU1C11	E-QL-------IQ-----R-S------TV-	SNY--
huAQC2-h2	E-QL-------IQ-----R-S------T--	-----
huAQC2-h1	--QL--------Q-----R-S---------	-----
mAQC2	DVKVVESGGGLVKPGGSLKLACAASGFSFS	RYTMS
huAQC2-c1	--QL--------Q-----R-S---------	-----
huAQC2-c2	E-QL--------Q-----R-S------T--	-----

	FR2	CDR2
AMU1C11	----A-G-G----S	V-YS--S---A-----
huAQC2-h2	----A-G-G-----	----------------
huAQC2-h1	----A-G-G-----	----------------
mAQC2	WVRQIPEKRLEWVA	TISGGGHTYYLDSVKG
huAQC2-c1	----A-G-G-----	----------------
huAQC2-c2	----A-G-G-----	----------------

	FR3	CDR3
AMU1C11	--------S--------N---A----V---AS	IRFLEWS--Y
huAQC2-h2	--------S--------N---A----V-----	----------
huAQC2-h1	--------S--------N---A----V-----	----------
mAQC2	RFTISRDNAKNTLYLQMSSLRSEDTAMYYCTR	GFGDGGYFDV
huAQC2-c1	--------S--------N---A----V-----	----------
huAQC2-c2	--------S--------N---A----V-----	----------

	FR4	Framework changes
AMU1C11	-----L-----	20
huAQC2-h2	-----L-----	16
huAQC2-h1	-----L-----	13
mAQC2	WGQGTTVTVSS***	0
huAQC2-c1	-----L-----	13
huAQC2-c2	-----L-----	15

*Dashes indicate identity with the mAQC2 amino acid sequence.
**Part of SEQ ID NO:1.
***Part of SEQ ID NO:2.

Some of the back mutations are discussed below.

(1) light chain:

1 D->Q This mutation was made in all versions since previous reshaping experiments (e.g. Kolbinger et al, *Protein Eng.* 6, p. 971 (1993)) suggested its importance for antigen binding.

4 M->L This is a vernier residue and was retained in all versions.

46 L->P This residue is both an interfacial and vernier residue and was retained only in h1 and c1.

47 L->W This is a vernier residue and was retained only in h1 and c1.

71 F->Y This residue is in an important canonical position and was retained

in all versions.

(2) heavy chain:

1 E->D This back mutation was made in h1 (i.e., c1) only.

12 I->V The residue I is unusual in human and was retained in the h2 only.

28 T->S This is a vernier residue and was retained in h1 only.

29 V->F This is a canonical residue and was retained in all versions.

49 S->A This is a vernier residue and was retained in all versions.

93 A->T This is a vernier residue and interfacial and was retained in all versions.

94 S->R This is a canonical residue and was retained in both versions.

The huAQC2 variable regions were made by USE mutagenesis as described above, using the chAQC2 variable domain plasmids as starting templates. The human acceptor framework ("FR") cDNA sequences were Kabat #Z37334 for the light chain and Kabat #U00490 for the heavy chain. To facilitate identification of mutated plasmids, silent mutations were introduced to change restriction sites. Mutated plasmids were identified by the restriction site changes. The variable region cDNA sequences in the resultant plasmids were confirmed by DNA sequencing.

The h1 and c1 versions of heavy chain (which were identical) were made by using plasmid pAND094 as template. The mutagenic primers were: FR1 primer 5'GGT GCC CAC TCC GAC GTC CAG CTG GTC GAG TCA GGG GGA GGC TTA GTC CAG CCT GGA GGG TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC 3' (SEQ ID NO:20), which introduced TaqI and PvuII sites, and eliminated a DdeI site; FR2 primer 5' ATG TCT TGG GTT CGC CAG GCT CCG GGG AAG GGG CTG GAG TGG GTC GCA ACC 3' (SEQ ID NO:21), which introduced a NciI site, and eliminated BspEI and EarI sites; FR3 primer 5' TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACC CTG TAC CTG CAG ATG AAC AGT CTG AGG GCC GAG GAC ACA GCC GTG TAT TAC TGT ACA AGA 3' (SEQ ID NO:22), which introduced PstI and DdeI sites; and FR4 primer 5' TGG GGC CAA GGT ACC CTG GTC ACC GTC TCC TCA GGT GAG 3' (SEQ ID NO:23),

which introduced KpnI and Eco0109I sites. The resultant h1 (i.e., c1) heavy chain plasmid was designated pAND104.

The c2 version of heavy chain were made by using pAND104 as template with the following mutagenic primers: FR1 primer 5' TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGG TAT ACT ATG TCT TGG GTT 3' (SEQ ID NO:24), which introduced an AccI site; and FR1 primer 5' GCA CCA GGT GCG CAC TCC GAG GTC CAG CTG GTC GAG TCA 3' (SEQ ID NO:25), which introduced an FspI site and eliminated an AatII site. The resultant c2 heavy chain plasmid was designated pAND115.

The h2 version of heavy chain were made by using pAND115 as template with the following primer: FR1 primer 5' GAG TCA GGG GGA GGC TTA ATC CAG CCT GGA GGG TCC CTG 3' (SEQ ID NO:26), which eliminated a DdeI site. The resultant h2 heavy chain plasmid was designated pAND113.

To generate expression vectors for the huAQC2 heavy chains, the 0.43 kb NotI-HindIII heavy chain variable domain fragment from pAND104, pAND115, or pAND113, and the 1.21 kb HindIII-NotI fragment from pEAG964 (*supra*) were subcloned into the NotI site of pCH269 (*supra*). The resultant heavy chain expression plasmids were designated pAND114 (h1), pAND121 (c2), and pAND124 (h2), respectively.

The h1 version of light chain were made by using plasmid pAND093 as template. The mutagenic primers were: FR1 primer 5' CAA ATT GTT CTC ACC CAG TCT CCA TCC TCC CTG TCT GCG TCT GTA GGG GAC AGA GTC ACC ATC ACA TGC AGT GCC AGC TCA 3' (SEQ ID NO:27), which removed BstEII and PstI sites; FR2 primer 5' TTC TGG TAT CAG CAG AAG CCC GGG AAA GCC CCC AAA CCC TGG ATT 3' (SEQ ID NO:28), which introduced an NciI site; FR3 primer 5' GCT TCT GGA GTC CCT TCA CGC TTC AGT GGC AGT GGG TCT GGG ACA GAT TAC ACT CTC ACA ATC AGC AGC CTG CAA CCT GAA GAT TTT GCC ACT TAT TAC TGC CAG 3' (SEQ ID NO:29), which introduced a DdeI site and eliminated EcoO109I and AvaII sites; and FR4 primer 5' GGT GGA GGC ACT AAG GTG GAG ATC TAA CGG GCT 3' (SEQ ID NO:30), which introduced DdeI and StyI sites. The resultant h1 light chain plasmid was designated pAND103.

The h2 version of light chain were made by using pAND103 as template with the following primer: FR2 primer 5' CCC GGG AAA GCG CCC AAA CTC CTG ATT TAT CTC ACA TCC 3' (SEQ ID NO:31), which introduced HhaI and HaeII sites. The resultant h2 light chain plasmid was designated pAND116.

The c1 version of light chain used plasmid pAND103 template with the following primers: FR1 primer 5' GCC TCA GTC ATA ATG TCC CGG GGA CAA ATT CAG CTC ACC CAG TCT CCA TCC 3' (SEQ ID NO:32), which introduced SmaI, NciI, and HpaII sites; FR4 primer 5' GGT AAC CCG TGG ACG TTC GGT CAG GGC ACT AAG GTG GAG ATC TAA CGG GCT 3' (SEQ ID NO:33), which introduced a Bsp1286I site. The resultant c1 light chain plasmid was designated pAND118.

The c2 version of light chain were made by using plasmid pAND116 template with the following primers: FR1 primer 5' GCC TCA GTC ATA ATG TCC CGG GGA CAA ATT CAG CTC ACC CAG TCT CCA TCC 3' (SEQ ID NO:34), which introduced SmaI, NciI, and HpaII sites; FR4 primer 5' GGT AAC CCG TGG ACG TTC GGT CAG GGC ACT AAG GTG GAG ATC TAA CGG GCT 3' (SEQ ID NO:35), which introduced a Bsp1286I site. The resultant c2 light chain plasmid was designated pAND119.

To generate expression vectors for the huAQC2 light chains, the 0.44 kb NotI-BglII light chain variable domain fragment from pAND103, pAND116, pAND118, or pAND119, and the 0.68 kb BclI-NotI fragment from pEAG963 (*supra*) were subcloned into the NotI site of pCH269 (*supra*). The resultant light chain expression vectors were designated pAND117 (h1), pAND120 (h2), pAND122 (c1), and pAND123 (c2), respectively.

The expression vectors were co-transfected into 293-EBNA cells, and transfected cells were tested for antibody secretion and specificity. Cells transfected with an empty vector served as negative control. The whole cell lysates and the conditioned medium were immuno-precipitated with protein A. Western blot analysis of the precipitates (developed with anti-human heavy and light chain antibodies) indicated that huAQC2-transfected cells synthesized and efficiently secreted heavy and light chains at levels similar to chAQC2-transfected cells.

FACS analysis of VLA-1-expressing K562α1 cells stained with conditioned medium from the transfected cells was then performed. To do so, the K562α1 cells were incubated with the conditioned medium on ice for 120 min. The cells were then washed three times with a FACS buffer (PBS with 5% FBS and 0.05% sodium azide). The washed cells were resuspended in the buffer and incubated with PE-conjugated anti-human IgG (H + L) (Jackson ImmunoResearch Laboratories, Inc.) on ice for 30 min on ice. After the incubation, the cells were washed three times with the FACS buffer, and resuspended in the FACS buffer for analysis. The data are shown in Table 2, in which HuAQC2-h1 refers to an mAb consisting of the h1 version of the huAQC2 heavy chain (HC) and the h1 version of the huAQC2 light chain (LC) (see Table 1). Likewise, huAQC-h2 is an mAb consisting of the h2 versions of the heavy and light chains, huAQC2-c1 the c1 versions, and huAQC2-c2 the c2 versions. In the table, relative MFI refers to mean MFI normalized to that observed for chAQC2 blocked. Data shown represents the average from two independent transfections. These data indicated that the huAQC2-h2 and -c2 mAbs bound less well than huAQC2-h1 and -c1 relative to chAQC2.

Table 2. FACS staining of K562α1 cells by chAQC2 and huAQC2

	Light chain	Heavy chain	Relative MFI
chAQC2	pAND102	pAND099	1.00
huAQC2-h1	pAND117	pAND114	1.50
huAQC2-h2	pAND120	pAND124	0.64
huAQC2-c1	pAND122	pAND114	1.50
huAQC2-c2	pAND123	pAND121	0.68
huAQC2 LC c1/HC c2	pAND122	pAND121	2.21
huAQC2 LC c2/HC c1	pAND123	pAND114	0.76
huAQC2 LC unblocked c1/HC c2	pAND150*	pAND121	0.75
huAQC2 LC L46P c2/HC c2	pAND133**	pAND121	1.50
huAQC2 LC L47W c2/HC c2	pAND132***	pAND121	1.00

*It encodes huAQC2 LC c1 with an unblocked N-terminus Q1D.
**It encodes huAQC2 LC c2 with L46P.
***It encodes huAQC2 LC c2 with L47W.

Co-transfections of 293-EBNA cells with chAQC2 and huAQC2-h1, -h2, -c1 and -c2 were scaled up. Antibodies in the conditioned media were purified with Protein A-Sepharose. Purified mAbs were assayed by FACS for activity. The protocol as follows.

1. Count cells from flask that was split 1:4 on the day prior to the assay.
2. Pellet cells and resuspend at 2.5e5 cells/ml in FACS buffer (5% FBS in PBS- with 0.02% NaAzide).
3. Pipette 100 μl of cells into the wells of a 96 well V bottom plate.
4. Prepare 1:3 serial dilutions of AQC2 starting at 3 μg/ml in FACS buffer.
5. Pellet the cells for 5 minutes at 800 X g and flick plate to remove buffer.
6. Resuspend the cells in 100 μl of the diluted antibody series.
7. Incubate for 2 hours on ice.
8. Wash plate. Pellet the cells for 3 minutes at 800 X g and flick plate to remove buffer.
9. Resuspend the cells in 100 μl of secondary antibody (diluted 1:100 in FACS buffer).
10. Incubate for 30 minutes on ice.
11. Wash plate (see above).
12. Resuspend cells in 25 μl of FACS buffer.
13. Centrifuge the FACS tubes briefly to ensure that the 50 μl is in the bottom of the tubes.
14. Vortex each tube vigorously and collect 5000 events.

The data are shown in Fig. 17. These data confirmed that huAQC2-h2 and -c2 bound less well than huAQC2-h1 and -c1 relative to chAQC2.

The consensus versions of huAQC2 were studied further because they would be less immunogenic when used to treat patients with chronic indications. Mix-and-match cotransfections were performed to identify whether a single chain was responsible for the apparent decrease in binding seen with huAQC2-c2. The co-transfections suggested that the reduction could be attributed to the c2 light chain (encoded by pAND123), which differed from the c1 light chain (encoded by pAND122) at only two residues in the FR2 region: P46L and W47L.

To examine the individual contributions of each of these two changes, new c2 light chain expression vectors were constructed. Plasmid pAND125, the L47W variant of the c2 light chain was made using pAND119 as a template with the

following mutagenic primer: FR2 primer 5' GGG AAA GCA CCC AAA CTC TGG ATC TAT CTC ACA TCC AAC 3' (SEQ ID NO:36), which introduced HhaI and HaeII sites. Plasmid pAND126, the L46P variant of the c2 light chain, was made by using pAND119 as a template with the following mutagenic primer: FR2 primer 5' AAG CCC GGG AAG GCG CCC AAA CCC CTG ATT TAT CTC ACA TCC AAC 3' (SEQ ID NO:37), which introduced BsaHI, BanI, and NarI sites. Expression vectors for these new huAQC2 light chains were made by subcloning the 0.44 kb NotI-BglII light chain variable domain fragment from pAND125 or pAND126, and the 0.68 kb BclI-NotI fragment from pEAG963 (*supra*) into the NotI site of pCH269 (*supra*). The resultant plasmids were designated pAND132 (c2 with L47W), and pAND133 (c2 with L46P), respectively.

Co-transfections of the new light chain plasmids with each of the huAQC2 heavy chain plasmids were performed. VLA-1 binding was examined by FACS. The data demonstrate that the L47W back mutation failed to improve binding. The L46P mutation improved the peak of the binding curve, but the EC50 was still right-shifted relative to the behavior of huAQC2 version 1 (Table 2, *supra*). These results suggested that both back mutations were needed for full binding activity.

A genetically unblocked c1 light chain was also made, since the Q1D variant would be one residue more "humanized." The Q1D mutant, designated pAND148, was made with the template pAND118 with the following mutagenic primer: FR1 primer 5' GTC ATA ATG TCC CGG GGA GAT ATC CAG CTC ACC CAG TCT 3' (SEQ ID NO:38), which introduced a new EcoRI site and removed an ApoI site. An expression vector for this last variant of the huAQC2 light chain was made by subcloning the 0.44 kb NotI-BglII light chain variable domain fragment from pAND148 and the 0.68 kb BclI-NotI fragment from pEAG963 into the NotI site of pCH269, producing the light chain expression vector pAND150 (c1 with unblocked N-terminus Q1D). Co-expression of the genetically unblocked light chain with the c2 heavy chain (i.e., "huAQC2 LC c1 unblocked/HC c2"; designated huAQC2-c4) was equivalent to that of "huAQC2 LC c1/HC c2" (designated as huAQC2-c3). VLA-1 binding was confirmed by FACS on VLA1-expressing K562α1 cells (Table 2).

Co-transfections of 293-EBNA cells with chAQC2 and huAQC2-h1, -h2, -c1, -c2, -c3, and -c4. Antibodies in the conditioned media were purified on Protein A-Sepharose. The purified mAbs were assayed for activity (Figs. 17 and 18). HuAQC2-c3 was chosen as the drug candidate, since its properties were more similar to chAQC2. Vectors were then designed for stable expression of huAQC2-c3 in CHO cells. The vectors contained a cDNA for the huAQC2 c1 LC or c2 HC, with the 5' and 3' UTRs eliminated and the heavy chain C-terminal lysine genetically deleted to ensure product homogeneity. The final vectors were pAND162 (light chain), pAND160 (heavy chain). As used herein, huAQC2-c3 is also called hAQC2.

The full polypeptide sequences of hAQC2 are as follows.

Light Chain (Plasmid: pAND162)

1 QIQLTQSPSS LSASVGDRVT ITCSASSSVN HMFWYQQKPG KAPKPWIYLT
51 SNLASGVPSR FSGSGSGTDY TLTISSLQPE DFATYYCQQW SGNPWTFGQG
101 TKVEIKRTVA APSVFIFPPS DEQLKSGTAS VVCLLNNFYP REAKVQWKVD
151 NALQSGNSQE SVTEQDSKDS TYSLSSTLTL SKADYEKHKV YACEVTHQGL
201 SSPVTKSFNR GEC
(SEQ ID NO:3)

Heavy Chain (Plasmid: pAND160)

1 EVQLVESGGG LVQPGGSLRL SCAASGFTFS RYTMSWVRQA PGKGLEWVAT
51 ISGGGHTYYL DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCTRGFG
101 DGGYFDVWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY
151 FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI

201 CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS VFLFPPKPKD
251 TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST
301 YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY
351 TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD
401 SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG
(SEQ ID NO:4)

Other heavy and light chain polypeptide and nucleotide sequences are shown below.

A. chAQC2 heavy chain (Pand099) (SEQ ID NOs:39 and 40. The former No refers to the nucleotide sequence and the latter to the polypeptide sequence. The same order is used in the following numbering.)

1
GACGTCAAGGTGGTGGAGTCAGGGGGAGGCTTAGTGAAGCCTGGAGGGTCCCTGAAACTC
D V K V V E S G G G L V K P G G S L K L

61
GCCTGTGCAGCCTCTGGATTCAGTTTCAGTAGATATACTATGTCTTGGGTTCGCCAGATT
A C A A S G F S F S R Y T M S W V R Q I

121
CCGGAGAAGAGGCTGGAGTGGGTCGCAACCATTAGTGGTGGTGGTCACACCTACTATCTA

P E K R L E W V A T I S G G G H T Y Y L

181
GACAGTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACACCCTGTACCTG
D S V K G R F T I S R D N A K N T L Y L

241
CAAATGAGCAGTCTGAGGTCTGAGGACACAGCCATGTATTACTGTACAAGAGGTTTTGGA
Q M S S L R S E D T A M Y Y C T R G F G

301
GACGGGGGGTACTTCGATGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
D G G Y F D V W G Q G T T V T V S S

B. hAQC2 HC h1 and c1 (pAND114) (SEQ ID NOs:41 and 42)

1
GACGTCCAGCTGGTCGAGTCAGGGGGAGGCTTAGTCCAGCCTGGAGGGTCCCTGAGACTC
D V Q L V E S G G G L V Q P G G S L R L

61
TCCTGTGCAGCCTCTGGATTCAGTTTCAGTAGATATACTATGTCTTGGGTTCGCCAGGCT
S C A A S G F S F S R Y T M S W V R Q A

121
CCGGGGAAGGGGCTGGAGTGGGTCGCAACCATTAGTGGTGGTGGTCACACCTACTAT
CTA
P G K G L E W V A T I S G G G H T Y
Y L

181
GACAGTGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACCCTGTAC
CTG
D S V K G R F T I S R D N S K N T L
Y L

241
CAGATGAACAGTCTGAGGGCCGAGGACACAGCCGTGTATTACTGTACAAGAGGTTTT
GGA
Q M N S L R A E D T A V Y Y C T R G
F G

301
GACGGGGGGTACTTCGATGTCTGGGGCCAAGGTACCCTGGTCACCGTCTCCTCA
D G G Y F D V W G Q G T L V T V S S

C. hAQC2 h2 heavy chain (pAND124) (SEQ ID NOs:43 and 44)

1
GAGGTCCAGCTGGTCGAGTCAGGGGGAGGCTTAATCCAGCCTGGAGGGTCCCTGAGA
CTC
E V Q L V E S G G G L I Q P G G S L
R L

61
TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGGTATACTATGTCTTGGGTTCGCCAG
GCT

S C A A S G F T F S R Y T M S W V R Q A

121
CCGGGGAAGGGGCTGGAGTGGGTCGCAACCATTAGTGGTGGTGGTCACACCTACTAT CTA
P G K G L E W V A T I S G G G H T Y Y L

181
GACAGTGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACCCTGTAC CTG
D S V K G R F T I S R D N S K N T L Y L

241
CAGATGAACAGTCTGAGGGCCGAGGACACAGCCGTGTATTACTGTACAAGAGGTTTT GGA
Q M N S L R A E D T A V Y Y C T R G F G

301
GACGGGGGGTACTTCGATGTCTGGGGCCAAGGTACCCTGGTCACCGTCTCCTCAGG
D G G Y F D V W G Q G T L V T V S S

D. hAQC2 c2 heavy chain (pAND121) (SEQ ID NOs:45 AND 2)

1
GAGGTCCAGCTGGTCGAGTCAGGGGGAGGCTTAGTCCAGCCTGGAGGGTCCCTGAGA CTC
E V Q L V E S G G G L V Q P G G S L R L

61
TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGGTATACTATGTCTTGGGTTCGCCAG
GCT
S C A A S G F T F S R Y T M S W V R
Q A

121
CCGGGGAAGGGGCTGGAGTGGGTCGCAACCATTAGTGGTGGTGGTCACACCTACTAT
CTA
P G K G L E W V A T I S G G G H T Y
Y L

181
GACAGTGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACCCTGTAC
CTG
D S V K G R F T I S R D N S K N T L
Y L

241
CAGATGAACAGTCTGAGGGCCGAGGACACAGCCGTGTATTACTGTACAAGAGGTTTT
GGA
Q M N S L R A E D T A V Y Y C T R G
F G

301
GACGGGGGGTACTTCGATGTCTGGGGCCAAGGTACCCTGGTCACCGTCTCCTCAGG
D G G Y F D V W G Q G T L V T V S S

E. chAQC2 blocked light chain (Pand102) (SEQ ID NOs:46 and 47)

1 CAAATTGTTCTCACCCAGTTTCCAGCACTCATGTCTGCGTCTCCAGGGGAGAAGGTCACC
Q I V L T Q F P A L M S A S P G E K
V T

61
ATGACCTGCAGTGCCAGCTCAAGTGTAAATCACATGTTCTGGTATCAGCAGAAGCCA
AAA
M T C S A S S S V N H M F W Y Q Q K
P K

121
TCCTCCCCCAAACCCTGGATTTATCTCACATCCAACCTGGCTTCTGGAGTCCCTGCT
CGC
S S P K P W I Y L T S N L A S G V P
A R

181
TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGCATGGAGGCT
GAA
F S G S G S G T S Y S L T I S S M E
A E

241
GATGCTGCCACTTATTACTGCCAGCAGTGGAGTGGTAACCCGTGGACGTTCGGTGGA
GGC
D A A T Y Y C Q Q W S G N P W T F G
G G
301 ACCAAGCTGGAGATCAAA
T K L E I K

F. hAQC2 h1 light chain (pAND117) (SEQ ID NOs:48 and 49)

```
1 CAAATTGTTCTCACCCAGTCTCCATCCTCCCTGTCTGCGTCTGTAGGGGACAGAGTCACC
   Q  I  V  L  T  Q  S  P  S  S  L  S  A  S  V  G  D  R
V  T

61
ATCACATGCAGTGCCAGCTCAAGTGTAAATCACATGTTCTGGTATCAGCAGAAGCCC
GGG
   I  T  C  S  A  S  S  S  V  N  H  M  F  W  Y  Q  Q  K
P  G

121
AAAGCCCCCAAACCCTGGATTTATCTCACATCCAACCTGGCTTCTGGAGTCCCTTCA
CGC
   K  A  P  K  P  W  I  Y  L  T  S  N  L  A  S  G  V  P
S  R

181
TTCAGTGGCAGTGGGTCTGGGACAGATTACACTCTCACAATCAGCAGCCTGCAACCT
GAA
   F  S  G  S  G  S  G  T  D  Y  T  L  T  I  S  S  L  Q
P  E

241
GATTTTGCCACTTATTACTGCCAGCAGTGGAGTGGTAACCCGTGGACGTTCGGTGGA
GGC
   D  F  A  T  Y  Y  C  Q  Q  W  S  G  N  P  W  T  F  G
G  G

301 ACTAAGGTGGAGATCAAA
   T  K  V  E  I  K
```

G. hAQC2 h2 light chain (pAND120) (SEQ ID NOs:50 and 51)

1
CAAATTGTTCTCACCCAGTCTCCATCCTCCCTGTCTGCGTCTGTAGGGGACAGAGTC
ACC
Q I V L T Q S P S S L S A S V G D R
V T

61
ATCACATGCAGTGCCAGCTCAAGTGTAAATCACATGTTCTGGTATCAGCAGAAGCCC
GGG
I T C S A S S S V N H M F W Y Q Q K
P G

121
AAAGCGCCCAAACTCCTGATTTATCTCACATCCAACCTGGCTTCTGGAGTCCCTTCA
CGC
K A P K L L I Y L T S N L A S G V P
S R

181
TTCAGTGGCAGTGGGTCTGGGACAGATTACACTCTCACAATCAGCAGCCTGCAACCT
GAA
F S G S G S G T D Y T L T I S S L Q
P E

241
GATTTTGCCACTTATTACTGCCAGCAGTGGAGTGGTAACCCGTGGACGTTCGGTGGA
GGC
D F A T Y Y C Q Q W S G N P W T F G
G G

301 ACTAAGGTGGAGATCAAA
T K V E I K

H. hAQC2 c1 light chain (pAND122) (SEQ ID NOs:52 and 1)

1
CAAATTCAGCTCACCCAGTCTCCATCCTCCCTGTCTGCGTCTGTAGGGGACAGAGTC
ACC
Q I Q L T Q S P S S L S A S V G D R
V T

61
ATCACATGCAGTGCCAGCTCAAGTGTAAATCACATGTTCTGGTATCAGCAGAAGCCC
GGG
I T C S A S S S V N H M F W Y Q Q K
P G

121
AAAGCCCCCAAACCCTGGATTTATCTCACATCCAACCTGGCTTCTGGAGTCCCTTCA
CGC
K A P K P W I Y L T S N L A S G V P
S R

181
TTCAGTGGCAGTGGGTCTGGGACAGATTACACTCTCACAATCAGCAGCCTGCAACCT
GAA
F S G S G S G T D Y T L T I S S L Q
P E

241
GATTTTGCCACTTATTACTGCCAGCAGTGGAGTGGTAACCCGTGGACGTTCGGTCAG
GGC
D F A T Y Y C Q Q W S G N P W T F G
Q G

301 ACTAAGGTGGAGATCAAA
T K V E I K

I. hAQC2 c2 light chain (pAND123) (SEQ ID NOs:53 and 54)

J. chAQC2 unblocked light chain (pAND098) (SEQ ID NOs:55 and 56)

1
GAAATTGTTCTCACCCAGTTTCCAGCACTCATGTCTGCGTCTCCAGGGGAGAAGGTC
ACC
E I V L T Q F P A L M S A S P G E K
V T

61
ATGACCTGCAGTGCCAGCTCAAGTGTAAATCACATGTTCTGGTATCAGCAGAAGCCA
AAA
M T C S A S S S V N H M F W Y Q Q K
P K

121
TCCTCCCCCAAACCCTGGATTTATCTCACATCCAACCTGGCTTCTGGAGTCCCTGCT
CGC
S S P K P W I Y L T S N L A S G V P
A R

181
TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGCATGGAGGCT
GAA
F S G S G S G T S Y S L T I S S M E
A E

241
GATGCTGCCACTTATTACTGCCAGCAGTGGAGTGGTAACCCGTGGACGTTCGGTGGA
GGC
D A A T Y Y C Q Q W S G N P W T F G
G G

301 ACCAAGCTGGAGATCAAA
T K L E I K

K. huAQC2 unblocked c1 light chain (pAND150) (SEQ ID NOs:57 and 58)

1
GATATCCAGCTCACCCAGTCTCCATCCTCCCTGTCTGCGTCTGTAGGGGACAGAGTCACC
D I Q L T Q S P S S L S A S V G D R V T

61
ATCACATGCAGTGCCAGCTCAAGTGTAAATCACATGTTCTGGTATCAGCAGAAGCCCGGG
I T C S A S S S V N H M F W Y Q Q K P G

121
AAAGCCCCCAAACCCTGGATTTATCTCACATCCAACCTGGCTTCTGGAGTCCCTTCACGC
K A P K P W I Y L T S N L A S G V P S R

181
TTCAGTGGCAGTGGGTCTGGGACAGATTACACTCTCACAATCAGCAGCCTGCAACCTGAA
F S G S G S G T D Y T L T I S S L Q P E

241
GATTTTGCCACTTATTACTGCCAGCAGTGGAGTGGTAACCCGTGGACGTTCGGTCAGGGC
D F A T Y Y C Q Q W S G N P W T F G Q G

301 ACTAAGGTGGAGATCAAA

T K V E I K

Example 22

This example describes the characterization of various AQC2 antibodies of the invention.

Solid-phase assay for α1 I domain binding. Fifty μl of 10 mg/ml α1 I domain-GST fusion protein was added to a CORNING COSTAR EASY WASH polystyrene 96-well plate (Gotwals et al., *Biochemistry*, 38, 8280-8 (1999)). Following incubation at 4°C for 16 hrs, the plate was washed four times with 350 μl of 0.1 % Tween-20 in PBS in a plate washer. The plate was blocked by addition of 180 μl of 3% BSA in TBS at 25°C for 60 min, and then washed as above. Dilutions of antibodies (50 μl/well) in TBS containing 1 mg/ml BSA (assay buffer) were prepared in a 96-well roundbottom plate, transferred to the α1 I domain-coated plate, and incubated for 60 min at 25°C. Following a final wash, 100 μl/well of TMB reagent (Pierce) was added. After 10 min, 100 μl of 1 M sulfuric acid was added, and the absorbance at 450 nm was read on a UV-Vis 96-well spectrophotometer.

Electrochemiluminescence assays for binding of α1β1 integrin or α1 I domain to collagen. Tosyl-activated DYNABEADS M-280 (Dynal, Inc.) were coated with 100 μg/ml type IV collagen (Sigma) according to the manufacturer's instructions. Cell lysates from α1-transfected K562 cells were prepared as follows. Cells were collected by centrifugation, resuspended at 10^8 cells/ml in a lysis buffer containing 25 mM Tris, pH 7.4, 1% NP-40, 1 mM $CaCl_2$, 1 mM $MnCl_2$, 1 mM $MgCl_2$, 2% BSA, and 1 mM PMSF, and incubated at 4°C for 60 min. Cell debris was removed by centrifugation at 12,000 rpm for 30 min and the resulting supernatant was used in subsequent experiments. Anti-β1 activating antibody TS2/16 and polyclonal anti-GST antibody (Pharmacia) were labeled with TAG-NHS ester (IGEN International, Inc., Gaithersburg, MD) according to the manufacturer's instructions. Labeled antibodies were purified by gel filtration chromatography on SEPHADEX G25M (Pharmacia).

To carry out the binding assay, collagen-coated beads (1 mg/ml) were blocked for 5 min with 8% Lewis rat plasma in an assay buffer containing 50 mM HEPES, pH 7.5, 150 mM NaCl, and 0.1% Triton X-100. For the α1β1 binding assay,

serial dilutions of antibodies were incubated with 10 μg of beads, cell lysate prepared from 10^5 α1-transfected K562 cells (*supra*), and 0.1 μg/ml of TAG-TS2/16 in an assay buffer containing 1 mM $MnCl_2$. For the α1 I domain binding assay, the antibodies were incubated with 10 μg of beads, 0.1 μg/ml α1 I domain GST fusion protein, and 1 μg/ml of TAG-anti-GST in an assay buffer containing 1 mM $MnCl_2$. After one to two hours of agitation at room temperature, 200 μl of the assay buffer was added and the samples were read on an ORIGEN 1.5 electrochemiluminescence detector (IGEN). Plots are presented with arbitrary electrochemiluminescence units (ECL) on the ordinate axis.

Biotinylated mAQC2 competition assay. A 96-well plate was coated with 50 μl of 5 μg/ml α1 I domain GST fusion protein and blocked with 3% BSA in TBS as described above. Dilutions of antibodies (60 μl/well) in the assay buffer were prepared in a 96-well roundbottom plate, and 60 μl of 0.1 μg/ml biotinylated murine AQC2 in the assay buffer was added. Fifty microliters from each well was transferred to the coated plate and incubated for 3 hrs at 25°C. The plate was then washed as above, 50 μl of 1 μg/ml peroxidase-conjugated EXTRAVIDIN (Sigma) was added, and the plate was incubated another 2 hrs at 25°C. After a final wash, 100 μl/well of TMB reagent (Pierce) was added. After 10 min, 100 μl of 1 M sulfuric acid was added, and the absorbance at 450 nm was read on a UV-Vis 96-well spectrophotometer.

Experimental results. The experimental results are shown in Figs. 16A-D and Table 3. The ability of mAQC2, chAQC2, hAQC2, and hAQC2' (i.e., huAQC2-c4; differing from hAQC2 only in that residue 1 of the hAQC2' light chain was D instead of Q) to (1) bind to human α1- transfected K562 cells (by FACS); (2) bind to immobilized α1-I domain (by ELISA); (3) compete with mAQC2 for binding to α1-I domain (ELISA); (4) block α1-I domain binding to collagen (Electrochemiluminescence assay); or (5) block α1β1 integrin binding to collagen (Electrochemiluminescence assay) was determined. The results are shown in Figs. 16A-D, and calculated IC50 (for inhibition) or EC50 (for binding) values are given in Table 3. In each assay, each of the humanized AQC2 forms showed a similar ability to either bind VLA1 (or the α1 domain) or block binding to collagen (Note that in

panel C, the observed difference in intensity between mAQC2 and the humanized forms derives from the use of an anti-murine-IgG secondary antibody, instead of an anti-human-IgG).

Table 3. Summary of assay results (all values in nM)

Antibody	FACS (EC50)	VLA1 Inhibition (IC50)	α1I Inhibition (IC50)	ELISA (EC50)	Competition with biotin-AQC2 (IC50)
mAQC2	n.d.	0.0726 (±0.014)	0.029 (±0.011)	0.061 (±0.015)	38 (±8.7)
Chimera	0.25	0.071 (±0.002)	0.027 (±0.007)	0.176 (±0.058)	30 (±6.9)
hAQC2	0.29	0.129 (±0.005)	0.035 (±0.005)	0.190 (±0.010)	65 (±2.2)
hAQC2'	0.43	0.125 (±0.018)	0.037 (±0.001)	0.313 (±0.072)	69 (±25.7)

We next tested whether changes at certain conservative residues in the CDRs could preserve the VLA-1 binding activity of hAQC2. DNA constructs encoding variants of hAQC2 with the following mutations were made by site-directed mutagenesis: (1) G55S in the heavy chain CDR2; (2) S24N in the light chain CDR1 (introducing an occupied N-linked glycosylation site); (3) G92S in the light chain CDR3; (4) a combination of (1) and (2); and (5) a combination of (1) and (3). The DNA constructs encoding both the heavy and light chains were then co-transfected into 293-EBNA cells, and the conditioned medium of the transfectants was assayed for antibody expression by Western blot and ELISA. The results indicated that the hAQC2 variants were expressed as efficiently as cognate hAQC2. FACS analysis using VLA-1-expressing K562 cells further showed that the VLA-1-binding activities

of these variants were similar to hAQC2 itself. In sum, the amino acid substitutions did not alter the VLA-1 binding activity of hAQC2. Indeed, X-ray crystal structure of the RΔH/hAQC2 Fab complex (*infra*) shows that S24 and G92 of the light chain and G55 of the heavy chain are not in the binding pocket that is in contact with the α1-I domain.

Example 23

The effector functions of an immunoglobulin couple the immunoglobulin's antigen-binding activity to the inflammatory, cytotoxic and stimulatory arms of the immune system. Effector functions may impair the safety and efficacy of an immunoglobulin therapeutic product. To reduce the potential effector functions of hAQC2, mutations of L234A and L235A were made to its heavy chain to generate hsAQC2. For the same reason, a single mutation of N297Q was made in the heavy chain of hAQC2 to generate an aglycosylated form of hAQC2, named haAQC2. Studies can be done to compare their efficacy, residual effector function, stability and immunogenicity to cognate hAQC2. Unless otherwise indicated, residue position numbers in constant regions as used herein are designated in accordance with the EU numbering convention.

The heavy chain polypeptide sequence of haAQC2 is as follows (Plasmid: pAND161):

```
1      EVQLVESGGG LVQPGGSLRL SCAASGFTFS RYTMSWVRQA
PGKGLEWVAT
51     ISGGGHTYYL DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT
AVYYCTRGFG
101    DGGYFDVWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT
AALGCLVKDY
151    FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP
SSSLGTQTYI
201    CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPELLGGPS
VFLFPPKPKD
251    TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT
KPREEQYQST
```

301 YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY
351 TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD
401 SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG (SEQ ID NO:5)

The heavy chain polypeptide sequence of hsAQC2 is as follows (Plasmid: pAND171):

1 EVQLVESGGG LVQPGGSLRL SCAASGFTFS RYTMSWVRQA PGKGLEWVAT
51 ISGGGHTYYL DSVKGRFTIS RDNSKNTLYL QMNSLRAEDT AVYYCTRGFG
101 DGGYFDVWGQ GTLVTVSSAS TKGPSVFPLA PSSKSTSGGT AALGCLVKDY
151 FPEPVTVSWN SGALTSGVHT FPAVLQSSGL YSLSSVVTVP SSSLGTQTYI
201 CNVNHKPSNT KVDKKVEPKS CDKTHTCPPC PAPEAAGGPS VFLFPPKPKD
251 TLMISRTPEV TCVVVDVSHE DPEVKFNWYV DGVEVHNAKT KPREEQYNST
301 YRVVSVLTVL HQDWLNGKEY KCKVSNKALP APIEKTISKA KGQPREPQVY
351 TLPPSRDELT KNQVSLTCLV KGFYPSDIAV EWESNGQPEN NYKTTPPVLD
401 SDGSFFLYSK LTVDKSRWQQ GNVFSCSVMH EALHNHYTQK SLSLSPG (SEQ ID NO:6)

Example 24

This example describes a method for determining the crystal structure of the complex of a rat/human chimeric α1-I domain of the α1β1 integrin and the hAQC2 Fab fragment.

Preparation of the protein complex

The hAQC2 Fab fragment was prepared from hAQC2 antibody using a variation of the procedure of the IMMUNOPURE® Fab preparation kit (Cat# 44885, Pierce, Rockford, IL). The intact hAQC2 antibody was concentrated to 12 mg/ml in a buffer containing 20 mM phosphate, 10 mM EDTA and 25 mM cysteine (pH 7.0). Immobilized papain was added at an enzyme to substrate ratio of 1:50, and digestion was allowed to occur overnight at 37° C. The immobilized papain was removed and the crude digest was dialyzed against 20 mM sodium acetate buffer (pH 4.5). The Fab fragment was separated from residual intact antibody, dimeric Fab fragment, and Fc fragment by cation exchange chromatography using a S-column (Poros HS/M , PERSEPTIVE Biosytems #PO42M26) with a shallow salt gradient. The Fab fragment was then exchanged into 0.1 M Hepes buffer (pH 8.0).

The chimeric α1-I domain used in the present invention is a rat/human chimeric I domain construct (mutant RΔH) containing residues Thr145-Phe336 of the rat α1 integrin chain, where residues Gly217, Arg218, Gln219 and Leu222 (crystal numbering) have been substituted with equivalent human residues Val, Gln, Arg and Arg, respectively, in order to restore antibody binding. The amino acid sequences of chimeric RΔH, rat, and human α1-I domains are given below in SEQ ID NOs:59, 60 and 61, respectively. Recombinant α1-I domain was expressed in *E. coli* as a GST-fusion protein. The RΔH α1-I domain was cleaved with thrombin and purified from a *Pichia pastoris* clone as described previously (Gotwals et al., 1999, *Biochemistry* 38:8280-8288).

```
145  TQLDIV
151  IVLDGSNSIY PWESVIAFLN DLLKRMDIGP KQTQVGIVQY
191  GENVTHEFNL NKYSSTEEVL VAANKIVQRG GRQTMTALGI
231  DTARKEAFTE ARGARRGVKK VMVIVTDGES HDNYRLKQVI
271  QDCEDENIQR FSIAILGHYN RGNLSTEKFV EEIKSIASEP
311  TEKHFFNVSD ELALVTIVKA LGERIF
```

(SEQ ID NO:59)

```
145  TQLDIV
151  IVLDGSNSIY PWESVIAFLN DLLKRMDIGP KQTQVGIVQY
```

191 GENVTHEFNL NKYSSTEEVL VAANKIGRQG GLQTMTALGI
231 DTARKEAFTE ARGARRGVKK VMVIVTDGES HDNYRLKQVI
271 QDCEDENIQR FSIAILGHYN RGNLSTEKFV EEIKSIASEP
311 TEKHFFNVSD ELALVTIVKA LGERIF
(SEQ ID NO:60)

145 TQLDIV
151 IVLDGSNSIY PWDSVTAFLN DLLKRMDIGP KQTQVGIVQY
191 GENVTHEFNL NKYSSTEEVL VAAKKIVQRG GRQTMTALGI
231 DTARKEAFTE ARGARRGVKK VMVIVTDGES HDNHRLKKVI
271 QDCEDENIQR FSIAILGSYN RGNLSTEKFV EEIKSIASEP
311 TEKHFFNVSD EIALVTIVKT LGERIF
(SEQ ID NO:61)

The hAQC2 Fab fragment was mixed with excess chimeric α1-I domain and incubated at 37° C for 15 minutes. The saturated α1/Fab complexes were separated from uncomplexed α1-I domain by size exclusion chromatography using a S200 Sephacryl column (Pharmacia, Gibco). The complex was further concentrated to 11 mg/ml in a 20 mM Tris (pH 7.4), 150 mM NaCl, 1 mM $MnCl_2$, 5 mM β-mercaptoethanol.

Preparation of crystals

Crystallization conditions were found using the CRYSTAL SCREEN™ KITs from Hampton Research (Laguna Niguel, CA). Crystals of the complex described above were grown at 20° C by vapor diffusion using an equal amount of protein complex solution and a 20-30% PEG 1500 reservoir solution. Typically, 2 μL of protein complex was added to 2 μL of well solution to yield drops of 4 μL. Crystals grew in two to seven days as hexagonal rods with dimensions 0.8 x 0.05 x 0.05 mm^3. The presence of the α1-I domain and hAQC2 Fab fragment was confirmed by SDS-PAGE analysis of dissolved crystals. In order to reduce the inherent radiation damage during data collection, X-ray diffraction data was collected at approximately 100 K. To prepare the crystals for data collection at this low

temperature, crystals were gradually equilibrated into a cryoprotectant solution containing 25% PEG 400 and 30% PEG 1500, and flash cooled in liquid nitrogen.

Structure determination

Native X-ray diffraction data to 2.8 Å resolution were collected from a single crystal at about 100 K using an ADSC Quantum 4 charged-coupled device detector at beamline X4A of the Brookhaven National Laboratory (BNL) National Synchrotron Light Source (NSLS). Data was processed using the software programs DENZO and SCALEPACK (Otwinowski & Minor, 1997, *Methods in Enzymol.* 276:307-326). Crystals belonged to the space group $P6_1$ or its enantiomorph $P6_5$, with unit cell dimensions a = b = 255.09 Å, c=38.64 Å. The data set was 96.6% complete and had an R-merge of 8.3%. The Matthews coefficient (Matthews, 1968, J. Mol. Biol. 33:491-497) was 2.59 $Å^3$ Da^{-1} with a solvent content of 52.1 %, which indicated that there were two complexes in the asymmetric unit. The two complexes in the asymmetric unit were related by non-crystallographic 2-fold symmetry. Data statistics are shown in Table 4.

Molecular replacement searches were done with the program AMoRe (Navaza, 1994, *Acta Cryst.* A50:157-163) from the CCP4 program package (Collaborative Computational Project No.4. The CCP4 Suite: programs for protein crystallography. 1994, *Acta Cryst.* D50:760-763), and molecular graphics manipulations were done with the program QUANTA. A single α1-I domain from the structure of the rat α1-I domain of α1β1 integrin (Protein Data Bank (PDB) accession number 1ck4; Nolte et al., 1999, *FEBS Lett.* 452:379-385) was used as a model or probe for rotation and translation searches. The translation function search indicated that the 1^{st} and 9^{th} highest peaks of the rotation function corresponded to the correct solutions for the two α1-I domains in the asymmetric unit (correlation coefficient (cc) = 21.1%, R=53.1 %) and that the space group was $P6_5$. Subsequently, searches for the hAQC2 Fab fragments were done, keeping the I domain solutions fixed and using a model of the Fv domain of the hAQC2 Fab as a search probe. A clear solution was found for one of the two Fv domains (cc=22.1%, R=52.6 %), but the second Fv could not be located. The position of the second Fv was derived using the non-crystallographic 2-fold symmetry. Rigid body refinement of the two I domains and

two Fv domains reduced the R-factor to 43.6% (R-free = 42.7 %). An 2Fo-Fc electron density map showed clear electron density for the constant domain (Fconst) of the first Fab fragment, but no density for the Fconst domain of the second Fab fragment. A model of the Fconst domain of the first Fab was manually fit in the observed electron density. Subsequent rigid body refinement with the software program CNX (Accelrys Inc., San Diego, CA ©2000; Brunger,1998, *Acta Cryst.* D54:905-921), using data in the 500-2.8 Å resolution range, optimized the position of all domains, reducing the R-factor to 39.7 % (R-free = 38.9%).

All subsequent refinement steps were carried out with the CNX program. To reduce model bias, partial models were used for 2Fo-Fc map calculation and model refinement. The initial partial model, was subjected to simulated annealing and grouped B-factor refinement with non-crystallographic symmetry restraints. The R-working and R-free factors dropped to 28.3% and 32.9%, respectively. Several cycles consisting of iterative model building, maximum likelihood positional refinement and B-factor refinement followed. Only model adjustments that resulted in a drop in the R-free factor were accepted. A bulk-solvent correction was employed after the complete model was built. The R-working and R-free factors of the final model are 21.3 % and 27.2 %, respectively for the data ($F > 2\sigma$) in the 500-2.8 Å resolution range.

The final 2Fo-Fc electron density map is of good quality for most of the complex with the exception of amino acid residues 288-295 of one I domain fragment (molecule A in Fig. 19) that are associated with weak electron density and have not been included in the model. In addition, the entire constant domain of one Fab fragment has no visible electron density, which indicates that it is disordered. This appears to be consequence of the absence of crystal contacts for the constant domain of the Fab fragment due to its position within a large solvent channel. This domain was also not included in the final model that consists of 1030 amino acid residues, constituting 6 polypeptide chains, and 2 manganese ions. The r.m.s. positional deviation between equivalent residues from the two complexes in the asymmetric unit is small (0.37 Å for 1660 equivalent main chain atoms). Stereochemistry statistics were calculated with the software programs PROCHECK

(Laskowski et al., 1993, *J. Appl. Cryst.* 26:283-291; Morris et al., 1992, *Proteins* 12:345-364) and CNX. Hydrogen bonds (< 3.6 Å) were found with the program CONTACT (Tadeusz Skarzynski, Imperial College, London, 1.12.88; Collaborative Computational Project No.4 . The CCP4 Suite: programs for protein crystallography. 1994, *Acta Cryst.* D50, 760-763). All non-glycine residues (except residue Thr50 of the L chain that will be discussed below) are in the allowed regions of the Ramachandran diagram and 86% of the residues are in the most favored regions. The average B-factor of the main chain atoms is 38.5 Å^2. Crystallographic analysis data are in Table 4.

Table 4: Summary of Data Statistics and Crystallographic Analysis

Data collection	
Cell dimensions a, b, c (Å)	255.09 , 255.09, 38.64
Space group	$P6_5$
Resolution (Å)	500-2.8 (2.9-2.8)†
Unique reflections	35275
Completeness (%)	96.6 (87.7)†
Average I/s	11.92 (2.29)†
Rmerge*(%)	8.3 (30.9)†
Model	
Number of non-H atoms	7950
Number of protein residues	1030
Contents of asymmetric unit	2 I domains, 1 Fab fragment, 1 Fv domain
Average B-factor ($Å^2$)	38.5
Refinement	
Resolution range used (F>2σ)	500-2.8
R-factor (R-working) (%)	21.3
R-free††(%)	27.2
Stereochemistry	
RMS deviations	
Bond lengths (Å)	0.007
Angles (°)	1.43

* Rmerge = $\Sigma_h \Sigma_i |I_{hi}-I_h| / \Sigma_{hi} I_{hi}$

† Values for the highest resolution shell given in parenthesis.

†† 8% of the data were allocated for the calculation of R-free factor.

Example 25

This example describes the crystal structure of the complex of a rat/human chimeric α1-I domain of the α1β1 integrin and the hAQC2 Fab fragment.

Architecture of Crystal Structure

The crystal structure of the complex of the rat/human chimeric α1-I domain of the α1β1 integrin and the hAQC2 Fab fragment has an elongated shape (Fig. 20). The dimensions of the complex are 100 Å x 50 Å x 35 Å.

The Fab fragment exhibits the typical immunoglobulin fold. The light chain and heavy chains of the Fab fragment each form two broad sheets of anti-parallel β-strands which pack tightly together to form a scaffold for the complementarity determining region (CDR) loops which extend from the packed sheets. Both the light chain and the heavy chain contain three CDR loops. The light chain loops are called L1, L2 and L3, while the heavy chain loops are referred to as H1, H2 and H3. The complementarity determining region (CDR) loops correspond to canonical structure 1 for light chain L1, L2 and L3 loops and for heavy chain H1 and H2 loops (Chothia et al., 1989, Nature 342:877-883). The heavy chain H3 loop has a tight β-hairpin-like conformation that is stabilized by internal hydrogen bonds as well as two aromatic residues (Tyr104 and Phe105) that are packed against the light chain. Residue Thr50 of L2 adopts mainchain dihedral angles that fall in the disallowed regions of the Ramachandran diagram. The same observation for the corresponding residue has been made for other antibodies (Muller et al., 1998, *Structure* 6, pp.1153-11567) which indicates that this is a natural characteristic of L2 loops.

The α1-I domain in the present invention has a structure very similar to the uncomplexed α1-I domain (PDB accession number 1ck4; Nolte et al., 1999, FEBS Lett. 452:379-385; PDB accession code 1qc5; Rich et al.,1999, *J. Biol. Chem.* 274:24906-24913). The I domain structure exhibits a "dinucleotide-binding" or "Rossman" fold (Rao & Rossman, 1973, J. Mol. Biol. 76:241-256) in which a central sheet of five parallel β-strands and one small antiparallel-strand is surrounded on both sides by a total of seven α-helices. The six β-strands of the structure in this invention will be referred to as βA, βB, βC, βD, βE, and βF and the seven α-helices are called α1, α2, α3, α4, α5, α6 and α7.

Three characteristic structural features exist for I domains. The first characteristic feature is the presence of an inserted small helix in the βE-α6 loop, termed as the C helix. Most of the C helix loop of molecule A (Fig. 19) in the present invention is associated with weak electron density, which suggests disorder. This appears to be a consequence of absence of crystal contacts or contacts with the Fab that would have stabilized the loop. However, the same loop in molecule B (Fig. 19) in the present invention has well-defined electron density and has been included in the model. The second characteristic feature of α1-I domains is the MIDAS or Metal-Ion-Dependent-Adhesion-Site where metal ions and ligands are implicated to bind to the I domain. Five key residues which form part of the MIDAS are referred to as the "DxSxS-T-D" motif. These residues, which are completely conserved among I domains, coordinate the metal ion (Gotwals et al., 1999, *Biochemistry* 38:8280-8288). The crystals in the present invention were grown in the presence of manganese and the MIDAS site of the I domain in this structure is observed to contain a Mn^{+2} metal ion. The ion is directly coordinated by the side chains of residues Ser156, Ser158 and Thr224. The 2Fo-Fc electron density map shows no evidence that MIDAS residues Asp154 and Asp257 make water-mediated indirect coordination of the metal ion (Fig. 20). However, the apparent absence of water molecules could be a consequence of the limited resolution (2.8 Å) of the electron density map. The third feature of I domains is that all determined structures of I domains belong to one of two conformations called "open" and "closed". The differences between the open and closed conformation include a different mode of metal ion coordination and a significant (about 10 Å) positional shift of the C-terminal helix of the I domain. The I domain in the complex in the present invention is in the closed conformation.

In the structure of the complex in the present invention, the Fab fragment binds to its epitope on the front upper surface of the I domain with a footprint 35 Å by 30 Å. The total buried surface area in the antibody-antigen interface is 1534 $Å^2$ which is typical of other antibody-antigen complexes (Davies et al., 1996, *Proc. Natl. Acad. Sci. USA* 93:7-12; Jones & Thornton, 1996, *Proc. Natl. Acad. Sci. USA* 93:13-20). The surface is 25% hydrophobic and 75% hydrophilic in character. The heavy chain contributes 65% of the buried surface area for the complex, while the

remaining 35% is contributed by the light chain. The antibody epitope consists of residues located in four loops of the I domain (Emsley et al., 2000, *Cell* 101:47-56). Three of the loops form the MIDAS site: loop 1 (βA- α1) which contains the conserved DXSXS sequence, loop 2 (α3-α4) which contains the MIDAS Thr224 and loop 3 (βD-α5) that contains MIDAS residue Asp257. The fourth loop is the C-helix loop and is involved in only in minor contacts.

The central feature of the antigen-antibody interaction is the coordination of the MIDAS site metal ion by Asp101 from the CDR H3 of the antibody (Fig. 20). The distance between the ion and Oδ1 of Asp101 is 2.4 Å. In addition, the Oδ2 atom of Asp101 is interacting with His261 of the I domain. Interestingly, the CDR H3 contains several glycine residues adjacent to Asp101 (sequence GFGDGGY)(SEQ ID NO:62), presumably to allow enough flexibility to the CDR loop to permit proper coordination of the metal ion. The CDR H3 sequence is essentially invariant in monoclonal antibodies that were raised against the same antigen and found to belong in the same class. Most of the antibody residues that are involved in antibody-antigen contacts are located in L3, H1, H2 and H3 CDR loops. A few residues from the L1 (Asn30) and L2 (Tyr48) loops appear to form minor Van Der Waals contacts. L3 primarily contributes to contacts through two large hydrophobic residues, Trp90 and Trp95. In addition, Asn93 from L3 forms hydrogen bonds with Gln223 of the I domain. The side chains of His56 and Tyr58 from the H2 loop form hydrogen bonds with main chain atoms of loop 2 of the I domain. Arg31 of H1 is in contact with Arg291 of loop 4 of the I domain. Arg222 from loop 2 of the I domain is sandwiched between several antibody residues including Tyr58, Trp95 and Asn93. This is the only residue out of the four mutated in the RΔH I domain, that is involved in contacts with the Fab. It is therefore likely to be the only residue responsible for restoring the binding of the antibody after the mutagenesis.

Comparison of the crystal structure of the complex of a rat/human chimeric α1-I domain and the hAQC2 Fab fragment with other I domain structures

The chimeric RΔH α1-I domain has four sequence differences with the rat α1-I domain (rat residues: 217G, 218R, 219Q and 222L), eight sequence differences with the human α1-I domain (human residues: 163D, 166T, 214K, 264H,

268K, 288S, 322I and 380T), and ten sequence differences with the clone used in the crystal structure studies of human α1-I domain (clone residues: 163D, 166T, 174E, 214K, 230I, 264H, 268K, 288S, 322I and 380T). In the unliganded rat α1β1 α1-I domain crystal structure (PDB accession code 1ck4; Nolte et al., 1999, *FEBS Lett.* 452:379-385), the α1-I domain contains no bound metal ions and adopts the "closed" conformation. In the unliganded human α1-I domain crystal structure (accession code 1qc5; Rich et al., 1999, *J. Biol. Chem.* 274:24906-24913), the α1-I domain contains bound Mg^{+2} and similarly adopts the closed conformation. Superimposition of these two structures with the complexed chimeric α1-I domain indicates that there are only minor conformational changes upon hAQC2 antibody binding. The r.m.s. positional deviation between the rat and chimeric α1-I domain is 1.04 Å for all 768 main chain atoms. The r.m.s. positional deviation between the human and chimeric α1-I domain is 0.69 Å for all 764 main chain atoms. The biggest differences (human and chimeric α1-I domain pair) are observed in loop 1 (r.m.s. deviations 1.24 Å for main chain atoms of residues 154-161) and the loop 4 (C helix loop) of the α1-I domain (r.m.s. deviations 1.55 Å for main chain atoms of residues 288-296). However, these differences can be more accurately described as shifts of the whole secondary structure elements rather than complex conformational changes. These are likely to be within the normal range of conformational flexibility of proteins. The r.m.s. positional deviation between the human and chimeric α1-I domain for backbone atoms of amino acid residues Glu192, Gln218, Arg219, Gly220, and Gly221 (crystal numbering) is 0.33 Å. The r.m.s. positional deviation between the rat and chimeric α1-I domain for backbone atoms of amino acid residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294 (crystal numbering) is 0.97 Å.

The I domain maintains the "closed" I domain conformation that has been observed only for unliganded I domains crystallized in the absence of ligands or pseudo-ligands bound to the MIDAS site. The r.m.s. positional deviation of the C-terminal helices of the human and chimeric I domains (calculated for the main chain atoms of residues 321-335) is 0.64 Å. A simulated annealing omit map calculated for the final refined model unambiguously confirms that the position of the

C-terminal helix and adjacent structural elements are consistent with the closed conformation.

In order to investigate the effects of ligand binding to the modes of metal ion coordination, the structure of the present invention was superimposed with the structures of the unliganded α2-I domain (PDB accession code 1aox; Emsley et al., 1997, *J. Biol. Chem.* 272:28512-28517) and the α2-I domain complexed with a collagen peptide (PDB accession code 1dzi; Emsley et al., 2000, *Cell* 101:47-56). The coordination of the metal ion by Asp101 from the antibody is remarkably similar to the coordination of the metal ion of the α2-I domain by a glutamic acid from the collagen peptide. Another feature that is conserved is the simultaneous interaction of the acidic group with His261 (His258 in the α2-I domain). All MIDAS residues of the I domain-Fab complex except Ser156 and Ser158 adopt conformations very similar to those observed in the unliganded I domain. In contrast, the side chains of Ser156 and Ser158, as well as the metal, adopt conformations similar with those of the liganded I domain. It is clear that the coordination of the metal ion by Asp101 does not allow the ion to maintain the position and coordination distances that are observed in the unliganded state. Thus, the metal ion is not directly coordinated by Asp257, a fact that permits the ion to maintain high electrophilicity.

Biological Implications

In the present invention, there is no direct coordination of the metal by Asp257, which may permit high affinity binding by lowering the energy barrier between a closed (no ligand bound) and open (ligand bound) conformation. However, the coordination of the metal by an aspartic acid from the antibody is not sufficient to induce the open conformation to the I domain in the present invention. The I domain - Fab complex structure indicates that it is possible to have strong binding to the I domain that adopts the closed conformation and that coordination of the metal ion by an acidic residue from the ligand may be necessary but not sufficient to induce a conformational change to the open state. Binding of the antibody is expected to stabilize the low affinity state of the integrin and prevent the outside-in signaling that would have accompanied integrin binding to collagen.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be apparent to those skilled in the art that certain changes and modifications will be practiced. Therefore, the description and examples should not be construed as limiting the scope of the invention.

What is claimed is:

1. An anti-VLA-1 antibody whose light chain complementarity determining regions are defined by amino acid residues 24 to 33, 49 to 55, and 88 to 96 of SEQ ID NO:1, and whose heavy chain complementarity determining regions are defined by amino acid residues 31 to 35, 50 to 65, and 98 to 107 of SEQ ID NO:2.

2. The antibody of claim 1, wherein the antibody comprises a light chain variable domain sequence of SEQ ID NO:1 and a heavy chain variable domain sequence of SEQ ID NO:2.

3. The antibody of claim 1, wherein the antibody comprises the same heavy and light chain polypeptide sequences as an antibody produced by hybridoma mAQC2 (ATCC accession number PTA3273).

4. The antibody of claim 1, wherein the antibody is a humanized antibody.

5. The antibody of claim 4, wherein the antibody comprises at least one of the following residues in its light chain: Q1, L4, P46, W47 and Y71; or at least one of the following residues in its heavy chain: D1, V12, S28, F29, A49, T93, R94 (Kabat numbering convention).

6. The antibody of claim 4, wherein the antibody comprises a light chain variable domain sequence defined by amino acid residues 1 to 106 of SEQ ID NO:3, and a heavy chain variable domain sequence defined by amino acid residues 1 to 118 of SEQ ID NO:4.

7. The antibody of claim 4, wherein the antibody comprises the same heavy and light chain polypeptide sequences as an antibody produced by cell line hAQC2 (ATCC accession number PTA3275).

8. The antibody of claim 4, wherein the heavy chain is mutated at one or more of amino acid residues selected from the group consisting of residues 234, 235, 236, 237, 297, 318, 320 and 322 (EU numbering system), thereby causing an alteration in an effector function while retaining binding to VLA-1 as compared with an unmodified antibody.

9. The antibody of claim 8, wherein the antibody comprises the mutations L234A and L235A (EU numbering system) in its heavy chain as compared with an unmodified antibody.

10. The antibody of claim 4, wherein the antibody comprises the same heavy and light polypeptide sequences as an antibody produced by cell line hsAQC2 (ATCC accession number PTA3356).

11. The antibody of claim 4, wherein the antibody is mutated at an amino acid residue that is a glycosylation site, thereby eliminating the glycosylation site.

12. The antibody of claim 11, wherein the antibody comprises the mutation N297Q in its heavy chain (EU numbering system).

13. The antibody of claim 4, wherein the antibody comprises the same heavy and light chain polypeptide sequences as an antibody produced by cell line haAQC2 (ATCC accession number PTA3274).

14. A composition comprising an antibody of any one of claims 4-13, and a pharmaceutically acceptable carrier.

15. An isolated nucleic acid comprising a coding sequence for SEQ ID NO:1.

16. An isolated nucleic acid comprising a coding sequence for SEQ ID NO:2.

17. An isolated nucleic acid comprising a coding sequence for the light chain of an antibody produced by hybridoma mAQC2 (ATCC accession number PTA3273).

18. An isolated nucleic acid comprising a coding sequence for the heavy chain of an antibody produced by hybridoma mAQC2 (ATCC accession number PTA3273).

19. An isolated nucleic acid comprising a coding sequence for the light chain of an antibody produced by cell line hAQC2 (ATCC accession number PTA3275).

20. An isolated nucleic acid comprising a coding sequence for the heavy chain of an antibody produced by cell line hAQC2 (ATCC accession number PTA3275).

21. An isolated nucleic acid comprising a coding sequence for the heavy chain of an antibody produced by cell line haAQC2 (ATCC accession number PTA3274).

22. An isolated nucleic acid comprising a coding sequence for the heavy chain of an antibody produced by cell line hsAQC2 (ATCC accession number PTA3356).

23. An isolated nucleic acid comprising a coding sequence for residues 1 to 106 of SEQ ID NO:3.

24. An isolated nucleic acid comprising a coding sequence for residues 1 to 118 of SEQ ID NO:4.

25. A method of treating a subject with an immunological disorder mediated by VLA-1, comprising administering to the subject the composition of claim 14.

26. A method of determining the level of VLA-1 in a tissue, comprising contacting the tissue with the antibody of claim 1, and detecting the binding of the antibody to the tissue, thereby determining the level of VLA-1 in the tissue.

27. A cell of hybridoma mAQC2 (ATCC accession number PTA3273).

28. A cell of cell line hAQC2 (ATCC accession number PTA3275).

29. A cell of cell line haAQC2 (ATCC accession number PTA3274).

30. A cell of cell line hsAQC2 (ATCC accession number PTA3356).

31. A computer for producing a three-dimensional representation of:

(a) a molecular complex, wherein said molecular complex is defined by the set of structure coordinates of a complex of a chimeric I domain of a $\alpha 1\beta 1$ integrin RΔH and a humanized antibody hAQC2, according to Fig. 19; or

(b) a homologue of said molecular complex, said homologue having a root mean square deviation from the backbone atoms of said amino acids of not more than 0.65 Å;

wherein said computer comprises:

(i) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said data comprises at least a portion of the structure coordinates of said complex, according to Fig. 19;

(ii) a working memory for storing instructions for processing said machine-readable data;

(iii) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine-readable data storage medium for processing said machine readable data into said three-dimensional representations; and

(iv) a display coupled to said central-processing unit for displaying said three-dimensional representation.

32. A computer for producing a three-dimensional representation of a molecule or molecular complex comprising:

a) a first binding site defined by structure coordinates of hAQC2 amino acids comprising at least seven of light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101 according to Fig. 19; or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a second binding site that has a root mean square deviation from the backbone atoms of the hAQC2 amino acids of not more than 1.10 Å; and wherein said computer comprises:

(i) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said data comprises the structure coordinates of hAQC2 amino acids comprising at least seven light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101 according to Fig. 19; and

(ii) a working memory for storing instructions for processing said machine-readable data;

(iii) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine-readable data storage medium for processing said machine readable data into said three-dimensional representations;

(iv) a display coupled to said central-processing unit for displaying said three-dimensional representation.

33. A computer for producing a three-dimensional representation of:

(a) a first binding site defined by structure coordinates of hAQC2 amino acids comprising at least seven of light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101, according to Fig. 19; or

(b) a second binding site of a homologue that has a root mean square deviation from the backbone atoms of the hAQC2 amino acids of not more than 1.10 Å;

wherein said computer comprises:

(i) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said data comprises the structure coordinates of hAQC2 amino acid acids selected from a group comprising at least seven of light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101, according to Fig. 19;

(ii) a working memory for storing instructions for processing said machine-readable data;

(iii) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine-readable data storage medium for processing said machine readable data into said three-dimensional representations;

(iv) a display coupled to said central-processing unit for displaying said three-dimensional representation.

34. A method for identifying an inhibitor of an I domain of an integrin comprising the steps of:

(a) using structure coordinates of hAQC2 amino acids comprising at least seven of light chain residues Asn30, Tyr48, Trp90, Ser91, Asn93 and Trp95, and heavy chain residues Ser30, Arg31, Trp47, Ser52, Gly53, His56, Tyr58, Phe99, Gly100 and Asp101, according to Fig. 19 or ± a root mean square deviation from the backbone atoms of said hAQC2 amino acids not more than 1.10 Å, to generate a three-dimensional structure of a binding site;

(b) employing said three-dimensional structure to design or select a potential antagonist;

(c) synthesizing said potential antagonist; and

(d) contacting said potential antagonist with hAQC2 to determine the ability of said potential antagonist to interact with hAQC2, wherein the ability of said potential antagonist to interact with hAQC2 indicates that the potential antagonist is an inhibitor of the I domain.

35. An inhibitor of I domain of integrin identified by the method according to claim 34.

36. A computer for producing a three-dimensional representation of a molecule or molecular complex comprising:

a) a first binding site defined by structure coordinates of I domain amino acid residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294, according to Fig. 19; or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a second binding site that has a root mean square deviation from the backbone atoms of said I domain amino acids not more than 0.92 Å; wherein said computer comprises:

(i) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said data comprises the

structure coordinates of I domain amino acid residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294, according to Fig. 19; and

(ii) a working memory for storing instructions for processing said machine-readable data;

(iii) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine-readable data storage medium for processing said machine readable data into said three-dimensional representations; and

(iv) a display coupled to said central-processing unit for displaying said three-dimensional representation.

37. A computer for producing a three-dimensional representation of:

(a) a first binding site defined by structure coordinates of I domain amino acids residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294, according to Fig. 19; or

(b) a second binding site of a homologue that has a root mean square deviation from the backbone atoms of said I domain amino acids not more than 0.92 Å;

wherein said computer comprises:

(i) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said data comprises structure coordinates of I domain amino residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294, according to Fig. 19; and

(ii) a working memory for storing instructions for processing said machine-readable data;

(iii) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said

machine-readable data storage medium for processing said machine readable data into said three-dimensional representations; and

(iv) a display coupled to said central-processing unit for displaying said three-dimensional representation;

38. A computer for producing a three-dimensional representation of a molecule or molecular complex comprising:

a) a first binding site defined by structure coordinates of I domain amino acids comprising at least three of residues Glu192, Gln218, Arg219, Gly220, and Gly221, according to Fig. 19; or

b) a homologue of said molecule or molecular complex, wherein said homologue comprises a second binding site that has a root mean square deviation from the backbone atoms of said I domain amino acids not more than 0.30 Å; wherein said computer comprises:

(i) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said data comprises the structure coordinates of I domain amino acids comprising at least three of residues Glu192, Gln218, Arg219, Gly220, and Gly221, according to Fig. 19; and

(ii) a working memory for storing instructions for processing said machine-readable data;

(iii) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine-readable data storage medium for processing said machine readable data into said three-dimensional representations; and

(iv) a display coupled to said central-processing unit for displaying said three-dimensional representation;

39. A computer for producing a three-dimensional representation of:

(a) a first binding site defined by structure coordinates of I domain amino acids comprising at least three of residues Glu192, Gln218, Arg219, Gly220, and Gly221, according to Fig. 19; or

(b) a second binding site of a homologue that has a root mean square deviation from the backbone atoms of said I domain amino acids not more than 0.30 Å;

wherein said computer comprises:

(i) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said data comprises the structure coordinates of I domain amino acids comprising at least three of residues Glu192, Gln218, Arg219, Gly220, and Gly221, according to Fig. 19;

(ii) a working memory for storing instructions for processing said machine-readable data;

(iii) a central-processing unit coupled to said working memory and to said machine-readable data storage medium for processing said machine-readable data storage medium for processing said machine readable data into said three-dimensional representations; and

(iv) a display coupled to said central-processing unit for displaying said three-dimensional representation;

40. A method for identifying an inhibitor of an I domain of an integrin comprising the steps of:

(a) using the structure coordinates of I domain amino acids residues Asp154, Ser156, Asn157, Ser158, Tyr160, Glu192, Gln218, Arg219, Gly220, Gly221, Arg222, Gln223, Thr224, Asp257, His261, Asn263, Arg291, and Leu294, according to Fig. 19, to generate a three-dimensional structure of a binding site;

(b) employing said three-dimensional structure to design or select a potential antagonist;

(c) synthesizing said potential antagonist; and

(d) contacting said potential antagonist with I domain to determine the ability of said potential antagonist to interact with I domain, wherein the ability of

said potential antagonist to interact with the I domain indicates that the potential antagonist is an inhibitor of the I domain.

41. A method for identifying an inhibitor of an I domain of an integrin comprising the steps of:

(a) using the structure coordinates of at least three of I domain amino acids comprising residues Glu192, Gln218, Arg219, Gly220, and Gly221, according to Fig. 19, or ± a root mean square deviation from the backbone atoms of said I domain amino acids not more than 0.30 Å, to generate a three-dimensional structure of a binding site;

(b) employing said three-dimensional structure to design or select a potential antagonist;

(c) synthesizing said potential antagonist; and

(d) contacting said potential antagonist with I domain to determine the ability of said potential antagonist to interact with I domain of integrin, wherein the ability of said potential antagonist to interact with the I domain indicates that the potential antagonist is an inhibitor of the I domain.

42. An inhibitor of I domain of integrin identified by the method according to any one of claims 40 and 41.

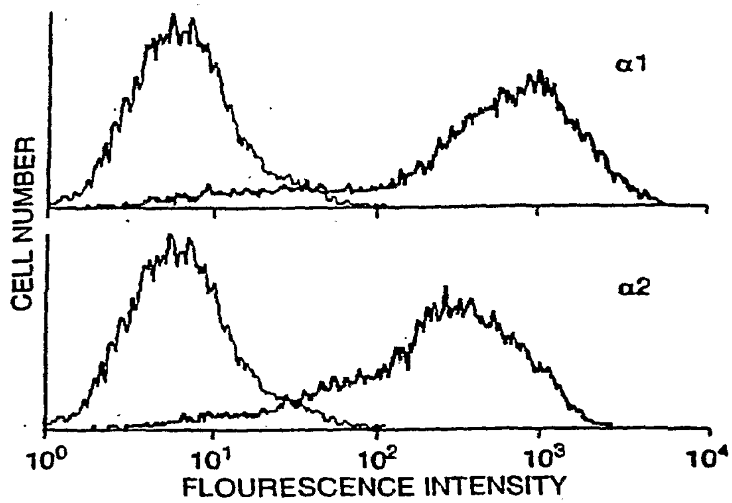

α1
α2
CELL NUMBER
10^0
10^1
10^2
10^3
10^4
FLOURESCENCE INTENSITY

FIG. 1A

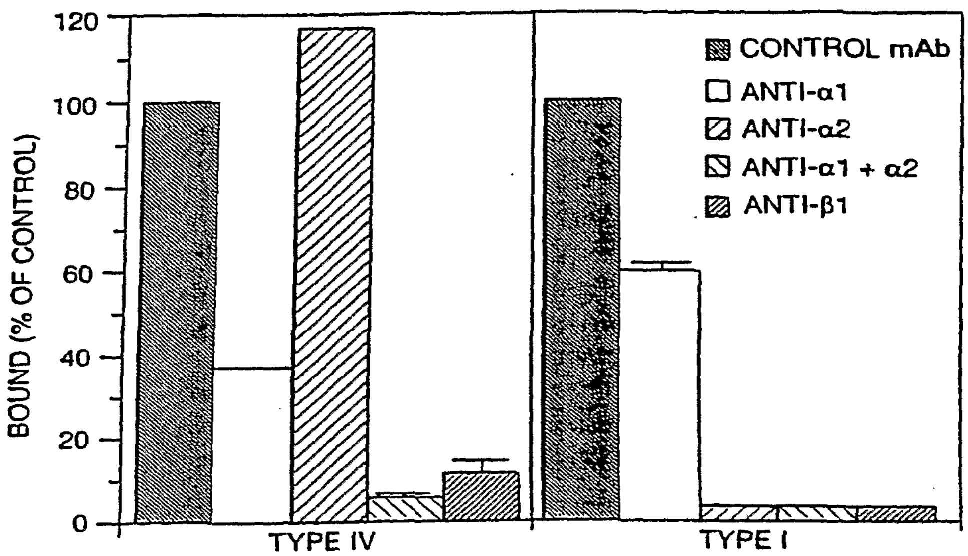

120
100
80
60
40
20
0
BOUND (% OF CONTROL)
CONTROL mAb
ANTI-α1
ANTI-α2
ANTI-α1 + α2
ANTI-β1
TYPE IV
TYPE I

FIG. 1B

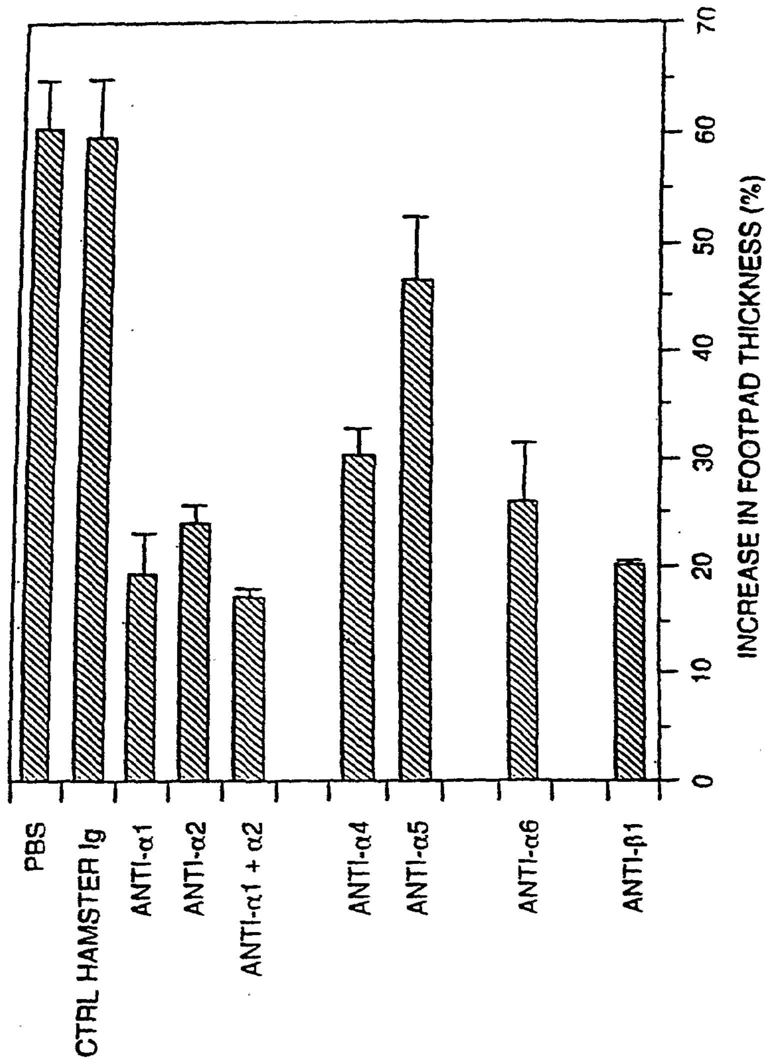

PBS
CTRL HAMSTER Ig
ANTI-α1
ANTI-α2
ANTI-α1 + α2
ANTI-α4
ANTI-α5
ANTI-α6
ANTI-β1
0
10
20
30
40
50
60
70
INCREASE IN FOOTPAD THICKNESS (%)

FIG. 2

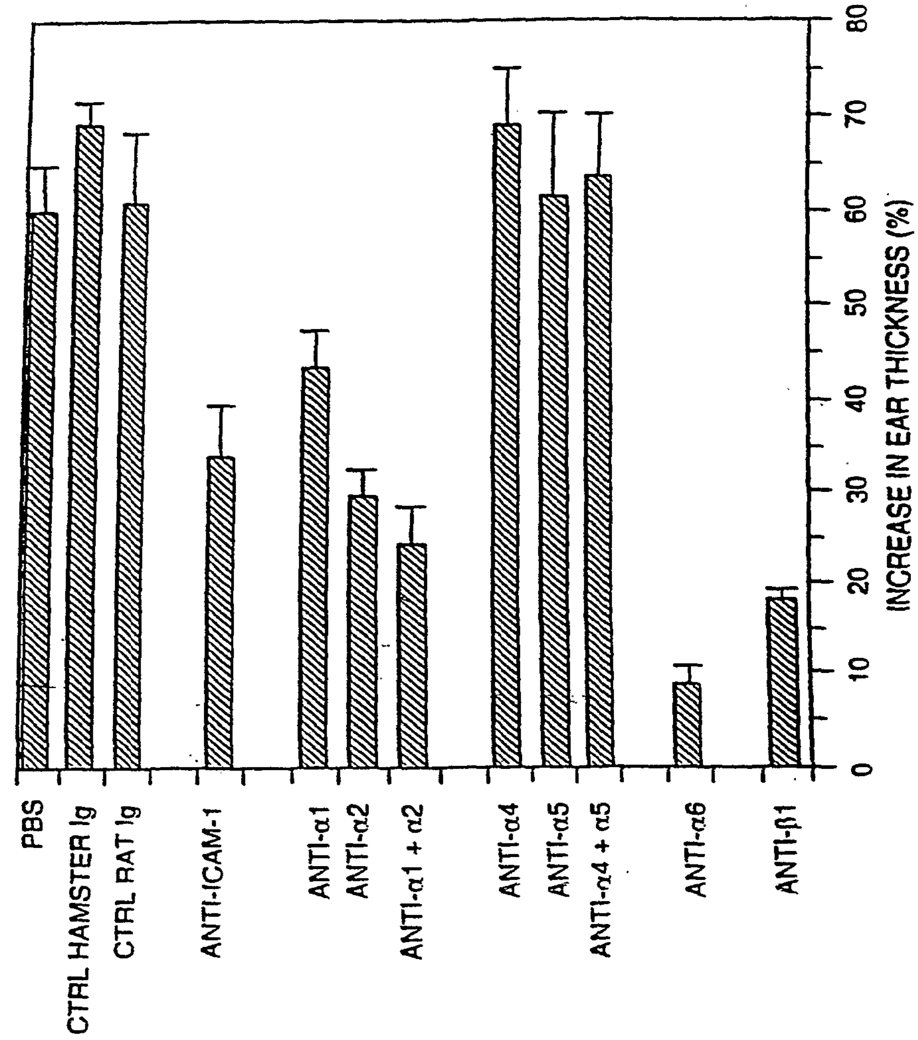

PBS
CTRL HAMSTER Ig
CTRL RAT Ig
ANTI-ICAM-1
ANTI-α1
ANTI-α2
ANTI-α1 + α2
ANTI-α4
ANTI-α5
ANTI-α4 + α5
ANTI-α6
ANTI-β1
0
10
20
30
40
50
60
70
80
INCREASE IN EAR THICKNESS (%)

FIG. 3

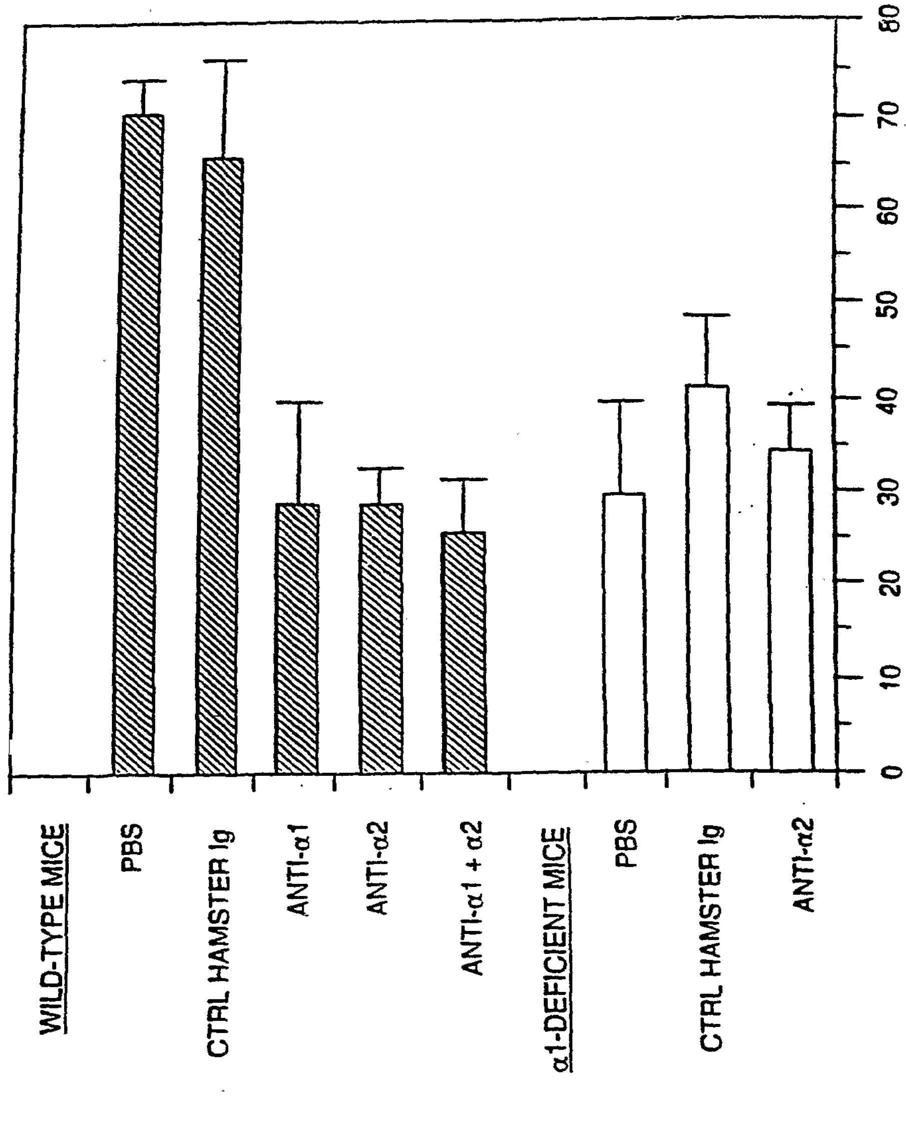

WILD-TYPE MICE
PBS
CTRL HAMSTER Ig
ANTI-α1
ANTI-α2
ANTI-α1 + α2
α1-DEFICIENT MICE
PBS
CTRL HAMSTER Ig
ANTI-α2
0
10
20
30
40
50
60
70
80
INCREASE IN EAR THICKNESS (%)

FIG. 4

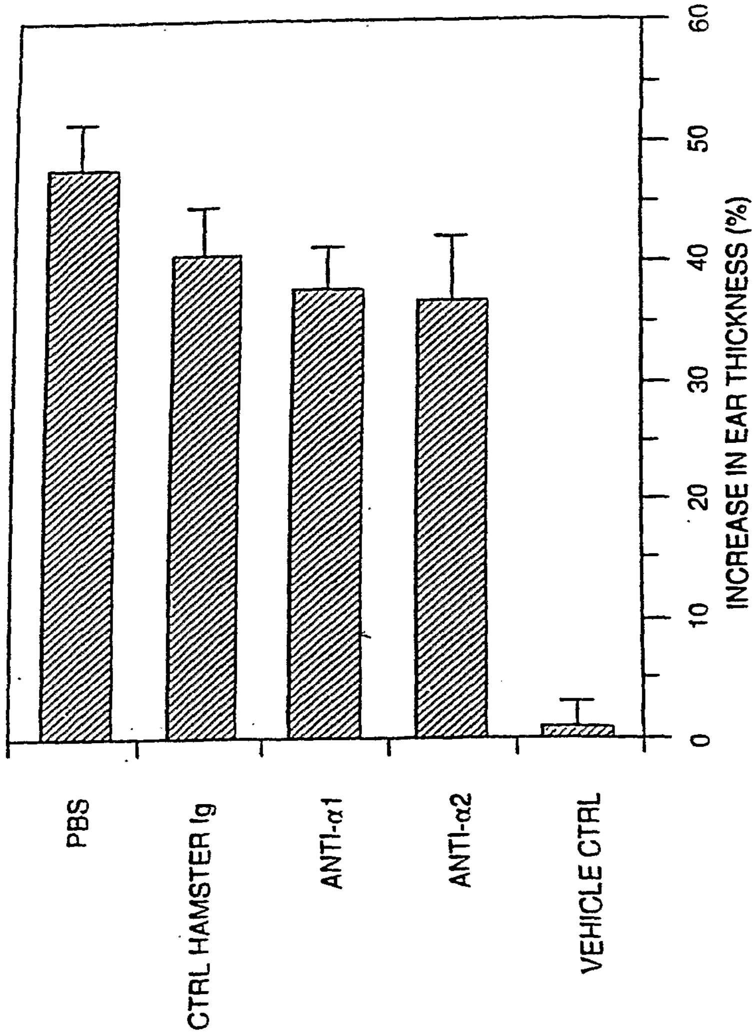

PBS
CTRL HAMSTER Ig
ANTI-α1
ANTI-α2
VEHICLE CTRL
0
10
20
30
40
50
60
INCREASE IN EAR THICKNESS (%)

FIG. 5

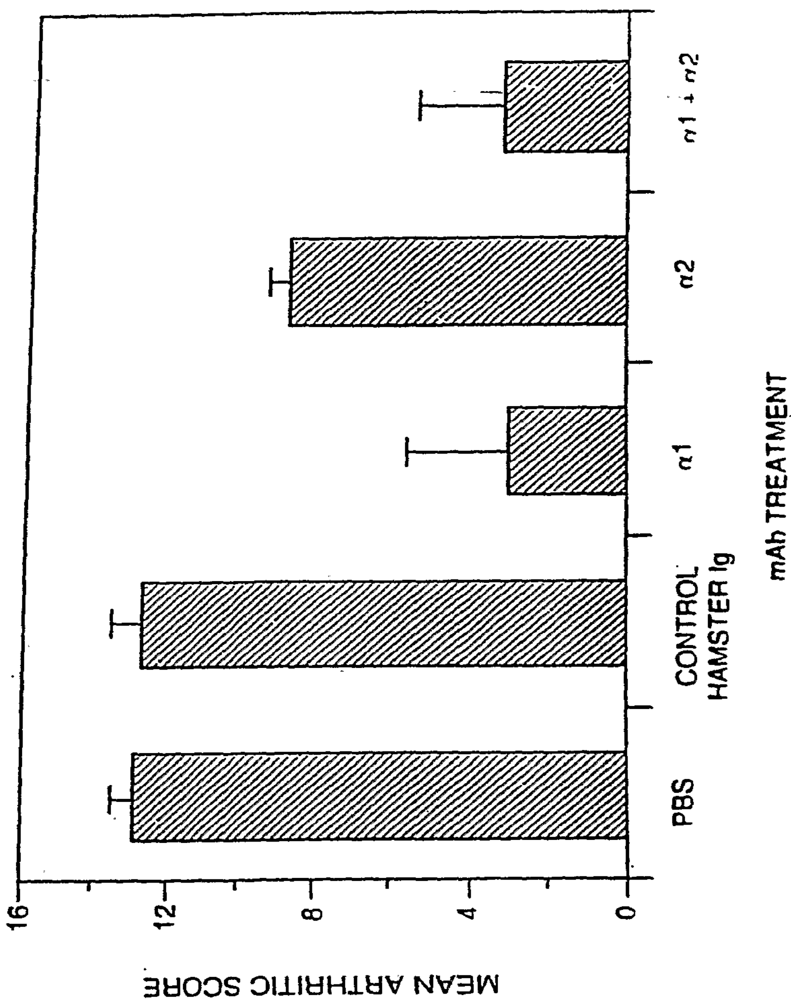

MEAN ARTHRITIC SCORE
16
12
8
4
0
PBS
CONTROL
HAMSTER Ig
α1
α2
α1 + α2
mAb TREATMENT

FIG. 6

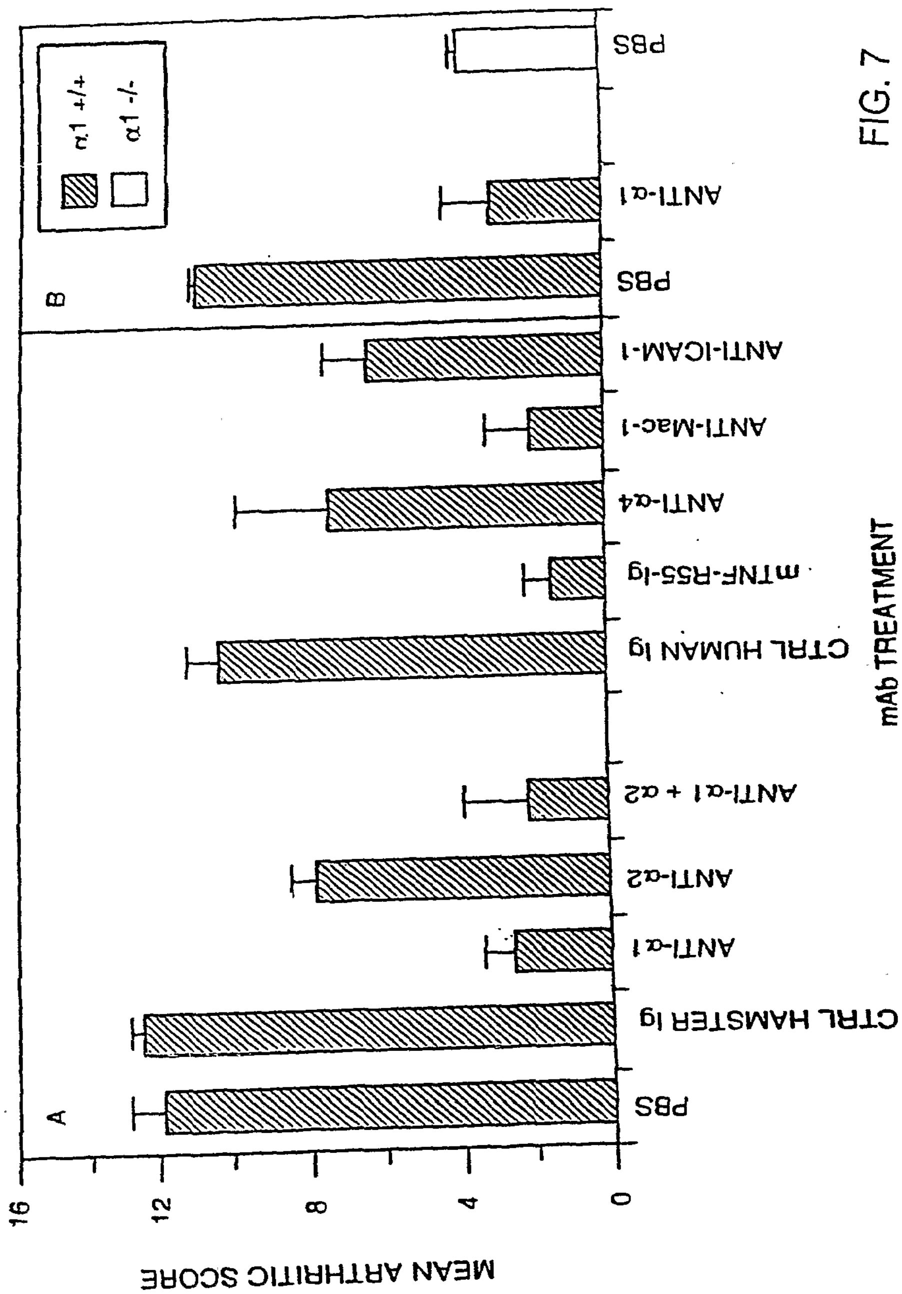

MEAN ARTHRITIC SCORE
16
12
8
4
0
A
B
α1 +/+
α1 -/-
PBS
CTRL HAMSTER Ig
ANTI-α1
ANTI-α2
ANTI-α1 + α2
CTRL HUMAN Ig
mTNF-R55-Ig
ANTI-α4
ANTI-Mac-1
ANTI-ICAM-1
PBS
ANTI-α1
PBS
mAb TREATMENT

FIG. 7

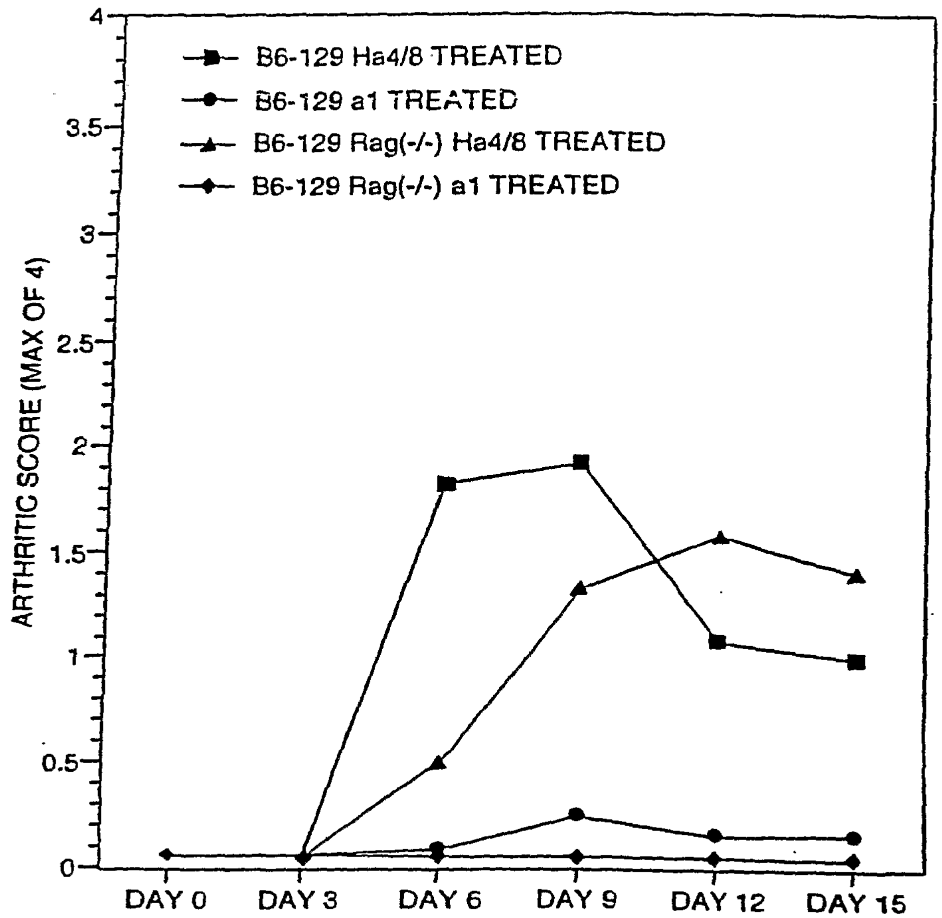

B6-129 Ha4/8 TREATED
B6-129 a1 TREATED
B6-129 Rag(-/-) Ha4/8 TREATED
B6-129 Rag(-/-) a1 TREATED
ARTHRITIC SCORE (MAX OF 4)
4
3.5
3
2.5
2
1.5
1
0.5
0
DAY 0
DAY 3
DAY 6
DAY 9
DAY 12
DAY 15

FIG. 8

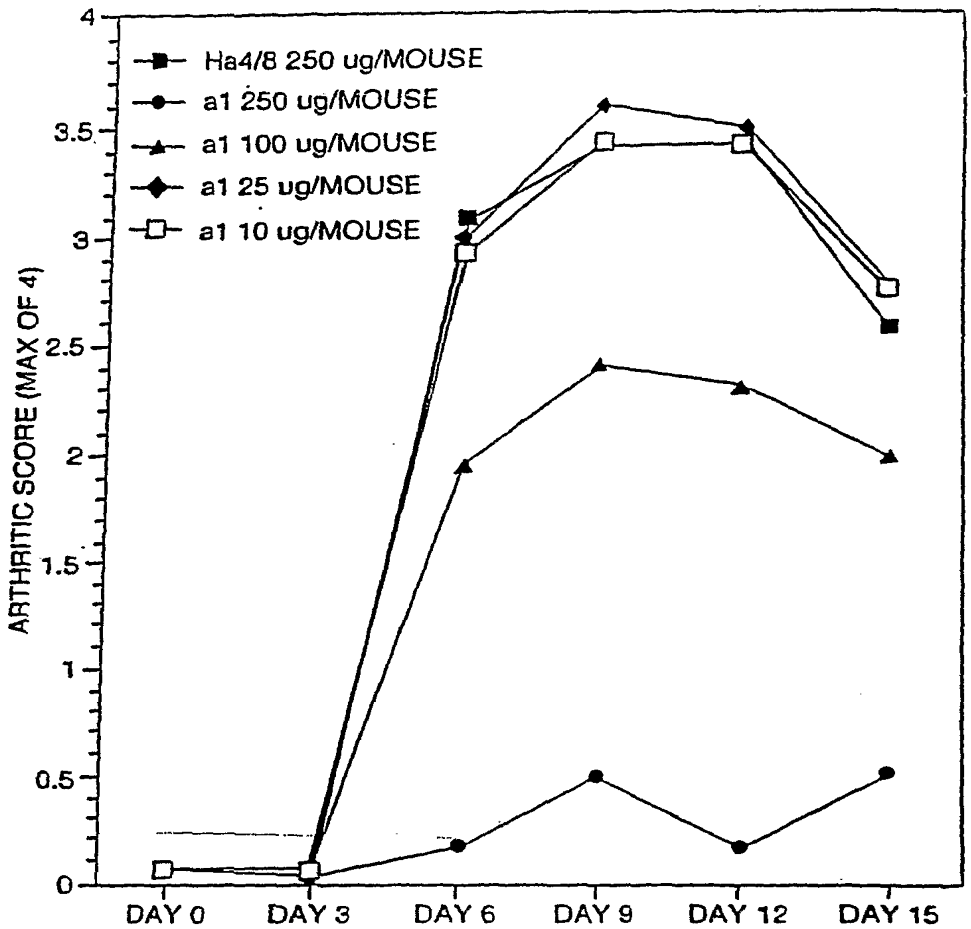

Ha4/8 250 ug/MOUSE
a1 250 ug/MOUSE
a1 100 ug/MOUSE
a1 25 ug/MOUSE
a1 10 ug/MOUSE
ARTHRITIC SCORE (MAX OF 4)
4
3.5
3
2.5
2
1.5
1
0.5
0
DAY 0
DAY 3
DAY 6
DAY 9
DAY 12
DAY 15

FIG. 9

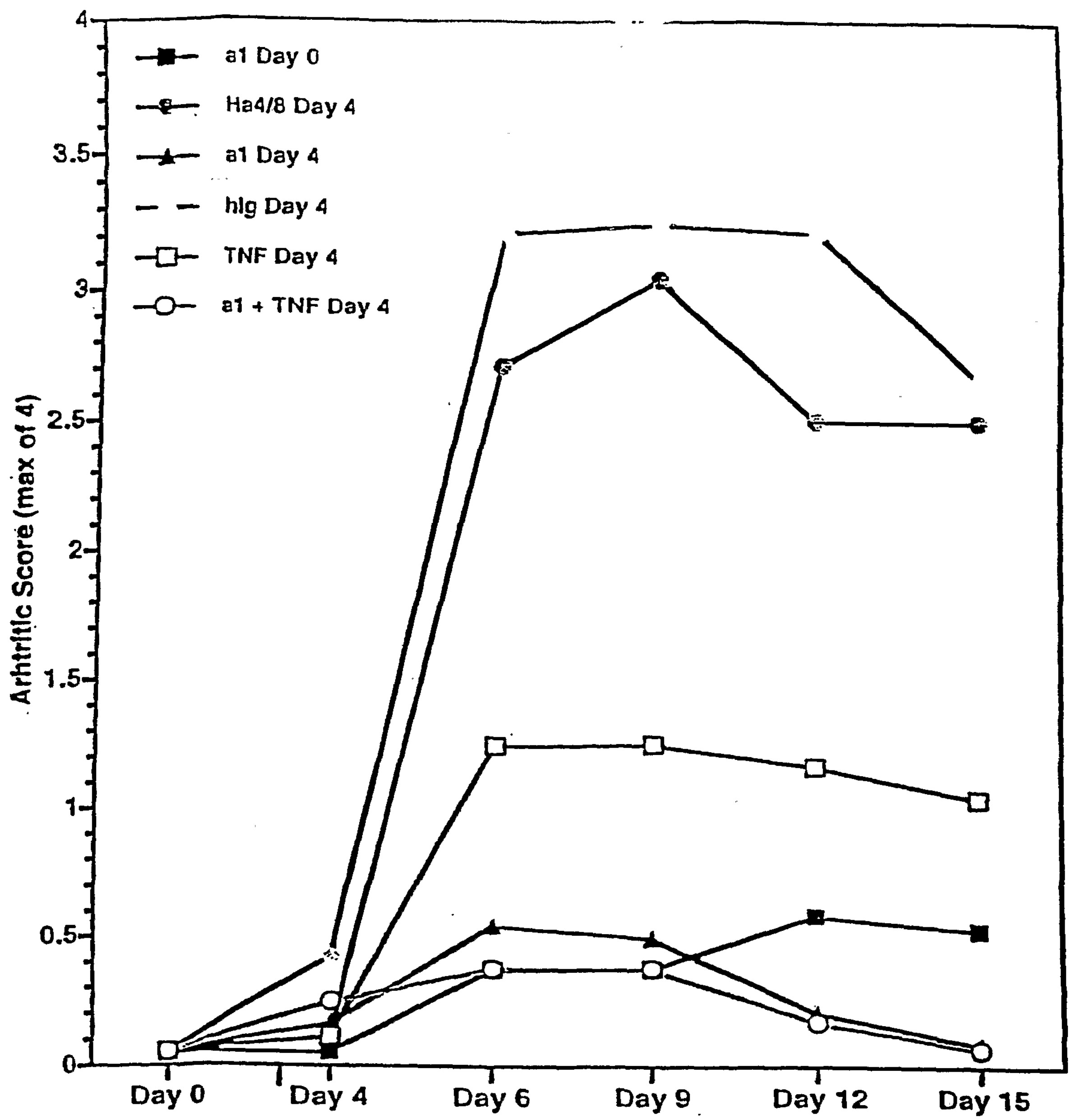

a1 Day 0
Ha4/8 Day 4
a1 Day 4
hIg Day 4
TNF Day 4
a1 + TNF Day 4
Arhtritic Score (max of 4)
4
3.5
3
2.5
2
1.5
1
0.5
0
Day 0
Day 4
Day 6
Day 9
Day 12
Day 15

FIG. 10

```
1    V S P T F Q V V N S F A P V Q E C S T C
                         I
21   L D I V I V L D G S N S I Y P W E S V I
                                     I     T
41   A F L N D L L K R M D I G P K C T C V G
61   I V Q Y G E N V T H E F N L N K Y S S T
81   E E V L V A A K K I G R Q G G L C T M T
                         V Q R G G R
101  A L G I D T A R K E A F T E A R G A R R
           T
121  G V K K V M V I V T D G E S H D N Y R L
                                       H
141  K Q V I Q D C E D E N I Q R F S I A I L
       K
161  G H Y N R G N L S T E K F V E E I K S I
       S
181  A S E P T E K H F F N V S D E L A L V T
201  I V K A L G E R I F A L E A
           T
```

FIG. 11A

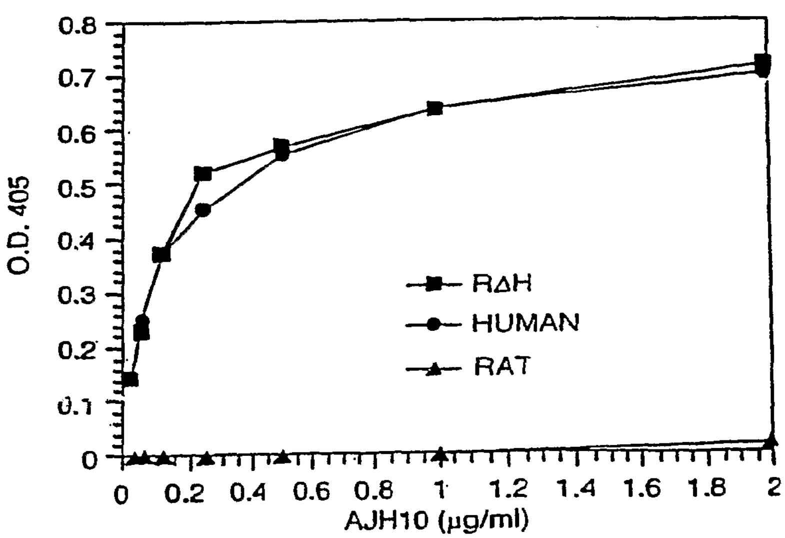


FIG. 11B

1	V S P T F Q V V N S I A P V Q E C S T Q
21	L D I V I V L D G S N S I Y P W D S V T
41	A F L N D L L K R M D I G P K Q T Q V G
61	I V Q Y G E N V T H E F N L N K Y S S T
81	E E V L V A A K K I $\boxed{\text{V Q R G G R Q}}$ T M T
101	A L G T D T A R K E A F T E A R G A R R
121	G V K K V M V I V T D G E S H D N H R L
141	K K V I Q D C E D E N I Q R F S I A I L
161	G S Y N R G N L S T E K F V E E I K S I
181	A S E P T E K H R F N V S D E L A L V T
201	I V K T L G E R I F A L E A

FIG. 12

FIG. 13A

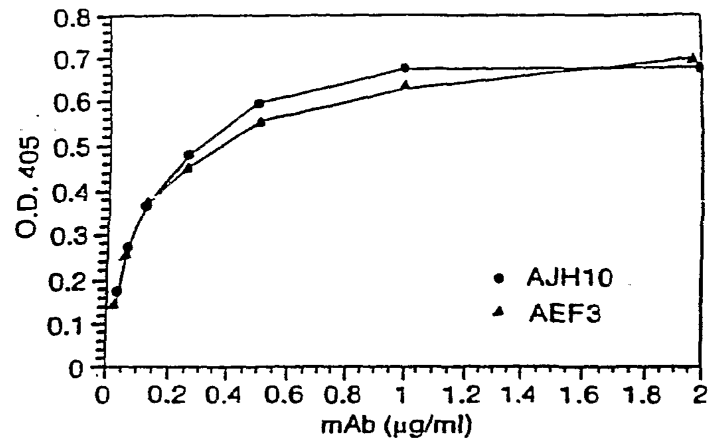


FIG. 13B

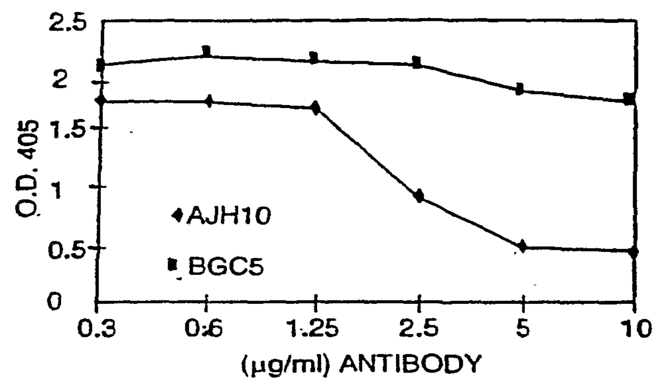
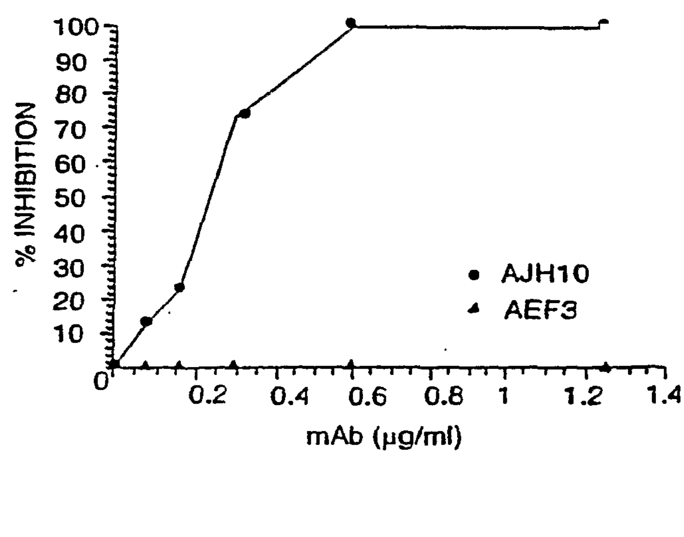


FIG. 13C



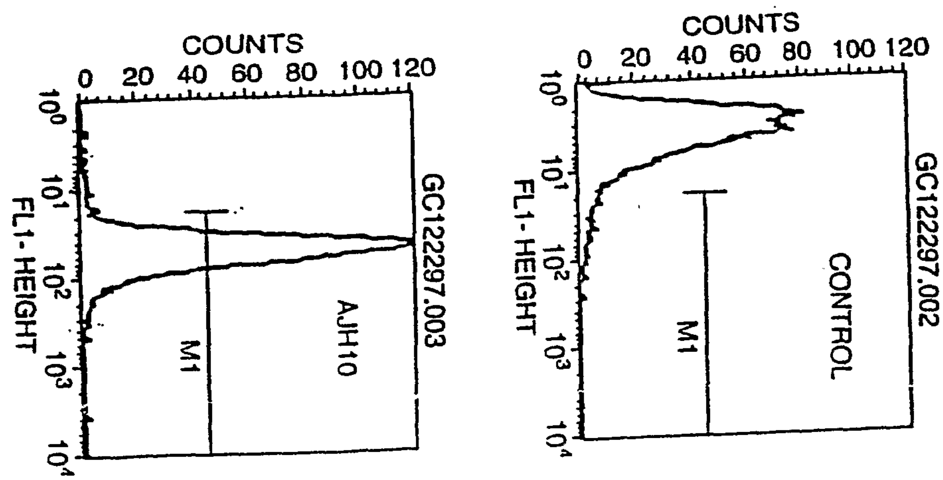

COUNTS
0 20 40 60 80 100 120
10^0
10^1
10^2
10^3
10^4
FL1 - HEIGHT
M1
AJH10
GC122297.003
COUNTS
0 20 40 60 80 100 120
10^0
10^1
10^2
10^3
10^4
FL1 - HEIGHT
M1
CONTROL
GC122297.002

FIG. 14

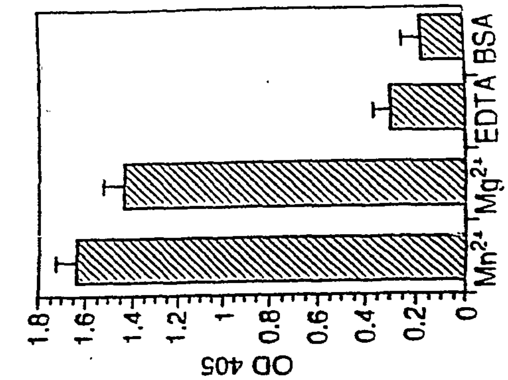


FIG. 15C

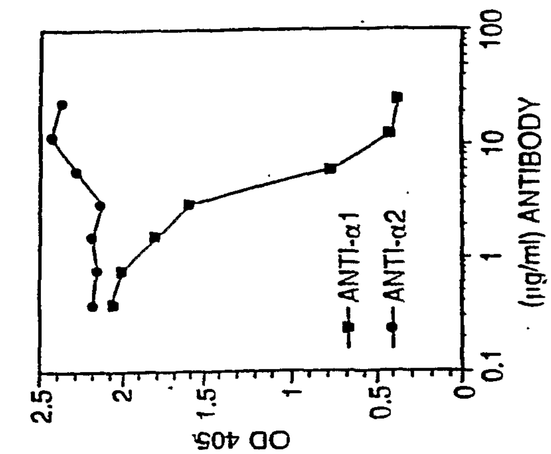


FIG. 15B

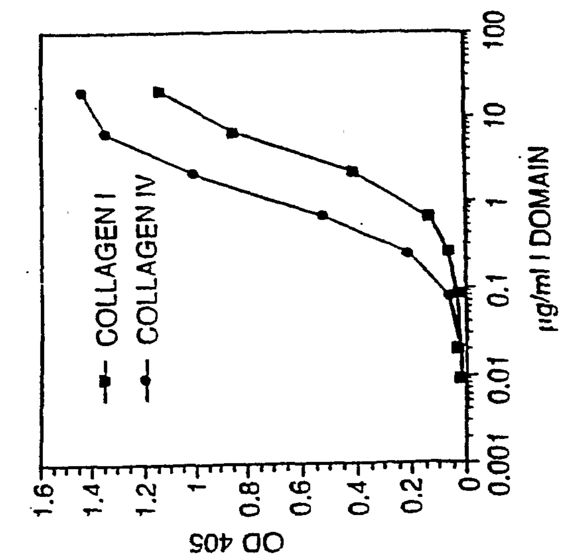
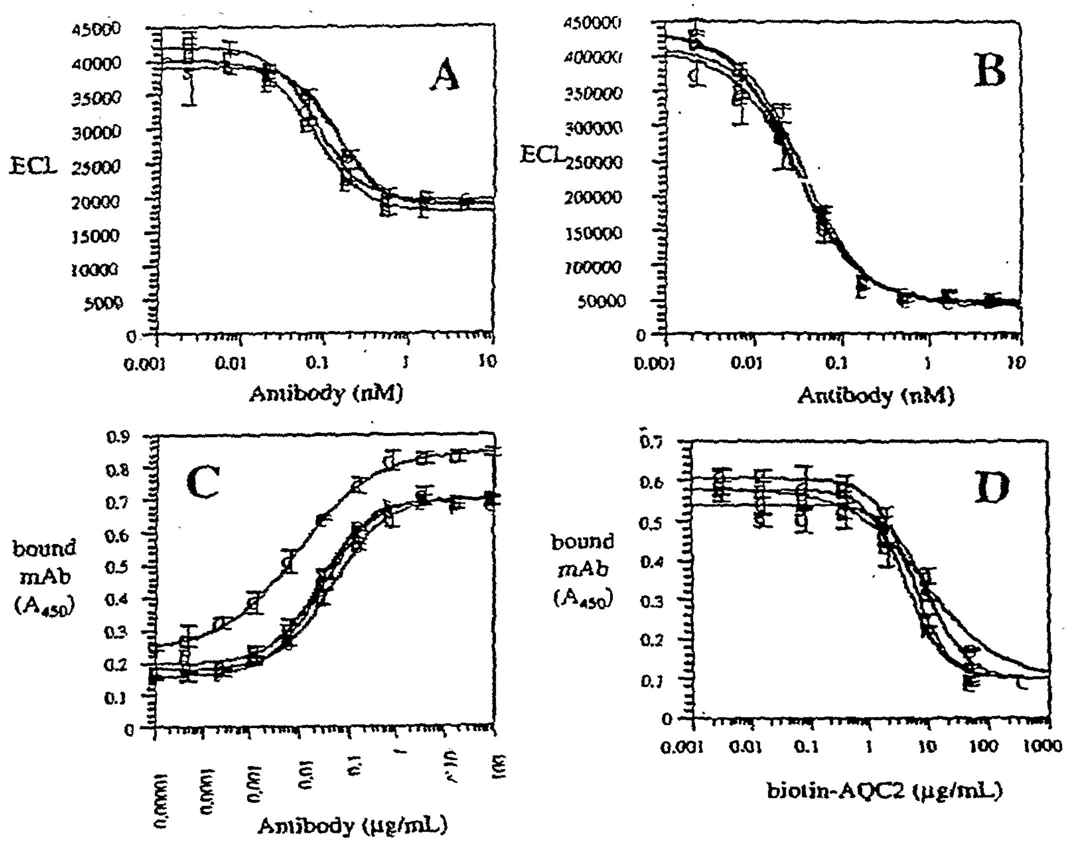


FIG. 15A


A
B
C
D
ECL
bound mAb (A_{450})
Antibody (nM)
Antibody (µg/mL)
biotin-AQC2 (µg/mL)
45000
40000
35000
30000
25000
20000
15000
10000
5000
0
450000
400000
350000
300000
250000
200000
150000
100000
50000
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.001
0.01
0.1
1
10
100
1000

FIGS. 16 A, B, C, D

Humanized AQ.C2 Antibodies tested by FACS on K562 α 1 cells

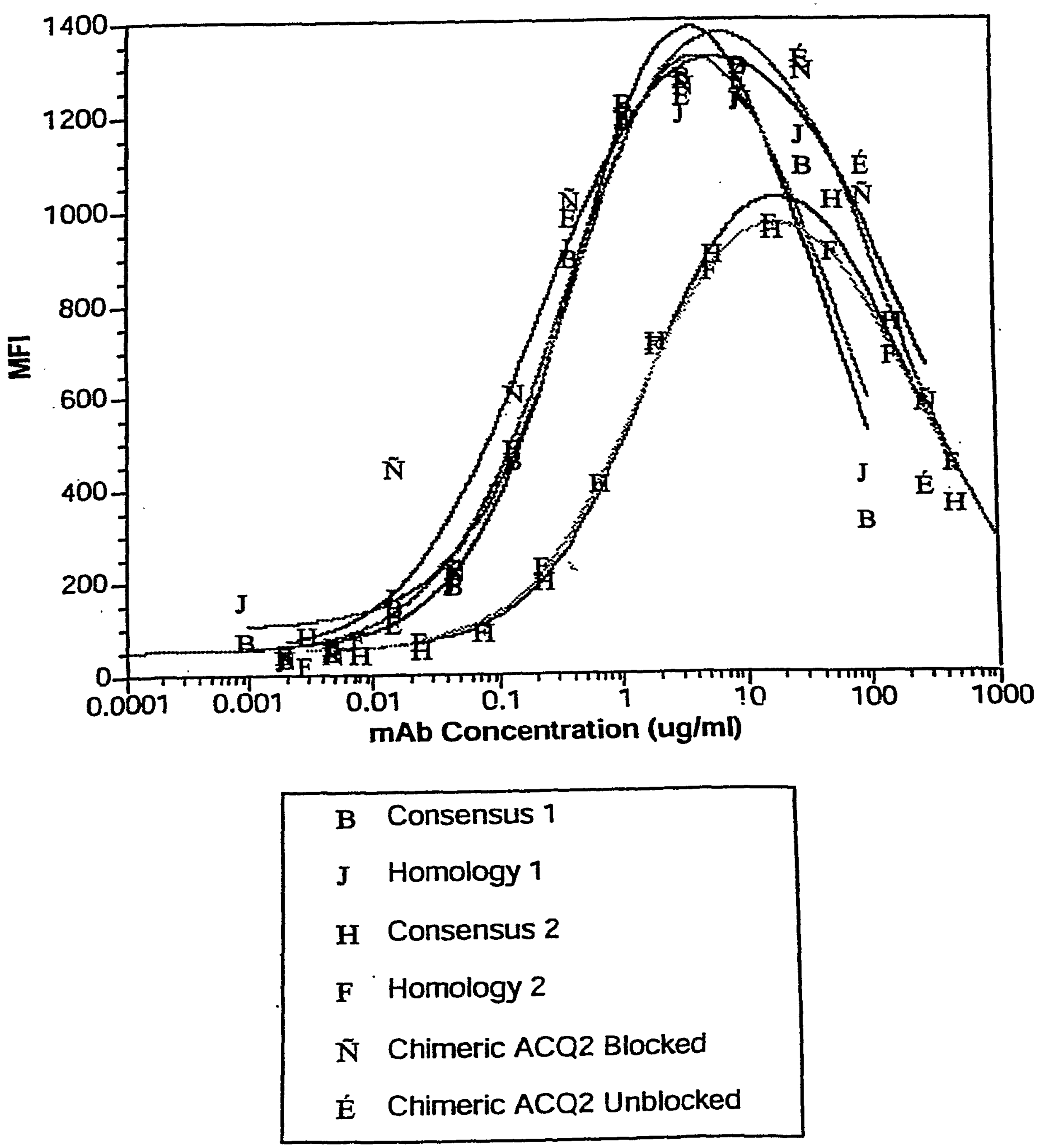


FIG. 17

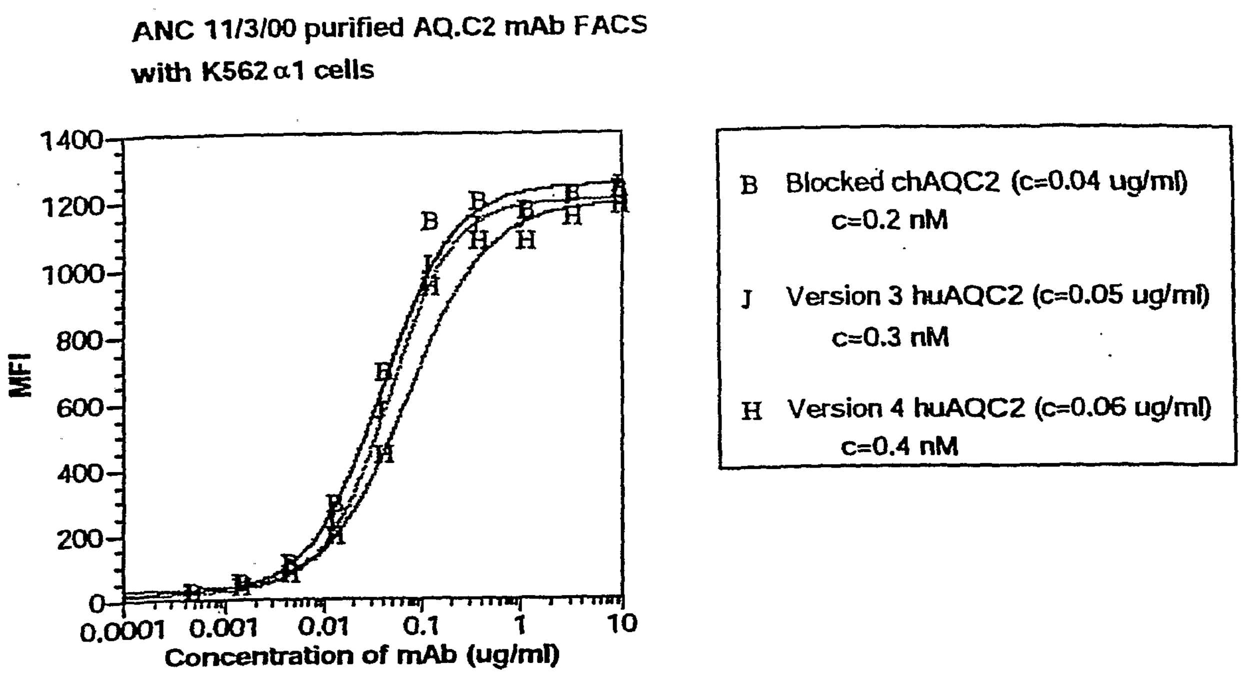

ANC 11/3/00 purified AQ.C2 mAb FACS
with K562 α1 cells
MFI
1400
1200
1000
800
600
400
200
0
0.0001
0.001
0.01
0.1
1
10
Concentration of mAb (ug/ml)
B Blocked chAQC2 (c=0.04 ug/ml)
c=0.2 nM
J Version 3 huAQC2 (c=0.05 ug/ml)
c=0.3 nM
H Version 4 huAQC2 (c=0.06 ug/ml)
c=0.4 nM

FIG. 18

Fig. 19: A-1

ATOM	1	CB	THR	145	131.250	52.244	-9.297	1.00	82.68	A	C
ATOM	2	OG1	THR	145	131.373	51.127	-10.191	1.00	82.68	A	O
ATOM	3	CG2	THR	145	132.601	52.936	-9.145	1.00	82.68	A	C
ATOM	4	C	THR	145	129.280	51.301	-8.080	1.00	146.54	A	C
ATOM	5	O	THR	145	128.489	51.352	-7.134	1.00	146.94	A	O
ATOM	6	N	THR	145	131.576	50.663	-7.360	1.00	144.92	A	N
ATOM	7	CA	THR	145	130.726	51.757	-7.915	1.00	144.52	A	C
ATOM	8	N	GLN	146	128.941	50.856	-9.288	1.00	36.14	A	N
ATOM	9	CA	GLN	146	127.592	50.397	-9.569	1.00	34.29	A	C
ATOM	10	CB	GLN	146	127.046	51.086	-10.823	1.00	99.89	A	C
ATOM	11	CG	GLN	146	127.887	50.902	-12.065	1.00	99.89	A	C
ATOM	12	CD	GLN	146	127.274	51.575	-13.279	1.00	99.89	A	C
ATOM	13	OE1	GLN	146	127.787	51.454	-14.392	1.00	99.89	A	O
ATOM	14	NE2	GLN	146	126.170	52.290	-13.070	1.00	99.89	A	N
ATOM	15	C	GLN	146	127.535	48.883	-9.721	1.00	34.71	A	C
ATOM	16	O	GLN	146	128.084	48.314	-10.667	1.00	36.57	A	O
ATOM	17	N	LEU	147	126.876	48.240	-8.762	1.00	33.54	A	N
ATOM	18	CA	LEU	147	126.718	46.794	-8.767	1.00	32.67	A	C
ATOM	19	CB	LEU	147	127.491	46.143	-7.609	1.00	35.25	A	C
ATOM	20	CG	LEU	147	128.963	46.398	-7.301	1.00	35.44	A	C
ATOM	21	CD1	LEU	147	129.205	47.877	-7.087	1.00	30.65	A	C
ATOM	22	CD2	LEU	147	129.325	45.637	-6.037	1.00	35.29	A	C
ATOM	23	C	LEU	147	125.247	46.451	-8.575	1.00	31.65	A	C
ATOM	24	O	LEU	147	124.506	47.194	-7.939	1.00	32.95	A	O
ATOM	25	N	ASP	148	124.832	45.325	-9.142	1.00	25.19	A	N
ATOM	26	CA	ASP	148	123.477	44.817	-8.976	1.00	22.65	A	C
ATOM	27	CB	ASP	148	122.907	44.329	-10.302	1.00	27.55	A	C
ATOM	28	CG	ASP	148	122.330	45.446	-11.125	1.00	27.17	A	C
ATOM	29	OD1	ASP	148	121.787	45.158	-12.208	1.00	26.28	A	O
ATOM	30	OD2	ASP	148	122.413	46.612	-10.686	1.00	25.35	A	O
ATOM	31	C	ASP	148	123.664	43.638	-8.025	1.00	19.03	A	C
ATOM	32	O	ASP	148	124.119	42.567	-8.422	1.00	18.33	A	O
ATOM	33	N	ILE	149	123.341	43.848	-6.760	1.00	16.75	A	N
ATOM	34	CA	ILE	149	123.502	42.809	-5.761	1.00	15.69	A	C
ATOM	35	CB	ILE	149	124.041	43.391	-4.442	1.00	18.53	A	C
ATOM	36	CG2	ILE	149	124.401	42.269	-3.485	1.00	13.54	A	C
ATOM	37	CG1	ILE	149	125.271	44.251	-4.718	1.00	14.25	A	C
ATOM	38	CD1	ILE	149	125.819	44.932	-3.497	1.00	17.00	A	C
ATOM	39	C	ILE	149	122.185	42.129	-5.456	1.00	17.34	A	C
ATOM	40	O	ILE	149	121.191	42.794	-5.181	1.00	17.74	A	O
ATOM	41	N	VAL	150	122.175	40.805	-5.526	1.00	11.00	A	N
ATOM	42	CA	VAL	150	120.987	40.036	-5.193	1.00	12.56	A	C
ATOM	43	CB	VAL	150	120.571	39.089	-6.336	1.00	16.85	A	C
ATOM	44	CG1	VAL	150	119.409	38.210	-5.885	1.00	19.04	A	C
ATOM	45	CG2	VAL	150	120.164	39.894	-7.555	1.00	18.66	A	C
ATOM	46	C	VAL	150	121.367	39.212	-3.970	1.00	10.12	A	C
ATOM	47	O	VAL	150	122.387	38.526	-3.973	1.00	8.27	A	O
ATOM	48	N	ILE	151	120.573	39.303	-2.912	1.00	20.50	A	N
ATOM	49	CA	ILE	151	120.856	38.537	-1.699	1.00	19.30	A	C
ATOM	50	CB	ILE	151	120.653	39.392	-0.439	1.00	14.22	A	C
ATOM	51	CG2	ILE	151	121.039	38.601	0.785	1.00	10.58	A	C
ATOM	52	CG1	ILE	151	121.515	40.659	-0.532	1.00	12.64	A	C
ATOM	53	CD1	ILE	151	121.283	41.660	0.593	1.00	14.62	A	C
ATOM	54	C	ILE	151	119.931	37.329	-1.646	1.00	17.42	A	C
ATOM	55	O	ILE	151	118.715	37.459	-1.777	1.00	17.66	A	O
ATOM	56	N	VAL	152	120.511	36.150	-1.470	1.00	17.56	A	N
ATOM	57	CA	VAL	152	119.741	34.915	-1.428	1.00	18.41	A	C
ATOM	58	CB	VAL	152	120.395	33.849	-2.309	1.00	11.45	A	C
ATOM	59	CG1	VAL	152	119.470	32.664	-2.460	1.00	10.58	A	C
ATOM	60	CG2	VAL	152	120.758	34.458	-3.667	1.00	7.89	A	C
ATOM	61	C	VAL	152	119.675	34.404	-0.003	1.00	16.31	A	C
ATOM	62	O	VAL	152	120.602	33.755	0.469	1.00	9.91	A	O
ATOM	63	N	LEU	153	118.568	34.692	0.672	1.00	19.79	A	N
ATOM	64	CA	LEU	153	118.367	34.297	2.061	1.00	19.90	A	C
ATOM	65	CB	LEU	153	117.530	35.361	2.766	1.00	21.44	A	C
ATOM	66	CG	LEU	153	118.250	36.403	3.623	1.00	23.22	A	C
ATOM	67	CD1	LEU	153	119.699	36.561	3.185	1.00	23.73	A	C
ATOM	68	CD2	LEU	153	117.494	37.721	3.530	1.00	25.76	A	C
ATOM	69	C	LEU	153	117.732	32.929	2.300	1.00	20.96	A	C
ATOM	70	O	LEU	153	116.724	32.574	1.690	1.00	19.96	A	O
ATOM	71	N	ASP	154	118.336	32.165	3.200	1.00	19.89	A	N
ATOM	72	CA	ASP	154	117.820	30.854	3.554	1.00	19.37	A	C
ATOM	73	CB	ASP	154	118.952	29.983	4.129	1.00	22.72	A	C

Fig. 19: A-2

ATOM	74	CG	ASP	154	118.486	28.601	4.546	1.00	21.92	A	C
ATOM	75	OD1	ASP	154	117.266	28.363	4.537	1.00	25.43	A	O
ATOM	76	OD2	ASP	154	119.340	27.754	4.893	1.00	18.24	A	O
ATOM	77	C	ASP	154	116.770	31.153	4.623	1.00	22.71	A	C
ATOM	78	O	ASP	154	117.062	31.802	5.630	1.00	19.03	A	O
ATOM	79	N	GLY	155	115.540	30.718	4.393	1.00	3.06	A	N
ATOM	80	CA	GLY	155	114.491	30.948	5.370	1.00	5.13	A	C
ATOM	81	C	GLY	155	113.840	29.638	5.788	1.00	6.39	A	C
ATOM	82	O	GLY	155	112.751	29.633	6.368	1.00	8.88	A	O
ATOM	83	N	SER	156	114.512	28.521	5.494	1.00	19.70	A	N
ATOM	84	CA	SER	156	114.011	27.191	5.832	1.00	24.28	A	C
ATOM	85	CB	SER	156	114.994	26.111	5.353	1.00	33.45	A	C
ATOM	86	OG	SER	156	116.261	26.252	5.967	1.00	36.37	A	O
ATOM	87	C	SER	156	113.773	27.054	7.330	1.00	21.27	A	C
ATOM	88	O	SER	156	114.270	27.843	8.128	1.00	24.45	A	O
ATOM	89	N	ASN	157	113.008	26.037	7.700	1.00	21.98	A	N
ATOM	90	CA	ASN	157	112.686	25.802	9.091	1.00	19.06	A	C
ATOM	91	CB	ASN	157	112.027	24.435	9.247	1.00	21.82	A	C
ATOM	92	CG	ASN	157	110.586	24.434	8.785	1.00	23.31	A	C
ATOM	93	OD1	ASN	157	109.944	23.385	8.706	1.00	20.38	A	O
ATOM	94	ND2	ASN	157	110.066	25.612	8.479	1.00	20.59	A	N
ATOM	95	C	ASN	157	113.859	25.913	10.048	1.00	17.03	A	C
ATOM	96	O	ASN	157	113.720	26.498	11.132	1.00	15.01	A	O
ATOM	97	N	SER	158	115.006	25.367	9.653	1.00	15.99	A	N
ATOM	98	CA	SER	158	116.179	25.378	10.510	1.00	14.20	A	C
ATOM	99	CB	SER	158	117.327	24.603	9.864	1.00	26.18	A	C
ATOM	100	OG	SER	158	117.597	25.067	8.562	1.00	28.89	A	O
ATOM	101	C	SER	158	116.656	26.753	10.941	1.00	14.97	A	C
ATOM	102	O	SER	158	117.053	26.930	12.097	1.00	12.14	A	O
ATOM	103	N	ILE	159	116.623	27.730	10.039	1.00	8.33	A	N
ATOM	104	CA	ILE	159	117.050	29.083	10.379	1.00	12.93	A	C
ATOM	105	CB	ILE	159	116.801	30.035	9.193	1.00	9.66	A	C
ATOM	106	CG2	ILE	159	117.138	31.479	9.592	1.00	9.57	A	C
ATOM	107	CG1	ILE	159	117.650	29.609	8.000	1.00	14.44	A	C
ATOM	108	CD1	ILE	159	119.134	29.804	8.204	1.00	19.60	A	C
ATOM	109	C	ILE	159	116.292	29.604	11.616	1.00	17.24	A	C
ATOM	110	O	ILE	159	115.059	29.575	11.659	1.00	16.65	A	O
ATOM	111	N	TYR	160	117.032	30.084	12.611	1.00	29.54	A	N
ATOM	112	CA	TYR	160	116.438	30.600	13.849	1.00	31.67	A	C
ATOM	113	CB	TYR	160	115.775	29.455	14.639	1.00	16.89	A	C
ATOM	114	CG	TYR	160	115.094	29.869	15.941	1.00	13.65	A	C
ATOM	115	CD1	TYR	160	113.717	30.089	15.993	1.00	16.07	A	C
ATOM	116	CE1	TYR	160	113.088	30.466	17.186	1.00	13.67	A	C
ATOM	117	CD2	TYR	160	115.828	30.038	17.116	1.00	11.30	A	C
ATOM	118	CE2	TYR	160	115.211	30.416	18.304	1.00	15.01	A	C
ATOM	119	CZ	TYR	160	113.841	30.627	18.338	1.00	14.36	A	C
ATOM	120	OH	TYR	160	113.227	30.987	19.522	1.00	19.36	A	O
ATOM	121	C	TYR	160	117.498	31.264	14.734	1.00	33.39	A	C
ATOM	122	O	TYR	160	118.567	30.703	14.970	1.00	39.31	A	O
ATOM	123	N	PRO	161	117.206	32.467	15.248	1.00	31.87	A	N
ATOM	124	CD	PRO	161	117.988	33.002	16.380	1.00	14.17	A	C
ATOM	125	CA	PRO	161	115.969	33.234	15.055	1.00	30.15	A	C
ATOM	126	CB	PRO	161	115.831	33.976	16.379	1.00	18.55	A	C
ATOM	127	CG	PRO	161	117.278	34.291	16.703	1.00	21.71	A	C
ATOM	128	C	PRO	161	116.038	34.183	13.852	1.00	28.81	A	C
ATOM	129	O	PRO	161	117.074	34.792	13.580	1.00	28.13	A	O
ATOM	130	N	TRP	162	114.919	34.320	13.149	1.00	29.23	A	N
ATOM	131	CA	TRP	162	114.839	35.170	11.967	1.00	30.30	A	C
ATOM	132	CB	TRP	162	113.388	35.250	11.493	1.00	29.17	A	C
ATOM	133	CG	TRP	162	113.214	35.826	10.120	1.00	29.69	A	C
ATOM	134	CD2	TRP	162	113.838	35.375	8.912	1.00	24.53	A	C
ATOM	135	CE2	TRP	162	113.338	36.175	7.859	1.00	28.08	A	C
ATOM	136	CE3	TRP	162	114.768	34.373	8.615	1.00	23.94	A	C
ATOM	137	CD1	TRP	162	112.387	36.854	9.758	1.00	28.88	A	C
ATOM	138	NE1	TRP	162	112.455	37.071	8.403	1.00	30.75	A	N
ATOM	139	CZ2	TRP	162	113.741	36.000	6.532	1.00	26.62	A	C
ATOM	140	CZ3	TRP	162	115.167	34.202	7.288	1.00	22.27	A	C
ATOM	141	CH2	TRP	162	114.652	35.012	6.268	1.00	27.18	A	C
ATOM	142	C	TRP	162	115.381	36.579	12.210	1.00	32.08	A	C
ATOM	143	O	TRP	162	116.074	37.133	11.352	1.00	31.23	A	O
ATOM	144	N	GLU	163	115.077	37.147	13.381	1.00	25.22	A	N
ATOM	145	CA	GLU	163	115.510	38.504	13.734	1.00	27.00	A	C
ATOM	146	CB	GLU	163	115.108	38.857	15.172	1.00	105.95	A	C

Fig. 19: A-3

ATOM	147	CG	GLU	163	115.906	38.145	16.248	1.00	112.26	A	C
ATOM	148	CD	GLU	163	115.816	38.833	17.603	1.00	114.40	A	C
ATOM	149	OE1	GLU	163	116.310	39.975	17.732	1.00	116.11	A	O
ATOM	150	OE2	GLU	163	115.253	38.232	18.541	1.00	113.36	A	O
ATOM	151	C	GLU	163	117.008	38.723	13.557	1.00	26.66	A	C
ATOM	152	O	GLU	163	117.448	39.799	13.136	1.00	22.83	A	O
ATOM	153	N	SER	164	117.800	37.709	13.865	1.00	20.71	A	N
ATOM	154	CA	SER	164	119.241	37.850	13.715	1.00	17.90	A	C
ATOM	155	CB	SER	164	119.955	36.647	14.335	1.00	27.61	A	C
ATOM	156	OG	SER	164	119.716	36.582	15.731	1.00	33.50	A	O
ATOM	157	C	SER	164	119.601	37.988	12.235	1.00	18.66	A	C
ATOM	158	O	SER	164	120.436	38.813	11.863	1.00	21.86	A	O
ATOM	159	N	VAL	165	118.956	37.179	11.398	1.00	9.03	A	N
ATOM	160	CA	VAL	165	119.189	37.213	9.961	1.00	8.42	A	C
ATOM	161	CB	VAL	165	118.303	36.166	9.226	1.00	21.53	A	C
ATOM	162	CG1	VAL	165	118.296	36.430	7.721	1.00	22.92	A	C
ATOM	163	CG2	VAL	165	118.826	34.760	9.505	1.00	24.53	A	C
ATOM	164	C	VAL	165	118.873	38.595	9.411	1.00	9.58	A	C
ATOM	165	O	VAL	165	119.610	39.131	8.574	1.00	11.40	A	O
ATOM	166	N	ILE	166	117.772	39.169	9.887	1.00	17.73	A	N
ATOM	167	CA	ILE	166	117.351	40.482	9.427	1.00	17.05	A	C
ATOM	168	CB	ILE	166	115.903	40.763	9.840	1.00	21.02	A	C
ATOM	169	CG2	ILE	166	115.489	42.162	9.413	1.00	20.23	A	C
ATOM	170	CG1	ILE	166	114.997	39.737	9.164	1.00	20.88	A	C
ATOM	171	CD1	ILE	166	113.538	39.919	9.499	1.00	17.28	A	C
ATOM	172	C	ILE	166	118.281	41.564	9.929	1.00	16.50	A	C
ATOM	173	O	ILE	166	118.560	42.520	9.206	1.00	18.25	A	O
ATOM	174	N	ALA	167	118.774	41.413	11.157	1.00	25.46	A	N
ATOM	175	CA	ALA	167	119.711	42.391	11.710	1.00	26.06	A	C
ATOM	176	CB	ALA	167	120.095	42.021	13.100	1.00	7.73	A	C
ATOM	177	C	ALA	167	120.941	42.371	10.823	1.00	27.27	A	C
ATOM	178	O	ALA	167	121.546	43.414	10.544	1.00	23.87	A	O
ATOM	179	N	PHE	168	121.303	41.167	10.383	1.00	18.13	A	N
ATOM	180	CA	PHE	168	122.442	40.989	9.498	1.00	16.65	A	C
ATOM	181	CB	PHE	168	122.626	39.513	9.158	1.00	32.51	A	C
ATOM	182	CG	PHE	168	123.514	39.273	7.970	1.00	31.01	A	C
ATOM	183	CD1	PHE	168	122.968	39.066	6.701	1.00	32.61	A	C
ATOM	184	CD2	PHE	168	124.894	39.290	8.106	1.00	29.32	A	C
ATOM	185	CE1	PHE	168	123.792	38.882	5.585	1.00	31.09	A	C
ATOM	186	CE2	PHE	168	125.724	39.109	7.000	1.00	31.14	A	C
ATOM	187	CZ	PHE	168	125.173	38.906	5.738	1.00	33.63	A	C
ATOM	188	C	PHE	168	122.222	41.796	8.227	1.00	17.51	A	C
ATOM	189	O	PHE	168	123.139	42.475	7.750	1.00	13.95	A	O
ATOM	190	N	LEU	169	121.007	41.719	7.680	1.00	16.88	A	N
ATOM	191	CA	LEU	169	120.677	42.467	6.471	1.00	19.47	A	C
ATOM	192	CB	LEU	169	119.262	42.140	6.000	1.00	14.12	A	C
ATOM	193	CG	LEU	169	119.041	40.860	5.213	1.00	13.28	A	C
ATOM	194	CD1	LEU	169	117.662	40.952	4.603	1.00	9.74	A	C
ATOM	195	CD2	LEU	169	120.100	40.694	4.127	1.00	10.14	A	C
ATOM	196	C	LEU	169	120.777	43.966	6.731	1.00	21.77	A	C
ATOM	197	O	LEU	169	121.409	44.694	5.968	1.00	23.20	A	O
ATOM	198	N	ASN	170	120.150	44.419	7.815	1.00	20.45	A	N
ATOM	199	CA	ASN	170	120.159	45.832	8.175	1.00	17.58	A	C
ATOM	200	CB	ASN	170	119.534	46.018	9.562	1.00	31.53	A	C
ATOM	201	CG	ASN	170	119.017	47.426	9.791	1.00	34.95	A	C
ATOM	202	OD1	ASN	170	119.740	48.282	10.284	1.00	30.48	A	O
ATOM	203	ND2	ASN	170	117.762	47.671	9.421	1.00	32.86	A	N
ATOM	204	C	ASN	170	121.587	46.341	8.151	1.00	17.59	A	C
ATOM	205	O	ASN	170	121.941	47.174	7.321	1.00	17.80	A	O
ATOM	206	N	ASP	171	122.412	45.812	9.040	1.00	11.82	A	N
ATOM	207	CA	ASP	171	123.816	46.218	9.120	1.00	13.94	A	C
ATOM	208	CB	ASP	171	124.588	45.282	10.048	1.00	56.27	A	C
ATOM	209	CG	ASP	171	124.405	45.627	11.508	1.00	63.92	A	C
ATOM	210	OD1	ASP	171	123.248	45.689	11.971	1.00	66.14	A	O
ATOM	211	OD2	ASP	171	125.427	45.834	12.196	1.00	65.78	A	O
ATOM	212	C	ASP	171	124.509	46.244	7.760	1.00	15.43	A	C
ATOM	213	O	ASP	171	125.223	47.194	7.435	1.00	14.15	A	O
ATOM	214	N	LEU	172	124.289	45.200	6.966	1.00	15.45	A	N
ATOM	215	CA	LEU	172	124.910	45.099	5.650	1.00	16.13	A	C
ATOM	216	CB	LEU	172	124.633	43.717	5.047	1.00	10.67	A	C
ATOM	217	CG	LEU	172	125.667	43.058	4.123	1.00	10.16	A	C
ATOM	218	CD1	LEU	172	124.905	42.379	2.979	1.00	7.76	A	C
ATOM	219	CD2	LEU	172	126.672	44.070	3.594	1.00	8.33	A	C

Fig. 19: A-4

ATOM	220	C	LEU	172	124.401	46.178	4.699	1.00	16.47	A	C
ATOM	221	O	LEU	172	125.182	46.951	4.156	1.00	16.46	A	O
ATOM	222	N	LEU	173	123.088	46.226	4.509	1.00	30.03	A	N
ATOM	223	CA	LEU	173	122.475	47.193	3.609	1.00	32.78	A	C
ATOM	224	CB	LEU	173	120.967	46.932	3.474	1.00	23.11	A	C
ATOM	225	CG	LEU	173	120.357	45.803	2.627	1.00	24.46	A	C
ATOM	226	CD1	LEU	173	121.069	45.702	1.292	1.00	27.98	A	C
ATOM	227	CD2	LEU	173	120.456	44.501	3.353	1.00	25.01	A	C
ATOM	228	C	LEU	173	122.675	48.663	3.984	1.00	34.21	A	C
ATOM	229	O	LEU	173	122.937	49.495	3.105	1.00	30.93	A	O
ATOM	230	N	LYS	174	122.558	48.989	5.271	1.00	33.34	A	N
ATOM	231	CA	LYS	174	122.684	50.379	5.693	1.00	33.56	A	C
ATOM	232	CB	LYS	174	122.428	50.508	7.193	1.00	32.34	A	C
ATOM	233	CG	LYS	174	123.590	50.195	8.102	1.00	32.67	A	C
ATOM	234	CD	LYS	174	123.170	50.471	9.551	1.00	31.92	A	C
ATOM	235	CE	LYS	174	124.365	50.601	10.504	1.00	27.17	A	C
ATOM	236	NZ	LYS	174	125.178	49.351	10.664	1.00	23.64	A	N
ATOM	237	C	LYS	174	124.004	51.046	5.317	1.00	31.92	A	C
ATOM	238	O	LYS	174	124.060	52.256	5.142	1.00	32.79	A	O
ATOM	239	N	ARG	175	125.059	50.255	5.176	1.00	34.34	A	N
ATOM	240	CA	ARG	175	126.385	50.759	4.797	1.00	36.57	A	C
ATOM	241	CB	ARG	175	127.468	49.712	5.125	1.00	50.56	A	C
ATOM	242	CG	ARG	175	127.708	49.400	6.606	1.00	57.49	A	C
ATOM	243	CD	ARG	175	128.550	48.120	6.760	1.00	61.77	A	C
ATOM	244	NE	ARG	175	129.398	48.107	7.957	1.00	66.67	A	N
ATOM	245	CZ	ARG	175	128.954	48.049	9.211	1.00	70.25	A	C
ATOM	246	NH1	ARG	175	127.653	47.997	9.461	1.00	70.45	A	N
ATOM	247	NH2	ARG	175	129.819	48.039	10.219	1.00	71.15	A	N
ATOM	248	C	ARG	175	126.461	51.051	3.288	1.00	34.10	A	C
ATOM	249	O	ARG	175	127.487	51.522	2.796	1.00	33.94	A	O
ATOM	250	N	MET	176	125.384	50.766	2.557	1.00	18.81	A	N
ATOM	251	CA	MET	176	125.371	50.959	1.104	1.00	15.29	A	C
ATOM	252	CB	MET	176	124.758	49.728	0.431	1.00	45.67	A	C
ATOM	253	CG	MET	176	125.646	48.505	0.474	1.00	42.57	A	C
ATOM	254	SD	MET	176	124.887	47.063	-0.292	1.00	46.71	A	S
ATOM	255	CE	MET	176	124.633	46.046	1.139	1.00	40.22	A	C
ATOM	256	C	MET	176	124.679	52.199	0.546	1.00	18.80	A	C
ATOM	257	O	MET	176	123.797	52.768	1.176	1.00	18.87	A	O
ATOM	258	N	ASP	177	125.098	52.605	-0.652	1.00	31.75	A	N
ATOM	259	CA	ASP	177	124.504	53.744	-1.344	1.00	34.24	A	C
ATOM	260	CB	ASP	177	125.584	54.671	-1.903	1.00	129.70	A	C
ATOM	261	CG	ASP	177	126.196	55.556	-0.838	1.00	132.65	A	C
ATOM	262	OD1	ASP	177	127.004	56.437	-1.194	1.00	132.32	A	O
ATOM	263	OD2	ASP	177	125.869	55.372	0.354	1.00	134.30	A	O
ATOM	264	C	ASP	177	123.638	53.207	-2.480	1.00	34.16	A	C
ATOM	265	O	ASP	177	124.085	53.107	-3.617	1.00	33.88	A	O
ATOM	266	N	ILE	178	122.402	52.848	-2.153	1.00	22.62	A	N
ATOM	267	CA	ILE	178	121.464	52.307	-3.122	1.00	22.76	A	C
ATOM	268	CB	ILE	178	120.326	51.524	-2.407	1.00	26.30	A	C
ATOM	269	CG2	ILE	178	119.208	51.207	-3.390	1.00	24.58	A	C
ATOM	270	CG1	ILE	178	120.866	50.222	-1.803	1.00	27.36	A	C
ATOM	271	CD1	ILE	178	121.188	50.292	-0.325	1.00	29.20	A	C
ATOM	272	C	ILE	178	120.848	53.398	-4.009	1.00	21.90	A	C
ATOM	273	O	ILE	178	120.532	54.501	-3.539	1.00	23.89	A	O
ATOM	274	N	GLY	179	120.669	53.077	-5.292	1.00	18.17	A	N
ATOM	275	CA	GLY	179	120.091	54.029	-6.226	1.00	17.89	A	C
ATOM	276	C	GLY	179	120.123	53.536	-7.658	1.00	18.65	A	C
ATOM	277	O	GLY	179	121.019	52.786	-8.023	1.00	16.80	A	O
ATOM	278	N	PRO	180	119.150	53.937	-8.498	1.00	18.34	A	N
ATOM	279	CD	PRO	180	117.980	54.770	-8.159	1.00	16.60	A	C
ATOM	280	CA	PRO	180	119.094	53.512	-9.901	1.00	19.40	A	C
ATOM	281	CB	PRO	180	118.044	54.442	-10.498	1.00	15.44	A	C
ATOM	282	CG	PRO	180	117.074	54.573	-9.365	1.00	17.83	A	C
ATOM	283	C	PRO	180	120.432	53.622	-10.597	1.00	21.18	A	C
ATOM	284	O	PRO	180	120.706	52.877	-11.529	1.00	21.82	A	O
ATOM	285	N	LYS	181	121.262	54.553	-10.139	1.00	25.85	A	N
ATOM	286	CA	LYS	181	122.581	54.751	-10.732	1.00	26.27	A	C
ATOM	287	CB	LYS	181	122.737	56.187	-11.253	1.00	26.21	A	C
ATOM	288	CG	LYS	181	121.801	56.557	-12.403	1.00	26.81	A	C
ATOM	289	CD	LYS	181	122.014	55.683	-13.627	1.00	25.67	A	C
ATOM	290	CE	LYS	181	121.014	56.031	-14.719	1.00	28.19	A	C
ATOM	291	NZ	LYS	181	121.097	55.146	-15.923	1.00	27.76	A	N
ATOM	292	C	LYS	181	123.684	54.451	-9.729	1.00	25.62	A	C

Fig. 19: A-5

ATOM	293	O	LYS	181	124.854	54.742	-9.975	1.00	23.94	A	O
ATOM	294	N	GLN	182	123.300	53.870	-8.599	1.00	34.95	A	N
ATOM	295	CA	GLN	182	124.246	53.513	-7.548	1.00	33.61	A	C
ATOM	296	CB	GLN	182	123.797	54.096	-6.207	1.00	89.66	A	C
ATOM	297	CG	GLN	182	123.331	55.528	-6.251	1.00	90.94	A	C
ATOM	298	CD	GLN	182	124.443	56.478	-6.597	1.00	92.56	A	C
ATOM	299	OE1	GLN	182	125.007	56.418	-7.686	1.00	93.40	A	O
ATOM	300	NE2	GLN	182	124.772	57.364	-5.667	1.00	93.92	A	N
ATOM	301	C	GLN	182	124.258	51.991	-7.439	1.00	32.52	A	C
ATOM	302	O	GLN	182	124.398	51.278	-8.429	1.00	36.85	A	O
ATOM	303	N	THR	183	124.096	51.507	-6.216	1.00	26.87	A	N
ATOM	304	CA	THR	183	124.052	50.083	-5.953	1.00	23.79	A	C
ATOM	305	CB	THR	183	124.642	49.767	-4.584	1.00	30.55	A	C
ATOM	306	OG1	THR	183	125.983	50.262	-4.526	1.00	27.00	A	O
ATOM	307	CG2	THR	183	124.629	48.274	-4.331	1.00	28.23	A	C
ATOM	308	C	THR	183	122.590	49.687	-5.944	1.00	23.45	A	C
ATOM	309	O	THR	183	121.752	50.380	-5.368	1.00	21.98	A	O
ATOM	310	N	GLN	184	122.269	48.592	-6.608	1.00	25.73	A	N
ATOM	311	CA	GLN	184	120.897	48.127	-6.612	1.00	21.38	A	C
ATOM	312	CB	GLN	184	120.399	47.898	-8.042	1.00	35.06	A	C
ATOM	313	CG	GLN	184	120.016	49.181	-8.770	1.00	34.81	A	C
ATOM	314	CD	GLN	184	118.982	48.942	-9.856	1.00	34.28	A	C
ATOM	315	OE1	GLN	184	119.215	48.164	-10.781	1.00	29.98	A	O
ATOM	316	NE2	GLN	184	117.834	49.604	-9.748	1.00	32.58	A	N
ATOM	317	C	GLN	184	120.862	46.839	-5.800	1.00	21.76	A	C
ATOM	318	O	GLN	184	121.832	46.087	-5.780	1.00	19.15	A	O
ATOM	319	N	VAL	185	119.753	46.599	-5.112	1.00	33.23	A	N
ATOM	320	CA	VAL	185	119.634	45.408	-4.298	1.00	31.60	A	C
ATOM	321	CB	VAL	185	119.868	45.742	-2.810	1.00	20.42	A	C
ATOM	322	CG1	VAL	185	119.572	44.535	-1.938	1.00	20.41	A	C
ATOM	323	CG2	VAL	185	121.294	46.148	-2.614	1.00	6.28	A	C
ATOM	324	C	VAL	185	118.297	44.701	-4.445	1.00	32.19	A	C
ATOM	325	O	VAL	185	117.237	45.322	-4.469	1.00	29.34	A	O
ATOM	326	N	GLY	186	118.369	43.382	-4.554	1.00	17.76	A	N
ATOM	327	CA	GLY	186	117.177	42.573	-4.672	1.00	19.39	A	C
ATOM	328	C	GLY	186	117.355	41.424	-3.711	1.00	17.37	A	C
ATOM	329	O	GLY	186	118.470	40.929	-3.543	1.00	22.73	A	O
ATOM	330	N	ILE	187	116.278	40.995	-3.073	1.00	15.41	A	N
ATOM	331	CA	ILE	187	116.395	39.906	-2.133	1.00	14.00	A	C
ATOM	332	CB	ILE	187	116.117	40.403	-0.675	1.00	10.12	A	C
ATOM	333	CG2	ILE	187	116.053	39.225	0.299	1.00	7.45	A	C
ATOM	334	CG1	ILE	187	117.232	41.364	-0.253	1.00	10.64	A	C
ATOM	335	CD1	ILE	187	117.156	41.817	1.176	1.00	11.69	A	C
ATOM	336	C	ILE	187	115.496	38.731	-2.485	1.00	13.29	A	C
ATOM	337	O	ILE	187	114.301	38.896	-2.768	1.00	12.19	A	O
ATOM	338	N	VAL	188	116.097	37.546	-2.473	1.00	16.67	A	N
ATOM	339	CA	VAL	188	115.403	36.303	-2.769	1.00	16.34	A	C
ATOM	340	CB	VAL	188	116.082	35.567	-3.951	1.00	11.96	A	C
ATOM	341	CG1	VAL	188	115.642	34.122	-3.993	1.00	7.23	A	C
ATOM	342	CG2	VAL	188	115.742	36.251	-5.248	1.00	12.38	A	C
ATOM	343	C	VAL	188	115.464	35.404	-1.536	1.00	14.88	A	C
ATOM	344	O	VAL	188	116.509	35.286	-0.895	1.00	14.29	A	O
ATOM	345	N	GLN	189	114.348	34.774	-1.194	1.00	30.23	A	N
ATOM	346	CA	GLN	189	114.335	33.873	-0.049	1.00	29.91	A	C
ATOM	347	CB	GLN	189	113.374	34.363	1.039	1.00	26.02	A	C
ATOM	348	CG	GLN	189	113.277	33.399	2.210	1.00	23.53	A	C
ATOM	349	CD	GLN	189	112.257	33.807	3.267	1.00	24.24	A	C
ATOM	350	OE1	GLN	189	111.891	32.998	4.125	1.00	25.46	A	O
ATOM	351	NE2	GLN	189	111.800	35.058	3.219	1.00	25.28	A	N
ATOM	352	C	GLN	189	113.911	32.490	-0.520	1.00	26.90	A	C
ATOM	353	O	GLN	189	113.056	32.366	-1.401	1.00	25.26	A	O
ATOM	354	N	TYR	190	114.516	31.455	0.063	1.00	12.87	A	N
ATOM	355	CA	TYR	190	114.196	30.084	-0.310	1.00	16.39	A	C
ATOM	356	CB	TYR	190	115.267	29.539	-1.257	1.00	17.86	A	C
ATOM	357	CG	TYR	190	116.599	29.241	-0.590	1.00	13.63	A	C
ATOM	358	CD1	TYR	190	116.887	27.963	-0.092	1.00	13.63	A	C
ATOM	359	CE1	TYR	190	118.104	27.687	0.517	1.00	13.63	A	C
ATOM	360	CD2	TYR	190	117.569	30.233	-0.453	1.00	13.63	A	C
ATOM	361	CE2	TYR	190	118.787	29.968	0.159	1.00	13.63	A	C
ATOM	362	CZ	TYR	190	119.053	28.698	0.640	1.00	13.63	A	C
ATOM	363	OH	TYR	190	120.278	28.442	1.228	1.00	13.63	A	O
ATOM	364	C	TYR	190	114.035	29.135	0.878	1.00	18.24	A	C
ATOM	365	O	TYR	190	114.456	29.424	2.003	1.00	18.32	A	O

Fig. 19: A-6

ATOM	366	N	GLY	191	113.417	27.994	0.588	1.00	15.40	A	N
ATOM	367	CA	GLY	191	113.171	26.954	1.572	1.00	13.15	A	C
ATOM	368	C	GLY	191	112.683	25.776	0.764	1.00	14.59	A	C
ATOM	369	O	GLY	191	113.482	25.084	0.139	1.00	17.97	A	O
ATOM	370	N	GLU	192	111.371	25.552	0.769	1.00	27.03	A	N
ATOM	371	CA	GLU	192	110.764	24.475	-0.020	1.00	29.04	A	C
ATOM	372	CB	GLU	192	109.400	24.089	0.537	1.00	28.96	A	C
ATOM	373	CG	GLU	192	109.412	23.507	1.929	1.00	29.34	A	C
ATOM	374	CD	GLU	192	108.020	23.089	2.390	1.00	29.53	A	C
ATOM	375	OE1	GLU	192	107.890	22.532	3.505	1.00	32.42	A	O
ATOM	376	OE2	GLU	192	107.051	23.322	1.633	1.00	27.40	A	O
ATOM	377	C	GLU	192	110.562	25.062	-1.410	1.00	28.85	A	C
ATOM	378	O	GLU	192	110.692	24.380	-2.422	1.00	30.22	A	O
ATOM	379	N	ASN	193	110.236	26.350	-1.433	1.00	34.68	A	N
ATOM	380	CA	ASN	193	110.019	27.088	-2.668	1.00	35.89	A	C
ATOM	381	CB	ASN	193	108.566	27.527	-2.769	1.00	60.91	A	C
ATOM	382	CG	ASN	193	107.606	26.388	-2.564	1.00	64.08	A	C
ATOM	383	OD1	ASN	193	107.545	25.804	-1.488	1.00	68.19	A	O
ATOM	384	ND2	ASN	193	106.849	26.058	-3.601	1.00	66.19	A	N
ATOM	385	C	ASN	193	110.910	28.315	-2.640	1.00	34.07	A	C
ATOM	386	O	ASN	193	111.759	28.459	-1.760	1.00	35.07	A	O
ATOM	387	N	VAL	194	110.712	29.206	-3.598	1.00	31.94	A	N
ATOM	388	CA	VAL	194	111.511	30.423	-3.660	1.00	34.28	A	C
ATOM	389	CB	VAL	194	112.524	30.365	-4.803	1.00	32.89	A	C
ATOM	390	CG1	VAL	194	113.514	31.495	-4.671	1.00	33.92	A	C
ATOM	391	CG2	VAL	194	113.227	29.036	-4.799	1.00	30.16	A	C
ATOM	392	C	VAL	194	110.601	31.608	-3.914	1.00	32.05	A	C
ATOM	393	O	VAL	194	109.651	31.507	-4.688	1.00	30.17	A	O
ATOM	394	N	THR	195	110.877	32.730	-3.261	1.00	26.46	A	N
ATOM	395	CA	THR	195	110.058	33.915	-3.474	1.00	27.64	A	C
ATOM	396	CB	THR	195	109.050	34.135	-2.307	1.00	36.45	A	C
ATOM	397	OG1	THR	195	109.728	34.654	-1.163	1.00	40.46	A	O
ATOM	398	CG2	THR	195	108.396	32.820	-1.918	1.00	38.08	A	C
ATOM	399	C	THR	195	110.927	35.161	-3.656	1.00	28.48	A	C
ATOM	400	O	THR	195	111.977	35.309	-3.032	1.00	31.07	A	O
ATOM	401	N	HIS	196	110.492	36.040	-4.545	1.00	36.83	A	N
ATOM	402	CA	HIS	196	111.196	37.281	-4.819	1.00	36.93	A	C
ATOM	403	CB	HIS	196	110.843	37.772	-6.225	1.00	33.18	A	C
ATOM	404	CG	HIS	196	111.434	36.951	-7.326	1.00	29.68	A	C
ATOM	405	CD2	HIS	196	110.933	35.910	-8.032	1.00	30.31	A	C
ATOM	406	ND1	HIS	196	112.707	37.169	-7.813	1.00	28.33	A	N
ATOM	407	CE1	HIS	196	112.965	36.296	-8.772	1.00	25.05	A	C
ATOM	408	NE2	HIS	196	111.905	35.521	-8.924	1.00	23.26	A	N
ATOM	409	C	HIS	196	110.730	38.315	-3.802	1.00	36.79	A	C
ATOM	410	O	HIS	196	109.687	38.933	-3.997	1.00	35.45	A	O
ATOM	411	N	GLU	197	111.480	38.508	-2.721	1.00	21.51	A	N
ATOM	412	CA	GLU	197	111.069	39.488	-1.732	1.00	18.84	A	C
ATOM	413	CB	GLU	197	112.091	39.588	-0.604	1.00	43.52	A	C
ATOM	414	CG	GLU	197	112.094	38.384	0.339	1.00	43.86	A	C
ATOM	415	CD	GLU	197	110.717	38.043	0.882	1.00	42.93	A	C
ATOM	416	OE1	GLU	197	109.909	38.967	1.100	1.00	41.51	A	O
ATOM	417	OE2	GLU	197	110.444	36.847	1.111	1.00	44.59	A	O
ATOM	418	C	GLU	197	110.882	40.832	-2.442	1.00	16.31	A	C
ATOM	419	O	GLU	197	109.802	41.419	-2.403	1.00	21.51	A	O
ATOM	420	N	PHE	198	111.921	41.325	-3.098	1.00	11.53	A	N
ATOM	421	CA	PHE	198	111.786	42.562	-3.845	1.00	13.33	A	C
ATOM	422	CB	PHE	198	111.803	43.785	-2.901	1.00	15.90	A	C
ATOM	423	CG	PHE	198	113.092	44.003	-2.153	1.00	14.15	A	C
ATOM	424	CD1	PHE	198	114.262	44.390	-2.823	1.00	20.29	A	C
ATOM	425	CD2	PHE	198	113.115	43.912	-0.756	1.00	10.34	A	C
ATOM	426	CE1	PHE	198	115.427	44.685	-2.113	1.00	16.32	A	C
ATOM	427	CE2	PHE	198	114.274	44.208	-0.039	1.00	14.80	A	C
ATOM	428	CZ	PHE	198	115.431	44.594	-0.719	1.00	18.60	A	C
ATOM	429	C	PHE	198	112.829	42.652	-4.956	1.00	16.01	A	C
ATOM	430	O	PHE	198	113.974	42.239	-4.771	1.00	17.30	A	O
ATOM	431	N	ASN	199	112.418	43.152	-6.123	1.00	19.42	A	N
ATOM	432	CA	ASN	199	113.321	43.265	-7.276	1.00	19.71	A	C
ATOM	433	CB	ASN	199	112.540	43.562	-8.548	1.00	30.06	A	C
ATOM	434	CG	ASN	199	111.465	42.548	-8.824	1.00	31.32	A	C
ATOM	435	OD1	ASN	199	111.726	41.350	-8.934	1.00	32.85	A	O
ATOM	436	ND2	ASN	199	110.236	43.029	-8.948	1.00	30.20	A	N
ATOM	437	C	ASN	199	114.458	44.288	-7.173	1.00	22.17	A	C
ATOM	438	O	ASN	199	114.430	45.215	-6.351	1.00	19.98	A	O

Fig. 19: A-7

ATOM	439	N	LEU	200	115.445	44.107	-8.044	1.00	18.99	A	N
ATOM	440	CA	LEU	200	116.619	44.958	-8.078	1.00	20.95	A	C
ATOM	441	CB	LEU	200	117.556	44.524	-9.212	1.00	24.87	A	C
ATOM	442	CG	LEU	200	118.631	43.490	-8.869	1.00	22.72	A	C
ATOM	443	CD1	LEU	200	119.348	43.048	-10.130	1.00	27.84	A	C
ATOM	444	CD2	LEU	200	119.617	44.089	-7.869	1.00	23.89	A	C
ATOM	445	C	LEU	200	116.282	46.415	-8.246	1.00	21.35	A	C
ATOM	446	O	LEU	200	116.960	47.274	-7.688	1.00	22.37	A	O
ATOM	447	N	ASN	201	115.231	46.691	-9.011	1.00	18.94	A	N
ATOM	448	CA	ASN	201	114.816	48.061	-9.284	1.00	20.79	A	C
ATOM	449	CB	ASN	201	114.546	48.208	-10.773	1.00	21.69	A	C
ATOM	450	CG	ASN	201	113.401	47.336	-11.236	1.00	23.97	A	C
ATOM	451	OD1	ASN	201	113.119	47.246	-12.424	1.00	24.11	A	O
ATOM	452	ND2	ASN	201	112.727	46.684	-10.292	1.00	21.81	A	N
ATOM	453	C	ASN	201	113.572	48.510	-8.509	1.00	20.84	A	C
ATOM	454	O	ASN	201	112.969	49.522	-8.851	1.00	16.74	A	O
ATOM	455	N	LYS	202	113.182	47.770	-7.477	1.00	23.30	A	N
ATOM	456	CA	LYS	202	111.998	48.137	-6.710	1.00	23.42	A	C
ATOM	457	CB	LYS	202	111.621	47.022	-5.741	1.00	34.18	A	C
ATOM	458	CG	LYS	202	110.337	47.265	-4.944	1.00	35.72	A	C
ATOM	459	CD	LYS	202	109.099	47.092	-5.803	1.00	37.63	A	C
ATOM	460	CE	LYS	202	109.162	45.813	-6.678	1.00	43.38	A	C
ATOM	461	NZ	LYS	202	109.316	44.491	-5.962	1.00	42.40	A	N
ATOM	462	C	LYS	202	112.188	49.428	-5.930	1.00	22.29	A	C
ATOM	463	O	LYS	202	111.338	50.313	-5.984	1.00	19.57	A	O
ATOM	464	N	TYR	203	113.292	49.538	-5.203	1.00	24.72	A	N
ATOM	465	CA	TYR	203	113.538	50.731	-4.407	1.00	24.40	A	C
ATOM	466	CB	TYR	203	113.769	50.348	-2.942	1.00	32.57	A	C
ATOM	467	CG	TYR	203	112.679	49.461	-2.396	1.00	31.24	A	C
ATOM	468	CD1	TYR	203	112.869	48.086	-2.282	1.00	31.85	A	C
ATOM	469	CE1	TYR	203	111.842	47.251	-1.844	1.00	28.32	A	C
ATOM	470	CD2	TYR	203	111.427	49.986	-2.050	1.00	34.13	A	C
ATOM	471	CE2	TYR	203	110.393	49.161	-1.611	1.00	36.88	A	C
ATOM	472	CZ	TYR	203	110.607	47.794	-1.512	1.00	36.50	A	C
ATOM	473	OH	TYR	203	109.590	46.962	-1.095	1.00	41.50	A	O
ATOM	474	C	TYR	203	114.713	51.541	-4.938	1.00	25.04	A	C
ATOM	475	O	TYR	203	115.755	50.986	-5.280	1.00	23.21	A	O
ATOM	476	N	SER	204	114.536	52.861	-4.998	1.00	28.94	A	N
ATOM	477	CA	SER	204	115.557	53.764	-5.513	1.00	30.79	A	C
ATOM	478	CB	SER	204	114.892	54.863	-6.338	1.00	29.83	A	C
ATOM	479	OG	SER	204	113.945	55.577	-5.558	1.00	31.66	A	O
ATOM	480	C	SER	204	116.372	54.402	-4.412	1.00	33.37	A	C
ATOM	481	O	SER	204	117.247	55.214	-4.680	1.00	33.88	A	O
ATOM	482	N	SER	205	116.089	54.027	-3.173	1.00	27.33	A	N
ATOM	483	CA	SER	205	116.787	54.615	-2.048	1.00	26.99	A	C
ATOM	484	CB	SER	205	115.874	55.628	-1.378	1.00	50.70	A	C
ATOM	485	OG	SER	205	116.409	56.032	-0.137	1.00	56.19	A	O
ATOM	486	C	SER	205	117.251	53.608	-1.016	1.00	25.12	A	C
ATOM	487	O	SER	205	116.650	52.551	-0.857	1.00	21.38	A	O
ATOM	488	N	THR	206	118.318	53.949	-0.301	1.00	23.44	A	N
ATOM	489	CA	THR	206	118.854	53.075	0.735	1.00	24.79	A	C
ATOM	490	CB	THR	206	120.176	53.614	1.286	1.00	12.85	A	C
ATOM	491	OG1	THR	206	121.137	53.683	0.227	1.00	11.66	A	O
ATOM	492	CG2	THR	206	120.696	52.712	2.392	1.00	11.22	A	C
ATOM	493	C	THR	206	117.889	52.879	1.900	1.00	25.38	A	C
ATOM	494	O	THR	206	117.798	51.785	2.447	1.00	28.17	A	O
ATOM	495	N	GLU	207	117.173	53.926	2.299	1.00	23.18	A	N
ATOM	496	CA	GLU	207	116.238	53.746	3.394	1.00	22.34	A	C
ATOM	497	CB	GLU	207	115.800	55.083	3.986	1.00	114.79	A	C
ATOM	498	CG	GLU	207	115.317	56.095	2.992	1.00	115.51	A	C
ATOM	499	CD	GLU	207	114.757	57.325	3.675	1.00	116.92	A	C
ATOM	500	OE1	GLU	207	115.428	57.857	4.587	1.00	116.15	A	O
ATOM	501	OE2	GLU	207	113.648	57.761	3.302	1.00	115.82	A	O
ATOM	502	C	GLU	207	115.038	52.937	2.908	1.00	22.84	A	C
ATOM	503	O	GLU	207	114.515	52.094	3.640	1.00	22.79	A	O
ATOM	504	N	GLU	208	114.614	53.163	1.668	1.00	31.71	A	N
ATOM	505	CA	GLU	208	113.485	52.412	1.126	1.00	33.44	A	C
ATOM	506	CB	GLU	208	113.168	52.841	-0.308	1.00	38.62	A	C
ATOM	507	CG	GLU	208	112.661	54.265	-0.441	1.00	36.09	A	C
ATOM	508	CD	GLU	208	112.288	54.633	-1.875	1.00	35.61	A	C
ATOM	509	OE1	GLU	208	111.943	55.811	-2.111	1.00	41.38	A	O
ATOM	510	OE2	GLU	208	112.338	53.757	-2.767	1.00	34.33	A	O
ATOM	511	C	GLU	208	113.808	50.920	1.148	1.00	34.14	A	C

Fig. 19: A-8

ATOM	512	O	GLU	208	112.942	50.093	1.426	1.00	35.14	A	O
ATOM	513	N	VAL	209	115.057	50.575	0.855	1.00	17.60	A	N
ATOM	514	CA	VAL	209	115.472	49.180	0.853	1.00	16.52	A	C
ATOM	515	CB	VAL	209	116.790	48.982	0.077	1.00	10.63	A	C
ATOM	516	CG1	VAL	209	117.501	47.719	0.538	1.00	10.96	A	C
ATOM	517	CG2	VAL	209	116.491	48.889	-1.398	1.00	11.65	A	C
ATOM	518	C	VAL	209	115.656	48.691	2.276	1.00	14.54	A	C
ATOM	519	O	VAL	209	115.278	47.558	2.596	1.00	13.50	A	O
ATOM	520	N	LEU	210	116.230	49.548	3.123	1.00	19.45	A	N
ATOM	521	CA	LEU	210	116.459	49.205	4.521	1.00	19.78	A	C
ATOM	522	CB	LEU	210	117.148	50.354	5.242	1.00	21.61	A	C
ATOM	523	CG	LEU	210	118.589	50.100	5.683	1.00	21.85	A	C
ATOM	524	CD1	LEU	210	119.093	51.347	6.358	1.00	18.40	A	C
ATOM	525	CD2	LEU	210	118.687	48.916	6.632	1.00	15.30	A	C
ATOM	526	C	LEU	210	115.148	48.894	5.223	1.00	18.04	A	C
ATOM	527	O	LEU	210	115.078	48.022	6.093	1.00	18.81	A	O
ATOM	528	N	VAL	211	114.107	49.618	4.839	1.00	25.49	A	N
ATOM	529	CA	VAL	211	112.798	49.443	5.432	1.00	25.25	A	C
ATOM	530	CB	VAL	211	111.916	50.685	5.175	1.00	19.83	A	C
ATOM	531	CG1	VAL	211	110.457	50.391	5.537	1.00	22.01	A	C
ATOM	532	CG2	VAL	211	112.446	51.859	5.989	1.00	20.44	A	C
ATOM	533	C	VAL	211	112.107	48.214	4.871	1.00	24.50	A	C
ATOM	534	O	VAL	211	111.437	47.483	5.593	1.00	25.18	A	O
ATOM	535	N	ALA	212	112.262	47.986	3.577	1.00	29.23	A	N
ATOM	536	CA	ALA	212	111.624	46.839	2.964	1.00	28.21	A	C
ATOM	537	CB	ALA	212	111.725	46.935	1.439	1.00	1.87	A	C
ATOM	538	C	ALA	212	112.275	45.559	3.465	1.00	26.02	A	C
ATOM	539	O	ALA	212	111.603	44.543	3.657	1.00	25.96	A	O
ATOM	540	N	ALA	213	113.587	45.618	3.680	1.00	33.07	A	N
ATOM	541	CA	ALA	213	114.339	44.464	4.147	1.00	34.24	A	C
ATOM	542	CB	ALA	213	115.803	44.787	4.176	1.00	20.72	A	C
ATOM	543	C	ALA	213	113.875	44.011	5.522	1.00	33.04	A	C
ATOM	544	O	ALA	213	113.659	42.824	5.746	1.00	30.67	A	O
ATOM	545	N	ASN	214	113.723	44.952	6.446	1.00	10.19	A	N
ATOM	546	CA	ASN	214	113.268	44.608	7.788	1.00	14.06	A	C
ATOM	547	CB	ASN	214	113.357	45.817	8.713	1.00	18.34	A	C
ATOM	548	CG	ASN	214	114.763	46.094	9.158	1.00	20.07	A	C
ATOM	549	OD1	ASN	214	115.597	46.563	8.377	1.00	22.00	A	O
ATOM	550	ND2	ASN	214	115.045	45.794	10.425	1.00	20.49	A	N
ATOM	551	C	ASN	214	111.847	44.081	7.828	1.00	16.45	A	C
ATOM	552	O	ASN	214	111.448	43.500	8.825	1.00	17.17	A	O
ATOM	553	N	LYS	215	111.080	44.289	6.764	1.00	16.88	A	N
ATOM	554	CA	LYS	215	109.705	43.817	6.744	1.00	17.32	A	C
ATOM	555	CB	LYS	215	108.804	44.772	5.926	1.00	20.45	A	C
ATOM	556	CG	LYS	215	108.670	46.176	6.531	1.00	28.03	A	C
ATOM	557	CD	LYS	215	107.387	46.902	6.115	1.00	31.57	A	C
ATOM	558	CE	LYS	215	107.304	47.155	4.607	1.00	35.03	A	C
ATOM	559	NZ	LYS	215	106.135	48.007	4.237	1.00	36.02	A	N
ATOM	560	C	LYS	215	109.617	42.399	6.193	1.00	15.45	A	C
ATOM	561	O	LYS	215	108.529	41.825	6.124	1.00	16.67	A	O
ATOM	562	N	ILE	216	110.757	41.824	5.812	1.00	28.84	A	N
ATOM	563	CA	ILE	216	110.754	40.475	5.262	1.00	25.66	A	C
ATOM	564	CB	ILE	216	112.088	40.123	4.594	1.00	13.08	A	C
ATOM	565	CG2	ILE	216	112.088	38.681	4.163	1.00	9.86	A	C
ATOM	566	CG1	ILE	216	112.298	41.002	3.362	1.00	9.76	A	C
ATOM	567	CD1	ILE	216	113.597	40.713	2.626	1.00	6.72	A	C
ATOM	568	C	ILE	216	110.459	39.445	6.333	1.00	24.10	A	C
ATOM	569	O	ILE	216	111.076	39.441	7.404	1.00	24.80	A	O
ATOM	570	N	VAL	217	109.503	38.574	6.017	1.00	14.68	A	N
ATOM	571	CA	VAL	217	109.065	37.511	6.904	1.00	16.45	A	C
ATOM	572	CB	VAL	217	107.535	37.425	6.901	1.00	9.81	A	C
ATOM	573	CG1	VAL	217	107.065	36.144	7.569	1.00	9.81	A	C
ATOM	574	CG2	VAL	217	106.967	38.647	7.626	1.00	9.81	A	C
ATOM	575	C	VAL	217	109.641	36.173	6.483	1.00	17.61	A	C
ATOM	576	O	VAL	217	109.794	35.895	5.298	1.00	17.07	A	O
ATOM	577	N	GLN	218	109.959	35.348	7.474	1.00	15.74	A	N
ATOM	578	CA	GLN	218	110.512	34.024	7.234	1.00	16.40	A	C
ATOM	579	CB	GLN	218	111.064	33.446	8.531	1.00	14.26	A	C
ATOM	580	CG	GLN	218	111.752	32.109	8.372	1.00	14.26	A	C
ATOM	581	CD	GLN	218	112.331	31.589	9.675	1.00	14.26	A	C
ATOM	582	OE1	GLN	218	113.166	30.685	9.668	1.00	14.26	A	O
ATOM	583	NE2	GLN	218	111.887	32.156	10.802	1.00	14.26	A	N
ATOM	584	C	GLN	218	109.392	33.151	6.719	1.00	15.85	A	C

Fig. 19: A-9

ATOM	585	O	GLN	218	108.335	33.103	7.328	1.00	19.60	A	O
ATOM	586	N	ARG	219	109.622	32.464	5.604	1.00	16.04	A	N
ATOM	587	CA	ARG	219	108.599	31.602	5.005	1.00	15.69	A	C
ATOM	588	CB	ARG	219	108.595	31.786	3.489	1.00	43.49	A	C
ATOM	589	CG	ARG	219	109.053	33.163	3.054	1.00	43.49	A	C
ATOM	590	CD	ARG	219	108.719	33.421	1.606	1.00	43.49	A	C
ATOM	591	NE	ARG	219	107.365	33.952	1.454	1.00	43.49	A	N
ATOM	592	CZ	ARG	219	107.042	35.232	1.606	1.00	43.49	A	C
ATOM	593	NH1	ARG	219	107.978	36.122	1.915	1.00	43.49	A	N
ATOM	594	NH2	ARG	219	105.786	35.621	1.443	1.00	43.49	A	N
ATOM	595	C	ARG	219	108.814	30.127	5.350	1.00	16.90	A	C
ATOM	596	O	ARG	219	108.073	29.253	4.886	1.00	16.91	A	O
ATOM	597	N	GLY	220	109.838	29.867	6.160	1.00	9.58	A	N
ATOM	598	CA	GLY	220	110.148	28.513	6.567	1.00	9.19	A	C
ATOM	599	C	GLY	220	110.442	27.562	5.422	1.00	8.86	A	C
ATOM	600	O	GLY	220	110.682	27.993	4.288	1.00	7.20	A	O
ATOM	601	N	GLY	221	110.435	26.266	5.730	1.00	16.50	A	N
ATOM	602	CA	GLY	221	110.682	25.265	4.718	1.00	15.07	A	C
ATOM	603	C	GLY	221	111.117	23.954	5.314	1.00	15.49	A	C
ATOM	604	O	GLY	221	112.038	23.928	6.124	1.00	12.29	A	O
ATOM	605	N	ARG	222	110.459	22.865	4.927	1.00	35.34	A	N
ATOM	606	CA	ARG	222	110.815	21.543	5.433	1.00	36.05	A	C
ATOM	607	CB	ARG	222	109.652	20.567	5.235	1.00	22.30	A	C
ATOM	608	CG	ARG	222	108.505	20.791	6.201	1.00	22.30	A	C
ATOM	609	CD	ARG	222	107.252	20.047	5.779	1.00	22.30	A	C
ATOM	610	NE	ARG	222	106.621	20.647	4.614	1.00	22.30	A	N
ATOM	611	CZ	ARG	222	105.459	20.247	4.103	1.00	22.30	A	C
ATOM	612	NH1	ARG	222	104.795	19.241	4.654	1.00	22.30	A	N
ATOM	613	NH2	ARG	222	104.951	20.857	3.042	1.00	22.30	A	N
ATOM	614	C	ARG	222	112.062	21.036	4.723	1.00	36.10	A	C
ATOM	615	O	ARG	222	112.626	20.017	5.107	1.00	36.87	A	O
ATOM	616	N	GLN	223	112.473	21.750	3.678	1.00	27.48	A	N
ATOM	617	CA	GLN	223	113.672	21.428	2.912	1.00	25.77	A	C
ATOM	618	CB	GLN	223	113.328	20.858	1.535	1.00	13.17	A	C
ATOM	619	CG	GLN	223	112.830	19.417	1.508	1.00	14.61	A	C
ATOM	620	CD	GLN	223	111.346	19.312	1.790	1.00	15.02	A	C
ATOM	621	OE1	GLN	223	110.533	20.016	1.190	1.00	15.42	A	O
ATOM	622	NE2	GLN	223	110.981	18.417	2.698	1.00	15.46	A	N
ATOM	623	C	GLN	223	114.498	22.706	2.724	1.00	26.51	A	C
ATOM	624	O	GLN	223	114.057	23.799	3.069	1.00	25.99	A	O
ATOM	625	N	THR	224	115.696	22.567	2.172	1.00	24.40	A	N
ATOM	626	CA	THR	224	116.581	23.704	1.948	1.00	22.28	A	C
ATOM	627	CB	THR	224	117.795	23.633	2.897	1.00	14.98	A	C
ATOM	628	OG1	THR	224	117.328	23.565	4.246	1.00	14.97	A	O
ATOM	629	CG2	THR	224	118.683	24.849	2.747	1.00	11.28	A	C
ATOM	630	C	THR	224	117.061	23.662	0.500	1.00	19.29	A	C
ATOM	631	O	THR	224	118.122	23.129	0.202	1.00	15.78	A	O
ATOM	632	N	MET	225	116.272	24.234	-0.395	1.00	14.15	A	N
ATOM	633	CA	MET	225	116.607	24.236	-1.810	1.00	15.04	A	C
ATOM	634	CB	MET	225	115.346	24.481	-2.636	1.00	22.98	A	C
ATOM	635	CG	MET	225	114.183	23.602	-2.267	1.00	20.41	A	C
ATOM	636	SD	MET	225	114.421	21.883	-2.704	1.00	28.15	A	S
ATOM	637	CE	MET	225	112.675	21.302	-2.554	1.00	24.73	A	C
ATOM	638	C	MET	225	117.653	25.275	-2.204	1.00	16.07	A	C
ATOM	639	O	MET	225	117.426	26.054	-3.136	1.00	17.53	A	O
ATOM	640	N	THR	226	118.791	25.297	-1.513	1.00	16.19	A	N
ATOM	641	CA	THR	226	119.841	26.259	-1.840	1.00	15.66	A	C
ATOM	642	CB	THR	226	121.155	25.905	-1.129	1.00	25.30	A	C
ATOM	643	OG1	THR	226	120.925	25.825	0.284	1.00	27.32	A	O
ATOM	644	CG2	THR	226	122.216	26.959	-1.414	1.00	23.02	A	C
ATOM	645	C	THR	226	120.100	26.337	-3.356	1.00	14.26	A	C
ATOM	646	O	THR	226	120.229	27.418	-3.917	1.00	8.95	A	O
ATOM	647	N	ALA	227	120.158	25.190	-4.019	1.00	9.41	A	N
ATOM	648	CA	ALA	227	120.408	25.162	-5.448	1.00	8.35	A	C
ATOM	649	CB	ALA	227	120.422	23.738	-5.939	1.00	23.80	A	C
ATOM	650	C	ALA	227	119.342	25.951	-6.188	1.00	9.01	A	C
ATOM	651	O	ALA	227	119.644	26.759	-7.067	1.00	9.81	A	O
ATOM	652	N	LEU	228	118.085	25.711	-5.842	1.00	28.18	A	N
ATOM	653	CA	LEU	228	116.985	26.410	-6.489	1.00	26.62	A	C
ATOM	654	CB	LEU	228	115.649	25.860	-5.988	1.00	14.81	A	C
ATOM	655	CG	LEU	228	114.372	26.485	-6.557	1.00	22.70	A	C
ATOM	656	CD1	LEU	228	114.356	26.363	-8.080	1.00	20.29	A	C
ATOM	657	CD2	LEU	228	113.163	25.801	-5.947	1.00	19.75	A	C

Fig. 19: A-10

ATOM	658	C	LEU	228	117.067	27.909	-6.221	1.00	25.80	A	C
ATOM	659	O	LEU	228	116.885	28.719	-7.129	1.00	28.78	A	O
ATOM	660	N	GLY	229	117.341	28.274	-4.971	1.00	23.50	A	N
ATOM	661	CA	GLY	229	117.449	29.679	-4.624	1.00	25.86	A	C
ATOM	662	C	GLY	229	118.464	30.407	-5.495	1.00	28.42	A	C
ATOM	663	O	GLY	229	118.149	31.428	-6.108	1.00	29.01	A	O
ATOM	664	N	ILE	230	119.682	29.876	-5.562	1.00	20.49	A	N
ATOM	665	CA	ILE	230	120.736	30.498	-6.354	1.00	21.82	A	C
ATOM	666	CB	ILE	230	122.096	29.779	-6.195	1.00	2.66	A	C
ATOM	667	CG2	ILE	230	123.168	30.546	-6.953	1.00	2.66	A	C
ATOM	668	CG1	ILE	230	122.486	29.692	-4.720	1.00	2.66	A	C
ATOM	669	CD1	ILE	230	123.773	28.920	-4.474	1.00	2.66	A	C
ATOM	670	C	ILE	230	120.386	30.508	-7.830	1.00	22.08	A	C
ATOM	671	O	ILE	230	120.614	31.498	-8.511	1.00	20.01	A	O
ATOM	672	N	ASP	231	119.841	29.409	-8.333	1.00	32.19	A	N
ATOM	673	CA	ASP	231	119.473	29.352	-9.743	1.00	30.59	A	C
ATOM	674	CB	ASP	231	118.959	27.958	-10.103	1.00	35.41	A	C
ATOM	675	CG	ASP	231	118.860	27.739	-11.604	1.00	42.41	A	C
ATOM	676	OD1	ASP	231	119.910	27.778	-12.281	1.00	41.17	A	O
ATOM	677	OD2	ASP	231	117.735	27.525	-12.103	1.00	45.95	A	O
ATOM	678	C	ASP	231	118.392	30.395	-10.048	1.00	31.57	A	C
ATOM	679	O	ASP	231	118.429	31.048	-11.090	1.00	28.79	A	O
ATOM	680	N	THR	232	117.443	30.554	-9.126	1.00	18.29	A	N
ATOM	681	CA	THR	232	116.347	31.510	-9.296	1.00	17.08	A	C
ATOM	682	CB	THR	232	115.287	31.347	-8.194	1.00	20.70	A	C
ATOM	683	OG1	THR	232	114.714	30.041	-8.279	1.00	19.21	A	O
ATOM	684	CG2	THR	232	114.191	32.370	-8.358	1.00	14.24	A	C
ATOM	685	C	THR	232	116.859	32.937	-9.264	1.00	17.71	A	C
ATOM	686	O	THR	232	116.390	33.801	-10.010	1.00	17.88	A	O
ATOM	687	N	ALA	233	117.815	33.187	-8.379	1.00	19.66	A	N
ATOM	688	CA	ALA	233	118.395	34.517	-8.270	1.00	22.31	A	C
ATOM	689	CB	ALA	233	119.364	34.580	-7.099	1.00	15.15	A	C
ATOM	690	C	ALA	233	119.125	34.796	-9.575	1.00	24.62	A	C
ATOM	691	O	ALA	233	119.187	35.929	-10.031	1.00	26.53	A	O
ATOM	692	N	ARG	234	119.666	33.746	-10.180	1.00	30.19	A	N
ATOM	693	CA	ARG	234	120.390	33.879	-11.434	1.00	33.29	A	C
ATOM	694	CB	ARG	234	121.241	32.637	-11.693	1.00	15.32	A	C
ATOM	695	CG	ARG	234	122.345	32.875	-12.693	1.00	15.32	A	C
ATOM	696	CD	ARG	234	122.760	31.617	-13.460	1.00	15.32	A	C
ATOM	697	NE	ARG	234	121.839	31.311	-14.554	1.00	15.32	A	N
ATOM	698	CZ	ARG	234	120.875	30.405	-14.481	1.00	15.32	A	C
ATOM	699	NH1	ARG	234	120.708	29.713	-13.368	1.00	15.32	A	N
ATOM	700	NH2	ARG	234	120.078	30.188	-15.511	1.00	15.32	A	N
ATOM	701	C	ARG	234	119.446	34.083	-12.619	1.00	35.42	A	C
ATOM	702	O	ARG	234	119.409	35.153	-13.215	1.00	35.47	A	O
ATOM	703	N	LYS	235	118.666	33.057	-12.941	1.00	67.48	A	N
ATOM	704	CA	LYS	235	117.767	33.124	-14.085	1.00	67.43	A	C
ATOM	705	CB	LYS	235	117.204	31.730	-14.397	1.00	53.18	A	C
ATOM	706	CG	LYS	235	115.965	31.308	-13.615	1.00	54.33	A	C
ATOM	707	CD	LYS	235	115.583	29.867	-13.970	1.00	54.15	A	C
ATOM	708	CE	LYS	235	114.146	29.517	-13.590	1.00	54.95	A	C
ATOM	709	NZ	LYS	235	113.873	29.660	-12.135	1.00	55.71	A	N
ATOM	710	C	LYS	235	116.628	34.134	-14.017	1.00	67.57	A	C
ATOM	711	O	LYS	235	116.074	34.500	-15.054	1.00	67.91	A	O
ATOM	712	N	GLU	236	116.277	34.596	-12.822	1.00	98.68	A	N
ATOM	713	CA	GLU	236	115.186	35.558	-12.693	1.00	100.30	A	C
ATOM	714	CB	GLU	236	114.087	34.999	-11.781	1.00	50.64	A	C
ATOM	715	CG	GLU	236	113.008	34.192	-12.510	1.00	53.41	A	C
ATOM	716	CD	GLU	236	112.199	33.276	-11.582	1.00	55.89	A	C
ATOM	717	OE1	GLU	236	111.660	33.760	-10.565	1.00	55.98	A	O
ATOM	718	OE2	GLU	236	112.098	32.065	-11.875	1.00	55.73	A	O
ATOM	719	C	GLU	236	115.627	36.917	-12.174	1.00	98.85	A	C
ATOM	720	O	GLU	236	115.638	37.900	-12.912	1.00	100.28	A	O
ATOM	721	N	ALA	237	115.991	36.969	-10.899	1.00	71.25	A	N
ATOM	722	CA	ALA	237	116.405	38.218	-10.276	1.00	68.72	A	C
ATOM	723	CB	ALA	237	117.046	37.934	-8.932	1.00	56.85	A	C
ATOM	724	C	ALA	237	117.349	39.046	-11.139	1.00	67.56	A	C
ATOM	725	O	ALA	237	117.225	40.267	-11.200	1.00	65.98	A	O
ATOM	726	N	PHE	238	118.283	38.385	-11.812	1.00	41.81	A	N
ATOM	727	CA	PHE	238	119.256	39.080	-12.651	1.00	41.24	A	C
ATOM	728	CB	PHE	238	120.606	38.369	-12.591	1.00	47.57	A	C
ATOM	729	CG	PHE	238	121.413	38.696	-11.378	1.00	46.60	A	C
ATOM	730	CD1	PHE	238	121.686	37.725	-10.419	1.00	47.83	A	C

Fig. 19: A-11

ATOM	731	CD2	PHE	238	121.931	39.970	-11.208	1.00	44.20	A	C
ATOM	732	CE1	PHE	238	122.476	38.023	-9.298	1.00	45.63	A	C
ATOM	733	CE2	PHE	238	122.719	40.282	-10.094	1.00	50.51	A	C
ATOM	734	CZ	PHE	238	122.993	39.305	-9.137	1.00	51.93	A	C
ATOM	735	C	PHE	238	118.861	39.252	-14.116	1.00	43.09	A	C
ATOM	736	O	PHE	238	119.699	39.129	-15.017	1.00	43.19	A	O
ATOM	737	N	THR	239	117.586	39.520	-14.362	1.00	28.84	A	N
ATOM	738	CA	THR	239	117.117	39.744	-15.724	1.00	32.78	A	C
ATOM	739	CB	THR	239	115.952	38.821	-16.086	1.00	22.29	A	C
ATOM	740	OG1	THR	239	114.866	39.059	-15.191	1.00	20.25	A	O
ATOM	741	CG2	THR	239	116.363	37.382	-15.988	1.00	25.20	A	C
ATOM	742	C	THR	239	116.655	41.202	-15.798	1.00	33.04	A	C
ATOM	743	O	THR	239	115.955	41.695	-14.902	1.00	33.54	A	O
ATOM	744	N	GLU	240	117.067	41.881	-16.868	1.00	73.11	A	N
ATOM	745	CA	GLU	240	116.755	43.291	-17.085	1.00	73.36	A	C
ATOM	746	CB	GLU	240	116.995	43.654	-18.549	1.00	97.49	A	C
ATOM	747	CG	GLU	240	117.147	45.141	-18.793	1.00	102.13	A	C
ATOM	748	CD	GLU	240	117.738	45.441	-20.152	1.00	105.04	A	C
ATOM	749	OE1	GLU	240	118.794	44.858	-20.483	1.00	105.14	A	O
ATOM	750	OE2	GLU	240	117.151	46.263	-20.885	1.00	105.11	A	O
ATOM	751	C	GLU	240	115.336	43.665	-16.689	1.00	74.71	A	C
ATOM	752	O	GLU	240	115.083	44.772	-16.210	1.00	75.92	A	O
ATOM	753	N	ALA	241	114.417	42.730	-16.885	1.00	32.59	A	N
ATOM	754	CA	ALA	241	113.016	42.952	-16.552	1.00	33.44	A	C
ATOM	755	CB	ALA	241	112.170	41.769	-17.051	1.00	4.05	A	C
ATOM	756	C	ALA	241	112.802	43.165	-15.044	1.00	32.91	A	C
ATOM	757	O	ALA	241	111.809	43.759	-14.622	1.00	34.37	A	O
ATOM	758	N	ARG	242	113.725	42.678	-14.223	1.00	31.60	A	N
ATOM	759	CA	ARG	242	113.585	42.851	-12.786	1.00	31.34	A	C
ATOM	760	CB	ARG	242	113.757	41.500	-12.079	1.00	27.81	A	C
ATOM	761	CG	ARG	242	112.489	40.658	-12.052	1.00	28.01	A	C
ATOM	762	CD	ARG	242	112.669	39.440	-11.160	1.00	28.87	A	C
ATOM	763	NE	ARG	242	111.425	39.010	-10.515	1.00	30.07	A	N
ATOM	764	CZ	ARG	242	110.582	38.106	-11.011	1.00	29.27	A	C
ATOM	765	NH1	ARG	242	110.846	37.525	-12.176	1.00	28.32	A	N
ATOM	766	NH2	ARG	242	109.485	37.769	-10.334	1.00	31.29	A	N
ATOM	767	C	ARG	242	114.557	43.898	-12.231	1.00	32.54	A	C
ATOM	768	O	ARG	242	114.824	43.954	-11.026	1.00	35.55	A	O
ATOM	769	N	GLY	243	115.080	44.733	-13.122	1.00	38.70	A	N
ATOM	770	CA	GLY	243	115.996	45.775	-12.706	1.00	36.85	A	C
ATOM	771	C	GLY	243	117.468	45.462	-12.890	1.00	35.13	A	C
ATOM	772	O	GLY	243	118.318	46.139	-12.308	1.00	34.75	A	O
ATOM	773	N	ALA	244	117.792	44.447	-13.683	1.00	32.25	A	N
ATOM	774	CA	ALA	244	119.190	44.119	-13.896	1.00	30.25	A	C
ATOM	775	CB	ALA	244	119.326	42.709	-14.442	1.00	67.28	A	C
ATOM	776	C	ALA	244	119.750	45.130	-14.886	1.00	32.13	A	C
ATOM	777	O	ALA	244	119.437	45.088	-16.068	1.00	31.59	A	O
ATOM	778	N	ARG	245	120.566	46.054	-14.401	1.00	18.96	A	N
ATOM	779	CA	ARG	245	121.154	47.074	-15.258	1.00	19.79	A	C
ATOM	780	CB	ARG	245	121.853	48.130	-14.399	1.00	36.60	A	C
ATOM	781	CG	ARG	245	120.888	49.043	-13.655	1.00	39.07	A	C
ATOM	782	CD	ARG	245	121.614	49.991	-12.741	1.00	39.28	A	C
ATOM	783	NE	ARG	245	122.309	49.254	-11.701	1.00	33.70	A	N
ATOM	784	CZ	ARG	245	122.997	49.824	-10.726	1.00	33.52	A	C
ATOM	785	NH1	ARG	245	123.084	51.145	-10.662	1.00	32.72	A	N
ATOM	786	NH2	ARG	245	123.590	49.075	-9.810	1.00	30.81	A	N
ATOM	787	C	ARG	245	122.131	46.493	-16.266	1.00	18.16	A	C
ATOM	788	O	ARG	245	123.003	45.710	-15.911	1.00	14.27	A	O
ATOM	789	N	ARG	246	121.985	46.896	-17.525	1.00	55.16	A	N
ATOM	790	CA	ARG	246	122.848	46.429	-18.607	1.00	57.95	A	C
ATOM	791	CB	ARG	246	122.447	47.078	-19.928	1.00	115.62	A	C
ATOM	792	CG	ARG	246	123.405	46.764	-21.067	1.00	120.98	A	C
ATOM	793	CD	ARG	246	123.057	47.546	-22.318	1.00	126.90	A	C
ATOM	794	NE	ARG	246	121.637	47.444	-22.641	1.00	129.81	A	N
ATOM	795	CZ	ARG	246	120.981	46.298	-22.804	1.00	132.92	A	C
ATOM	796	NH1	ARG	246	121.615	45.138	-22.676	1.00	132.61	A	N
ATOM	797	NH2	ARG	246	119.685	46.314	-23.094	1.00	133.70	A	N
ATOM	798	C	ARG	246	124.313	46.736	-18.364	1.00	55.77	A	C
ATOM	799	O	ARG	246	124.671	47.879	-18.092	1.00	58.40	A	O
ATOM	800	N	GLY	247	125.151	45.711	-18.475	1.00	47.75	A	N
ATOM	801	CA	GLY	247	126.587	45.878	-18.302	1.00	50.33	A	C
ATOM	802	C	GLY	247	127.097	46.294	-16.934	1.00	50.40	A	C
ATOM	803	O	GLY	247	128.129	46.958	-16.824	1.00	53.36	A	O

Fig. 19: A-12

ATOM	804	N	VAL	248	126.382	45.911	-15.887	1.00	40.38	A	N
ATOM	805	CA	VAL	248	126.790	46.248	-14.535	1.00	38.39	A	C
ATOM	806	CB	VAL	248	125.653	46.928	-13.780	1.00	41.70	A	C
ATOM	807	CG1	VAL	248	126.049	47.136	-12.331	1.00	39.35	A	C
ATOM	808	CG2	VAL	248	125.331	48.250	-14.436	1.00	33.47	A	C
ATOM	809	C	VAL	248	127.173	44.970	-13.807	1.00	41.41	A	C
ATOM	810	O	VAL	248	126.530	43.936	-13.993	1.00	45.46	A	O
ATOM	811	N	LYS	249	128.208	45.036	-12.975	1.00	30.45	A	N
ATOM	812	CA	LYS	249	128.645	43.852	-12.250	1.00	31.36	A	C
ATOM	813	CB	LYS	249	129.799	44.186	-11.299	1.00	85.59	A	C
ATOM	814	CG	LYS	249	130.426	42.940	-10.690	1.00	91.11	A	C
ATOM	815	CD	LYS	249	130.844	41.943	-11.782	1.00	92.18	A	C
ATOM	816	CE	LYS	249	131.040	40.539	-11.224	1.00	94.54	A	C
ATOM	817	NZ	LYS	249	131.548	39.546	-12.218	1.00	97.36	A	N
ATOM	818	C	LYS	249	127.503	43.190	-11.473	1.00	30.02	A	C
ATOM	819	O	LYS	249	126.706	43.862	-10.815	1.00	29.84	A	O
ATOM	820	N	LYS	250	127.432	41.864	-11.559	1.00	29.51	A	N
ATOM	821	CA	LYS	250	126.396	41.110	-10.879	1.00	29.16	A	C
ATOM	822	CB	LYS	250	125.763	40.134	-11.871	1.00	45.59	A	C
ATOM	823	CG	LYS	250	125.050	40.864	-12.996	1.00	44.19	A	C
ATOM	824	CD	LYS	250	124.892	40.022	-14.263	1.00	45.74	A	C
ATOM	825	CE	LYS	250	123.827	38.928	-14.135	1.00	44.90	A	C
ATOM	826	NZ	LYS	250	123.513	38.274	-15.453	1.00	46.72	A	N
ATOM	827	C	LYS	250	126.979	40.391	-9.663	1.00	28.51	A	C
ATOM	828	O	LYS	250	127.849	39.541	-9.804	1.00	28.19	A	O
ATOM	829	N	VAL	251	126.493	40.754	-8.474	1.00	23.05	A	N
ATOM	830	CA	VAL	251	126.954	40.173	-7.219	1.00	22.96	A	C
ATOM	831	CB	VAL	251	127.504	41.263	-6.307	1.00	28.85	A	C
ATOM	832	CG1	VAL	251	127.901	40.676	-4.959	1.00	27.00	A	C
ATOM	833	CG2	VAL	251	128.678	41.928	-6.974	1.00	30.06	A	C
ATOM	834	C	VAL	251	125.863	39.421	-6.451	1.00	21.44	A	C
ATOM	835	O	VAL	251	124.778	39.945	-6.232	1.00	17.44	A	O
ATOM	836	N	MET	252	126.168	38.199	-6.023	1.00	19.32	A	N
ATOM	837	CA	MET	252	125.212	37.383	-5.278	1.00	20.30	A	C
ATOM	838	CB	MET	252	124.949	36.073	-6.024	1.00	19.49	A	C
ATOM	839	CG	MET	252	123.850	35.212	-5.425	1.00	18.18	A	C
ATOM	840	SD	MET	252	123.556	33.701	-6.379	1.00	22.23	A	S
ATOM	841	CE	MET	252	123.009	34.366	-7.960	1.00	13.54	A	C
ATOM	842	C	MET	252	125.730	37.072	-3.875	1.00	19.32	A	C
ATOM	843	O	MET	252	126.880	36.675	-3.704	1.00	21.69	A	O
ATOM	844	N	VAL	253	124.886	37.261	-2.869	1.00	11.70	A	N
ATOM	845	CA	VAL	253	125.286	36.971	-1.505	1.00	12.85	A	C
ATOM	846	CB	VAL	253	125.173	38.221	-0.593	1.00	5.67	A	C
ATOM	847	CG1	VAL	253	125.508	37.856	0.842	1.00	7.09	A	C
ATOM	848	CG2	VAL	253	126.118	39.310	-1.079	1.00	5.31	A	C
ATOM	849	C	VAL	253	124.370	35.881	-0.974	1.00	12.42	A	C
ATOM	850	O	VAL	253	123.166	36.093	-0.870	1.00	10.86	A	O
ATOM	851	N	ILE	254	124.936	34.716	-0.649	1.00	26.88	A	N
ATOM	852	CA	ILE	254	124.142	33.597	-0.126	1.00	23.78	A	C
ATOM	853	CB	ILE	254	124.457	32.266	-0.847	1.00	10.72	A	C
ATOM	854	CG2	ILE	254	123.584	31.171	-0.294	1.00	7.19	A	C
ATOM	855	CG1	ILE	254	124.220	32.397	-2.352	1.00	9.30	A	C
ATOM	856	CD1	ILE	254	125.307	33.140	-3.078	1.00	8.93	A	C
ATOM	857	C	ILE	254	124.379	33.370	1.359	1.00	21.87	A	C
ATOM	858	O	ILE	254	125.508	33.431	1.833	1.00	23.74	A	O
ATOM	859	N	VAL	255	123.300	33.105	2.084	1.00	38.19	A	N
ATOM	860	CA	VAL	255	123.379	32.858	3.516	1.00	36.93	A	C
ATOM	861	CB	VAL	255	122.733	33.994	4.328	1.00	13.80	A	C
ATOM	862	CG1	VAL	255	123.224	33.949	5.753	1.00	12.25	A	C
ATOM	863	CG2	VAL	255	123.056	35.325	3.713	1.00	14.44	A	C
ATOM	864	C	VAL	255	122.592	31.594	3.798	1.00	34.68	A	C
ATOM	865	O	VAL	255	121.431	31.491	3.403	1.00	36.68	A	O
ATOM	866	N	THR	256	123.210	30.632	4.474	1.00	19.22	A	N
ATOM	867	CA	THR	256	122.514	29.387	4.798	1.00	20.04	A	C
ATOM	868	CB	THR	256	122.477	28.457	3.566	1.00	10.08	A	C
ATOM	869	OG1	THR	256	122.032	27.147	3.952	1.00	6.12	A	O
ATOM	870	CG2	THR	256	123.851	28.387	2.926	1.00	8.93	A	C
ATOM	871	C	THR	256	123.128	28.650	5.995	1.00	23.52	A	C
ATOM	872	O	THR	256	124.303	28.831	6.310	1.00	19.68	A	O
ATOM	873	N	ASP	257	122.323	27.829	6.663	1.00	46.58	A	N
ATOM	874	CA	ASP	257	122.794	27.097	7.830	1.00	46.96	A	C
ATOM	875	CB	ASP	257	122.069	27.585	9.091	1.00	21.89	A	C
ATOM	876	CG	ASP	257	120.655	27.009	9.225	1.00	27.25	A	C

Fig. 19: A-13

ATOM	877	OD1	ASP	257	120.089	26.573	8.191	1.00	27.72	A	O
ATOM	878	OD2	ASP	257	120.110	27.006	10.362	1.00	32.52	A	O
ATOM	879	C	ASP	257	122.599	25.596	7.693	1.00	43.55	A	C
ATOM	880	O	ASP	257	122.525	24.883	8.695	1.00	42.79	A	O
ATOM	881	N	GLY	258	122.510	25.106	6.461	1.00	42.38	A	N
ATOM	882	CA	GLY	258	122.330	23.678	6.283	1.00	44.80	A	C
ATOM	883	C	GLY	258	122.618	23.150	4.896	1.00	48.62	A	C
ATOM	884	O	GLY	258	122.523	23.871	3.903	1.00	44.34	A	O
ATOM	885	N	GLU	259	122.984	21.876	4.832	1.00	88.78	A	N
ATOM	886	CA	GLU	259	123.265	21.230	3.562	1.00	90.66	A	C
ATOM	887	CB	GLU	259	123.650	19.770	3.782	1.00	87.02	A	C
ATOM	888	CG	GLU	259	124.983	19.588	4.461	1.00	94.80	A	C
ATOM	889	CD	GLU	259	125.130	18.214	5.070	1.00	98.61	A	C
ATOM	890	OE1	GLU	259	126.256	17.861	5.481	1.00	105.36	A	O
ATOM	891	OE2	GLU	259	124.115	17.490	5.147	1.00	98.63	A	O
ATOM	892	C	GLU	259	122.004	21.298	2.727	1.00	89.52	A	C
ATOM	893	O	GLU	259	120.927	20.906	3.174	1.00	86.69	A	O
ATOM	894	N	SER	260	122.140	21.815	1.517	1.00	31.72	A	N
ATOM	895	CA	SER	260	121.007	21.922	0.615	1.00	34.88	A	C
ATOM	896	CB	SER	260	121.435	22.606	-0.685	1.00	104.64	A	C
ATOM	897	OG	SER	260	122.467	21.872	-1.325	1.00	105.15	A	O
ATOM	898	C	SER	260	120.489	20.526	0.304	1.00	34.78	A	C
ATOM	899	O	SER	260	121.257	19.571	0.315	1.00	30.81	A	O
ATOM	900	N	HIS	261	119.192	20.409	0.039	1.00	119.42	A	N
ATOM	901	CA	HIS	261	118.609	19.114	-0.284	1.00	123.77	A	C
ATOM	902	CB	HIS	261	117.107	19.116	0.020	1.00	89.56	A	C
ATOM	903	CG	HIS	261	116.789	19.030	1.482	1.00	92.76	A	C
ATOM	904	CD2	HIS	261	116.610	19.997	2.413	1.00	91.87	A	C
ATOM	905	ND1	HIS	261	116.648	17.830	2.147	1.00	94.24	A	N
ATOM	906	CE1	HIS	261	116.393	18.065	3.422	1.00	94.31	A	C
ATOM	907	NE2	HIS	261	116.365	19.372	3.610	1.00	91.58	A	N
ATOM	908	C	HIS	261	118.866	18.815	-1.754	1.00	124.83	A	C
ATOM	909	O	HIS	261	118.732	17.676	-2.203	1.00	122.05	A	O
ATOM	910	N	ASP	262	119.251	19.850	-2.495	1.00	94.20	A	N
ATOM	911	CA	ASP	262	119.556	19.709	-3.913	1.00	99.17	A	C
ATOM	912	CB	ASP	262	118.838	20.798	-4.732	1.00	77.35	A	C
ATOM	913	CG	ASP	262	118.558	22.065	-3.929	1.00	77.35	A	C
ATOM	914	OD1	ASP	262	119.382	22.429	-3.067	1.00	77.35	A	O
ATOM	915	OD2	ASP	262	117.515	22.708	-4.179	1.00	77.35	A	O
ATOM	916	C	ASP	262	121.065	19.758	-4.191	1.00	99.22	A	C
ATOM	917	O	ASP	262	121.510	20.456	-5.104	1.00	99.08	A	O
ATOM	918	N	ASN	263	121.842	19.009	-3.406	1.00	48.33	A	N
ATOM	919	CA	ASN	263	123.300	18.956	-3.558	1.00	49.50	A	C
ATOM	920	CB	ASN	263	123.896	17.820	-2.719	1.00	78.20	A	C
ATOM	921	CG	ASN	263	123.359	17.781	-1.303	1.00	82.57	A	C
ATOM	922	OD1	ASN	263	123.578	18.703	-0.511	1.00	84.07	A	O
ATOM	923	ND2	ASN	263	122.651	16.702	-0.974	1.00	77.07	A	N
ATOM	924	C	ASN	263	123.657	18.684	-5.012	1.00	50.14	A	C
ATOM	925	O	ASN	263	124.574	19.286	-5.572	1.00	49.04	A	O
ATOM	926	N	TYR	264	122.915	17.754	-5.601	1.00	83.05	A	N
ATOM	927	CA	TYR	264	123.112	17.330	-6.976	1.00	80.90	A	C
ATOM	928	CB	TYR	264	121.905	16.512	-7.431	1.00	165.37	A	C
ATOM	929	CG	TYR	264	121.684	15.297	-6.568	1.00	165.37	A	C
ATOM	930	CD1	TYR	264	121.294	15.427	-5.234	1.00	165.37	A	C
ATOM	931	CE1	TYR	264	121.137	14.312	-4.419	1.00	165.37	A	C
ATOM	932	CD2	TYR	264	121.909	14.016	-7.067	1.00	165.37	A	C
ATOM	933	CE2	TYR	264	121.753	12.892	-6.262	1.00	165.37	A	C
ATOM	934	CZ	TYR	264	121.369	13.048	-4.939	1.00	165.37	A	C
ATOM	935	OH	TYR	264	121.224	11.940	-4.139	1.00	165.37	A	O
ATOM	936	C	TYR	264	123.396	18.439	-7.977	1.00	79.55	A	C
ATOM	937	O	TYR	264	124.509	18.536	-8.498	1.00	76.68	A	O
ATOM	938	N	ARG	265	122.406	19.283	-8.245	1.00	83.26	A	N
ATOM	939	CA	ARG	265	122.605	20.340	-9.224	1.00	82.16	A	C
ATOM	940	CB	ARG	265	121.297	20.636	-9.957	1.00	36.62	A	C
ATOM	941	CG	ARG	265	120.182	21.225	-9.142	1.00	37.07	A	C
ATOM	942	CD	ARG	265	119.267	21.953	-10.110	1.00	38.90	A	C
ATOM	943	NE	ARG	265	118.140	22.620	-9.464	1.00	44.29	A	N
ATOM	944	CZ	ARG	265	117.562	23.714	-9.947	1.00	44.46	A	C
ATOM	945	NH1	ARG	265	118.016	24.257	-11.071	1.00	49.09	A	N
ATOM	946	NH2	ARG	265	116.528	24.258	-9.321	1.00	48.43	A	N
ATOM	947	C	ARG	265	123.211	21.644	-8.720	1.00	81.41	A	C
ATOM	948	O	ARG	265	123.137	22.668	-9.396	1.00	82.72	A	O
ATOM	949	N	LEU	266	123.819	21.614	-7.543	1.00	27.19	A	N

Fig. 19: A-14

ATOM	950	CA	LEU	266	124.435	22.815	-7.003	1.00	28.76	A	C
ATOM	951	CB	LEU	266	124.798	22.601	-5.539	1.00	4.24	A	C
ATOM	952	CG	LEU	266	125.336	23.820	-4.797	1.00	3.45	A	C
ATOM	953	CD1	LEU	266	124.393	24.999	-4.976	1.00	5.79	A	C
ATOM	954	CD2	LEU	266	125.502	23.466	-3.320	1.00	1.87	A	C
ATOM	955	C	LEU	266	125.684	23.084	-7.828	1.00	31.58	A	C
ATOM	956	O	LEU	266	126.086	24.226	-8.022	1.00	31.46	A	O
ATOM	957	N	LYS	267	126.286	22.007	-8.317	1.00	45.65	A	N
ATOM	958	CA	LYS	267	127.479	22.088	-9.149	1.00	47.96	A	C
ATOM	959	CB	LYS	267	127.949	20.673	-9.497	1.00	72.30	A	C
ATOM	960	CG	LYS	267	129.239	20.583	-10.298	1.00	72.30	A	C
ATOM	961	CD	LYS	267	130.428	20.277	-9.403	1.00	72.30	A	C
ATOM	962	CE	LYS	267	131.649	19.894	-10.230	1.00	72.30	A	C
ATOM	963	NZ	LYS	267	132.793	19.452	-9.381	1.00	72.30	A	N
ATOM	964	C	LYS	267	127.103	22.842	-10.427	1.00	47.45	A	C
ATOM	965	O	LYS	267	127.763	23.810	-10.809	1.00	46.97	A	O
ATOM	966	N	GLN	268	126.032	22.389	-11.074	1.00	32.65	A	N
ATOM	967	CA	GLN	268	125.553	22.999	-12.303	1.00	31.62	A	C
ATOM	968	CB	GLN	268	124.292	22.295	-12.798	1.00	88.56	A	C
ATOM	969	CG	GLN	268	124.449	20.845	-13.182	1.00	88.56	A	C
ATOM	970	CD	GLN	268	123.119	20.227	-13.576	1.00	88.56	A	C
ATOM	971	OE1	GLN	268	123.059	19.078	-14.010	1.00	88.56	A	O
ATOM	972	NE2	GLN	268	122.041	20.992	-13.423	1.00	88.56	A	N
ATOM	973	C	GLN	268	125.221	24.474	-12.100	1.00	27.37	A	C
ATOM	974	O	GLN	268	125.678	25.332	-12.851	1.00	28.55	A	O
ATOM	975	N	VAL	269	124.410	24.767	-11.089	1.00	11.19	A	N
ATOM	976	CA	VAL	269	124.007	26.140	-10.830	1.00	8.94	A	C
ATOM	977	CB	VAL	269	123.088	26.223	-9.598	1.00	22.95	A	C
ATOM	978	CG1	VAL	269	122.650	27.667	-9.374	1.00	18.60	A	C
ATOM	979	CG2	VAL	269	121.872	25.334	-9.801	1.00	20.81	A	C
ATOM	980	C	VAL	269	125.198	27.076	-10.649	1.00	8.53	A	C
ATOM	981	O	VAL	269	125.286	28.093	-11.318	1.00	11.37	A	O
ATOM	982	N	ILE	270	126.114	26.744	-9.746	1.00	5.57	A	N
ATOM	983	CA	ILE	270	127.291	27.585	-9.535	1.00	6.19	A	C
ATOM	984	CB	ILE	270	128.281	26.944	-8.533	1.00	12.81	A	C
ATOM	985	CG2	ILE	270	129.592	27.731	-8.504	1.00	7.43	A	C
ATOM	986	CG1	ILE	270	127.671	26.926	-7.135	1.00	10.37	A	C
ATOM	987	CD1	ILE	270	127.367	28.317	-6.591	1.00	11.49	A	C
ATOM	988	C	ILE	270	128.001	27.775	-10.870	1.00	10.06	A	C
ATOM	989	O	ILE	270	128.549	28.838	-11.140	1.00	8.84	A	O
ATOM	990	N	GLN	271	127.981	26.729	-11.696	1.00	7.96	A	N
ATOM	991	CA	GLN	271	128.605	26.751	-13.011	1.00	10.02	A	C
ATOM	992	CB	GLN	271	128.434	25.394	-13.698	1.00	84.89	A	C
ATOM	993	CG	GLN	271	129.267	25.214	-14.947	1.00	86.79	A	C
ATOM	994	CD	GLN	271	130.744	25.366	-14.665	1.00	89.29	A	C
ATOM	995	OE1	GLN	271	131.244	26.477	-14.506	1.00	89.62	A	O
ATOM	996	NE2	GLN	271	131.451	24.243	-14.583	1.00	90.86	A	N
ATOM	997	C	GLN	271	127.962	27.842	-13.860	1.00	12.48	A	C
ATOM	998	O	GLN	271	128.644	28.733	-14.348	1.00	15.17	A	O
ATOM	999	N	ASP	272	126.648	27.770	-14.031	1.00	33.57	A	N
ATOM	1000	CA	ASP	272	125.929	28.758	-14.818	1.00	34.85	A	C
ATOM	1001	CB	ASP	272	124.430	28.459	-14.786	1.00	74.39	A	C
ATOM	1002	CG	ASP	272	124.084	27.142	-15.454	1.00	76.01	A	C
ATOM	1003	OD1	ASP	272	123.000	26.589	-15.163	1.00	78.08	A	O
ATOM	1004	OD2	ASP	272	124.893	26.665	-16.278	1.00	82.27	A	O
ATOM	1005	C	ASP	272	126.194	30.163	-14.283	1.00	35.65	A	C
ATOM	1006	O	ASP	272	126.190	31.131	-15.042	1.00	33.10	A	O
ATOM	1007	N	CYS	273	126.426	30.280	-12.978	1.00	42.88	A	N
ATOM	1008	CA	CYS	273	126.698	31.582	-12.387	1.00	41.31	A	C
ATOM	1009	CB	CYS	273	126.630	31.516	-10.862	1.00	24.14	A	C
ATOM	1010	SG	CYS	273	124.940	31.489	-10.191	1.00	22.24	A	S
ATOM	1011	C	CYS	273	128.059	32.090	-12.826	1.00	41.68	A	C
ATOM	1012	O	CYS	273	128.244	33.288	-13.008	1.00	35.99	A	O
ATOM	1013	N	GLU	274	129.010	31.178	-12.994	1.00	20.07	A	N
ATOM	1014	CA	GLU	274	130.364	31.531	-13.440	1.00	22.87	A	C
ATOM	1015	CB	GLU	274	131.317	30.338	-13.298	1.00	39.18	A	C
ATOM	1016	CG	GLU	274	132.090	30.309	-11.989	1.00	44.30	A	C
ATOM	1017	CD	GLU	274	133.041	31.490	-11.836	1.00	49.41	A	C
ATOM	1018	OE1	GLU	274	133.622	31.659	-10.740	1.00	51.28	A	O
ATOM	1019	OE2	GLU	274	133.212	32.251	-12.812	1.00	53.97	A	O
ATOM	1020	C	GLU	274	130.345	31.984	-14.893	1.00	25.29	A	C
ATOM	1021	O	GLU	274	131.031	32.931	-15.266	1.00	27.49	A	O
ATOM	1022	N	ASP	275	129.550	31.298	-15.707	1.00	41.03	A	N

Fig. 19: A-15

ATOM	1023	CA	ASP	275	129.421	31.625	-17.119	1.00	39.77	A	C
ATOM	1024	CB	ASP	275	128.538	30.594	-17.822	1.00	63.42	A	C
ATOM	1025	CG	ASP	275	129.106	29.203	-17.757	1.00	64.69	A	C
ATOM	1026	OD1	ASP	275	129.987	28.959	-16.906	1.00	68.39	A	O
ATOM	1027	OD2	ASP	275	128.657	28.352	-18.551	1.00	66.35	A	O
ATOM	1028	C	ASP	275	128.789	32.996	-17.295	1.00	38.76	A	C
ATOM	1029	O	ASP	275	128.883	33.595	-18.367	1.00	34.31	A	O
ATOM	1030	N	GLU	276	128.137	33.485	-16.247	1.00	28.36	A	N
ATOM	1031	CA	GLU	276	127.479	34.771	-16.328	1.00	28.01	A	C
ATOM	1032	CB	GLU	276	126.019	34.617	-15.913	1.00	53.33	A	C
ATOM	1033	CG	GLU	276	125.310	33.520	-16.700	1.00	53.20	A	C
ATOM	1034	CD	GLU	276	123.807	33.493	-16.487	1.00	54.30	A	C
ATOM	1035	OE1	GLU	276	123.150	32.629	-17.102	1.00	55.01	A	O
ATOM	1036	OE2	GLU	276	123.280	34.330	-15.717	1.00	51.24	A	O
ATOM	1037	C	GLU	276	128.172	35.841	-15.504	1.00	26.84	A	C
ATOM	1038	O	GLU	276	127.621	36.919	-15.288	1.00	27.95	A	O
ATOM	1039	N	ASN	277	129.382	35.535	-15.050	1.00	28.50	A	N
ATOM	1040	CA	ASN	277	130.185	36.472	-14.268	1.00	28.47	A	C
ATOM	1041	CB	ASN	277	130.607	37.655	-15.140	1.00	86.35	A	C
ATOM	1042	CG	ASN	277	131.230	37.218	-16.439	1.00	91.27	A	C
ATOM	1043	OD1	ASN	277	132.263	36.548	-16.451	1.00	91.09	A	O
ATOM	1044	ND2	ASN	277	130.601	37.589	-17.550	1.00	90.23	A	N
ATOM	1045	C	ASN	277	129.493	37.014	-13.018	1.00	24.82	A	C
ATOM	1046	O	ASN	277	129.476	38.226	-12.790	1.00	25.80	A	O
ATOM	1047	N	ILE	278	128.925	36.127	-12.207	1.00	15.37	A	N
ATOM	1048	CA	ILE	278	128.261	36.560	-10.989	1.00	15.82	A	C
ATOM	1049	CB	ILE	278	126.963	35.773	-10.747	1.00	17.43	A	C
ATOM	1050	CG2	ILE	278	126.304	36.243	-9.454	1.00	18.82	A	C
ATOM	1051	CG1	ILE	278	126.016	35.949	-11.932	1.00	14.88	A	C
ATOM	1052	CD1	ILE	278	124.742	35.153	-11.796	1.00	17.16	A	C
ATOM	1053	C	ILE	278	129.168	36.345	-9.780	1.00	16.42	A	C
ATOM	1054	O	ILE	278	129.363	35.212	-9.354	1.00	16.76	A	O
ATOM	1055	N	GLN	279	129.737	37.426	-9.244	1.00	26.25	A	N
ATOM	1056	CA	GLN	279	130.578	37.335	-8.053	1.00	25.85	A	C
ATOM	1057	CB	GLN	279	131.035	38.716	-7.605	1.00	41.76	A	C
ATOM	1058	CG	GLN	279	131.959	39.382	-8.574	1.00	47.54	A	C
ATOM	1059	CD	GLN	279	133.158	38.524	-8.894	1.00	51.46	A	C
ATOM	1060	OE1	GLN	279	133.992	38.255	-8.023	1.00	45.70	A	O
ATOM	1061	NE2	GLN	279	133.252	38.078	-10.146	1.00	51.05	A	N
ATOM	1062	C	GLN	279	129.716	36.736	-6.958	1.00	23.72	A	C
ATOM	1063	O	GLN	279	128.609	37.216	-6.692	1.00	20.64	A	O
ATOM	1064	N	ARG	280	130.214	35.697	-6.310	1.00	16.06	A	N
ATOM	1065	CA	ARG	280	129.440	35.054	-5.258	1.00	17.58	A	C
ATOM	1066	CB	ARG	280	129.107	33.620	-5.661	1.00	19.51	A	C
ATOM	1067	CG	ARG	280	128.413	33.488	-6.997	1.00	18.14	A	C
ATOM	1068	CD	ARG	280	128.274	32.021	-7.371	1.00	17.81	A	C
ATOM	1069	NE	ARG	280	129.576	31.365	-7.441	1.00	14.86	A	N
ATOM	1070	CZ	ARG	280	130.427	31.489	-8.452	1.00	18.77	A	C
ATOM	1071	NH1	ARG	280	130.131	32.241	-9.493	1.00	21.69	A	N
ATOM	1072	NH2	ARG	280	131.579	30.846	-8.422	1.00	23.71	A	N
ATOM	1073	C	ARG	280	130.123	35.037	-3.892	1.00	17.24	A	C
ATOM	1074	O	ARG	280	131.269	34.592	-3.750	1.00	16.97	A	O
ATOM	1075	N	PHE	281	129.406	35.539	-2.894	1.00	21.33	A	N
ATOM	1076	CA	PHE	281	129.889	35.538	-1.527	1.00	23.32	A	C
ATOM	1077	CB	PHE	281	129.848	36.933	-0.924	1.00	12.67	A	C
ATOM	1078	CG	PHE	281	130.754	37.900	-1.603	1.00	15.70	A	C
ATOM	1079	CD1	PHE	281	130.419	38.434	-2.837	1.00	19.55	A	C
ATOM	1080	CD2	PHE	281	131.968	38.250	-1.024	1.00	17.43	A	C
ATOM	1081	CE1	PHE	281	131.281	39.305	-3.487	1.00	19.61	A	C
ATOM	1082	CE2	PHE	281	132.842	39.120	-1.665	1.00	15.16	A	C
ATOM	1083	CZ	PHE	281	132.498	39.650	-2.900	1.00	16.59	A	C
ATOM	1084	C	PHE	281	128.925	34.646	-0.785	1.00	24.03	A	C
ATOM	1085	O	PHE	281	127.710	34.867	-0.821	1.00	26.40	A	O
ATOM	1086	N	SER	282	129.449	33.613	-0.141	1.00	13.47	A	N
ATOM	1087	CA	SER	282	128.594	32.705	0.602	1.00	15.32	A	C
ATOM	1088	CB	SER	282	128.746	31.272	0.084	1.00	11.38	A	C
ATOM	1089	OG	SER	282	130.081	30.816	0.216	1.00	7.93	A	O
ATOM	1090	C	SER	282	128.947	32.782	2.069	1.00	17.20	A	C
ATOM	1091	O	SER	282	130.066	33.135	2.435	1.00	21.06	A	O
ATOM	1092	N	ILE	283	127.969	32.477	2.908	1.00	24.08	A	N
ATOM	1093	CA	ILE	283	128.164	32.504	4.343	1.00	22.00	A	C
ATOM	1094	CB	ILE	283	127.517	33.733	4.968	1.00	17.91	A	C
ATOM	1095	CG2	ILE	283	127.843	33.791	6.442	1.00	18.72	A	C

Fig. 19: A-16

ATOM	1096	CG1	ILE	283	128.045	34.986	4.281	1.00	14.38	A	C
ATOM	1097	CD1	ILE	283	127.103	36.171	4.383	1.00	17.94	A	C
ATOM	1098	C	ILE	283	127.510	31.273	4.912	1.00	21.07	A	C
ATOM	1099	O	ILE	283	126.394	30.917	4.536	1.00	20.93	A	O
ATOM	1100	N	ALA	284	128.204	30.618	5.823	1.00	29.93	A	N
ATOM	1101	CA	ALA	284	127.663	29.421	6.412	1.00	29.95	A	C
ATOM	1102	CB	ALA	284	128.548	28.253	6.070	1.00	1.87	A	C
ATOM	1103	C	ALA	284	127.507	29.536	7.920	1.00	28.08	A	C
ATOM	1104	O	ALA	284	128.482	29.740	8.641	1.00	26.74	A	O
ATOM	1105	N	ILE	285	126.270	29.422	8.389	1.00	31.23	A	N
ATOM	1106	CA	ILE	285	125.997	29.457	9.817	1.00	25.43	A	C
ATOM	1107	CB	ILE	285	124.529	29.859	10.107	1.00	43.54	A	C
ATOM	1108	CG2	ILE	285	124.187	29.569	11.555	1.00	38.36	A	C
ATOM	1109	CG1	ILE	285	124.306	31.344	9.791	1.00	38.87	A	C
ATOM	1110	CD1	ILE	285	124.206	31.670	8.315	1.00	40.01	A	C
ATOM	1111	C	ILE	285	126.227	28.022	10.296	1.00	28.75	A	C
ATOM	1112	O	ILE	285	125.523	27.106	9.872	1.00	30.49	A	O
ATOM	1113	N	LEU	286	127.205	27.818	11.169	1.00	38.23	A	N
ATOM	1114	CA	LEU	286	127.497	26.471	11.649	1.00	38.71	A	C
ATOM	1115	CB	LEU	286	128.999	26.313	11.876	1.00	50.51	A	C
ATOM	1116	CG	LEU	286	129.917	26.722	10.727	1.00	53.33	A	C
ATOM	1117	CD1	LEU	286	131.340	26.363	11.105	1.00	55.89	A	C
ATOM	1118	CD2	LEU	286	129.513	26.019	9.441	1.00	55.00	A	C
ATOM	1119	C	LEU	286	126.760	26.069	12.923	1.00	39.16	A	C
ATOM	1120	O	LEU	286	127.068	25.036	13.517	1.00	40.00	A	O
ATOM	1121	N	GLY	287	125.789	26.875	13.339	1.00	72.80	A	N
ATOM	1122	CA	GLY	287	125.042	26.579	14.551	1.00	71.58	A	C
ATOM	1123	C	GLY	287	124.586	25.139	14.700	1.00	69.16	A	C
ATOM	1124	O	GLY	287	125.056	24.419	15.583	1.00	73.26	A	O
ATOM	1125	N	THR	296	131.112	19.210	10.542	1.00	87.02	A	N
ATOM	1126	CA	THR	296	130.609	20.333	9.766	1.00	87.06	A	C
ATOM	1127	CB	THR	296	130.702	21.652	10.554	1.00	100.17	A	C
ATOM	1128	OG1	THR	296	132.071	21.903	10.895	1.00	105.23	A	O
ATOM	1129	CG2	THR	296	129.861	21.592	11.817	1.00	100.04	A	C
ATOM	1130	C	THR	296	131.387	20.535	8.479	1.00	88.04	A	C
ATOM	1131	O	THR	296	130.985	21.331	7.631	1.00	86.85	A	O
ATOM	1132	N	GLU	297	132.497	19.825	8.322	1.00	78.34	A	N
ATOM	1133	CA	GLU	297	133.304	20.020	7.128	1.00	81.80	A	C
ATOM	1134	CB	GLU	297	134.577	19.171	7.169	1.00	125.47	A	C
ATOM	1135	CG	GLU	297	134.403	17.709	6.851	1.00	132.50	A	C
ATOM	1136	CD	GLU	297	135.690	17.103	6.342	1.00	133.75	A	C
ATOM	1137	OE1	GLU	297	135.709	15.886	6.067	1.00	135.24	A	O
ATOM	1138	OE2	GLU	297	136.682	17.853	6.212	1.00	137.19	A	O
ATOM	1139	C	GLU	297	132.550	19.770	5.832	1.00	79.84	A	C
ATOM	1140	O	GLU	297	132.581	20.609	4.931	1.00	79.34	A	O
ATOM	1141	N	LYS	298	131.865	18.638	5.728	1.00	42.69	A	N
ATOM	1142	CA	LYS	298	131.125	18.352	4.505	1.00	42.69	A	C
ATOM	1143	CB	LYS	298	130.281	17.087	4.678	1.00	102.63	A	C
ATOM	1144	CG	LYS	298	129.695	16.562	3.376	1.00	111.34	A	C
ATOM	1145	CD	LYS	298	129.117	15.166	3.545	1.00	113.06	A	C
ATOM	1146	CE	LYS	298	130.167	14.187	4.057	1.00	116.88	A	C
ATOM	1147	NZ	LYS	298	131.378	14.159	3.195	1.00	121.20	A	N
ATOM	1148	C	LYS	298	130.228	19.547	4.143	1.00	40.29	A	C
ATOM	1149	O	LYS	298	130.032	19.853	2.964	1.00	41.17	A	O
ATOM	1150	N	PHE	299	129.700	20.218	5.167	1.00	38.43	A	N
ATOM	1151	CA	PHE	299	128.839	21.380	4.978	1.00	36.67	A	C
ATOM	1152	CB	PHE	299	128.100	21.712	6.283	1.00	55.97	A	C
ATOM	1153	CG	PHE	299	127.256	22.967	6.209	1.00	48.41	A	C
ATOM	1154	CD1	PHE	299	126.319	23.146	5.186	1.00	44.86	A	C
ATOM	1155	CD2	PHE	299	127.400	23.970	7.160	1.00	46.14	A	C
ATOM	1156	CE1	PHE	299	125.545	24.307	5.117	1.00	44.27	A	C
ATOM	1157	CE2	PHE	299	126.627	25.132	7.095	1.00	40.55	A	C
ATOM	1158	CZ	PHE	299	125.701	25.299	6.073	1.00	39.06	A	C
ATOM	1159	C	PHE	299	129.684	22.573	4.544	1.00	37.02	A	C
ATOM	1160	O	PHE	299	129.439	23.190	3.504	1.00	32.83	A	O
ATOM	1161	N	VAL	300	130.682	22.896	5.352	1.00	13.94	A	N
ATOM	1162	CA	VAL	300	131.551	24.010	5.034	1.00	18.89	A	C
ATOM	1163	CB	VAL	300	132.752	24.068	5.993	1.00	40.51	A	C
ATOM	1164	CG1	VAL	300	133.769	25.076	5.493	1.00	44.08	A	C
ATOM	1165	CG2	VAL	300	132.282	24.451	7.382	1.00	44.52	A	C
ATOM	1166	C	VAL	300	132.061	23.893	3.607	1.00	17.53	A	C
ATOM	1167	O	VAL	300	132.177	24.889	2.906	1.00	18.03	A	O
ATOM	1168	N	GLU	301	132.365	22.679	3.164	1.00	18.30	A	N

Fig. 19: A-17

ATOM	1169	CA	GLU	301	132.866	22.513	1.808	1.00	18.96	A	C
ATOM	1170	CB	GLU	301	133.407	21.094	1.605	1.00	40.16	A	C
ATOM	1171	CG	GLU	301	134.058	20.854	0.243	1.00	42.43	A	C
ATOM	1172	CD	GLU	301	135.049	21.943	-0.155	1.00	48.24	A	C
ATOM	1173	OE1	GLU	301	135.956	22.267	0.645	1.00	47.79	A	O
ATOM	1174	OE2	GLU	301	134.918	22.469	-1.282	1.00	50.51	A	O
ATOM	1175	C	GLU	301	131.770	22.832	0.791	1.00	17.53	A	C
ATOM	1176	O	GLU	301	132.034	23.458	-0.242	1.00	15.61	A	O
ATOM	1177	N	GLU	302	130.541	22.420	1.097	1.00	32.12	A	N
ATOM	1178	CA	GLU	302	129.412	22.667	0.210	1.00	31.93	A	C
ATOM	1179	CB	GLU	302	128.127	22.084	0.801	1.00	76.04	A	C
ATOM	1180	CG	GLU	302	126.894	22.274	-0.071	1.00	75.79	A	C
ATOM	1181	CD	GLU	302	125.659	21.594	0.501	1.00	72.72	A	C
ATOM	1182	OE1	GLU	302	125.651	20.349	0.584	1.00	72.70	A	O
ATOM	1183	OE2	GLU	302	124.698	22.302	0.872	1.00	77.14	A	O
ATOM	1184	C	GLU	302	129.237	24.158	-0.033	1.00	35.00	A	C
ATOM	1185	O	GLU	302	129.040	24.580	-1.170	1.00	34.26	A	O
ATOM	1186	N	ILE	303	129.334	24.953	1.031	1.00	23.69	A	N
ATOM	1187	CA	ILE	303	129.171	26.405	0.936	1.00	23.74	A	C
ATOM	1188	CB	ILE	303	128.933	27.019	2.326	1.00	28.42	A	C
ATOM	1189	CG2	ILE	303	128.556	28.480	2.199	1.00	23.60	A	C
ATOM	1190	CG1	ILE	303	127.823	26.245	3.046	1.00	26.02	A	C
ATOM	1191	CD1	ILE	303	126.599	25.926	2.183	1.00	22.48	A	C
ATOM	1192	C	ILE	303	130.340	27.129	0.267	1.00	25.77	A	C
ATOM	1193	O	ILE	303	130.133	28.036	-0.553	1.00	28.26	A	O
ATOM	1194	N	LYS	304	131.564	26.740	0.612	1.00	28.18	A	N
ATOM	1195	CA	LYS	304	132.733	27.363	0.003	1.00	28.98	A	C
ATOM	1196	CB	LYS	304	134.018	26.713	0.501	1.00	31.11	A	C
ATOM	1197	CG	LYS	304	134.415	27.051	1.915	1.00	37.78	A	C
ATOM	1198	CD	LYS	304	135.810	26.502	2.190	1.00	39.31	A	C
ATOM	1199	CE	LYS	304	136.298	26.803	3.599	1.00	42.04	A	C
ATOM	1200	NZ	LYS	304	137.673	26.262	3.857	1.00	44.22	A	N
ATOM	1201	C	LYS	304	132.665	27.210	-1.512	1.00	25.07	A	C
ATOM	1202	O	LYS	304	133.033	28.118	-2.252	1.00	29.15	A	O
ATOM	1203	N	SER	305	132.195	26.054	-1.965	1.00	30.32	A	N
ATOM	1204	CA	SER	305	132.100	25.785	-3.386	1.00	27.48	A	C
ATOM	1205	CB	SER	305	131.702	24.329	-3.635	1.00	18.09	A	C
ATOM	1206	OG	SER	305	130.352	24.088	-3.293	1.00	14.77	A	O
ATOM	1207	C	SER	305	131.094	26.709	-4.044	1.00	28.00	A	C
ATOM	1208	O	SER	305	131.137	26.917	-5.263	1.00	30.57	A	O
ATOM	1209	N	ILE	306	130.181	27.258	-3.247	1.00	37.08	A	N
ATOM	1210	CA	ILE	306	129.180	28.176	-3.783	1.00	33.83	A	C
ATOM	1211	CB	ILE	306	127.990	28.319	-2.831	1.00	15.00	A	C
ATOM	1212	CG2	ILE	306	127.190	29.565	-3.167	1.00	15.73	A	C
ATOM	1213	CG1	ILE	306	127.118	27.069	-2.929	1.00	17.63	A	C
ATOM	1214	CD1	ILE	306	125.993	27.029	-1.916	1.00	15.34	A	C
ATOM	1215	C	ILE	306	129.812	29.544	-4.008	1.00	31.59	A	C
ATOM	1216	O	ILE	306	129.361	30.333	-4.851	1.00	32.12	A	O
ATOM	1217	N	ALA	307	130.874	29.805	-3.251	1.00	20.26	A	N
ATOM	1218	CA	ALA	307	131.584	31.062	-3.349	1.00	22.45	A	C
ATOM	1219	CB	ALA	307	132.444	31.260	-2.118	1.00	5.65	A	C
ATOM	1220	C	ALA	307	132.441	31.113	-4.611	1.00	22.11	A	C
ATOM	1221	O	ALA	307	132.622	30.103	-5.302	1.00	21.10	A	O
ATOM	1222	N	SER	308	132.953	32.307	-4.906	1.00	24.29	A	N
ATOM	1223	CA	SER	308	133.796	32.533	-6.072	1.00	27.22	A	C
ATOM	1224	CB	SER	308	133.489	33.899	-6.700	1.00	15.61	A	C
ATOM	1225	OG	SER	308	132.299	33.860	-7.460	1.00	19.00	A	O
ATOM	1226	C	SER	308	135.264	32.482	-5.690	1.00	30.87	A	C
ATOM	1227	O	SER	308	135.625	32.797	-4.555	1.00	28.21	A	O
ATOM	1228	N	GLU	309	136.103	32.069	-6.640	1.00	26.43	A	N
ATOM	1229	CA	GLU	309	137.542	32.008	-6.418	1.00	29.92	A	C
ATOM	1230	CB	GLU	309	138.224	31.266	-7.569	1.00	73.14	A	C
ATOM	1231	CG	GLU	309	137.811	29.809	-7.737	1.00	78.51	A	C
ATOM	1232	CD	GLU	309	138.181	28.950	-6.541	1.00	81.27	A	C
ATOM	1233	OE1	GLU	309	138.103	27.708	-6.651	1.00	83.60	A	O
ATOM	1234	OE2	GLU	309	138.544	29.514	-5.487	1.00	85.42	A	O
ATOM	1235	C	GLU	309	138.009	33.461	-6.396	1.00	30.67	A	C
ATOM	1236	O	GLU	309	137.580	34.257	-7.230	1.00	32.32	A	O
ATOM	1237	N	PRO	310	138.882	33.834	-5.442	1.00	19.51	A	N
ATOM	1238	CD	PRO	310	139.395	35.217	-5.381	1.00	49.07	A	C
ATOM	1239	CA	PRO	310	139.483	33.029	-4.377	1.00	19.70	A	C
ATOM	1240	CB	PRO	310	140.703	33.851	-3.982	1.00	50.90	A	C
ATOM	1241	CG	PRO	310	140.182	35.231	-4.065	1.00	50.46	A	C

Fig. 19: A-18

ATOM	1242	C	PRO	310	138.569	32.751	-3.178	1.00	20.19	A	C
ATOM	1243	O	PRO	310	138.229	33.654	-2.394	1.00	16.98	A	O
ATOM	1244	N	THR	311	138.197	31.483	-3.043	1.00	25.93	A	N
ATOM	1245	CA	THR	311	137.352	31.013	-1.957	1.00	26.80	A	C
ATOM	1246	CB	THR	311	137.618	29.521	-1.695	1.00	73.61	A	C
ATOM	1247	OG1	THR	311	137.053	29.145	-0.434	1.00	77.77	A	O
ATOM	1248	CG2	THR	311	139.118	29.244	-1.696	1.00	76.69	A	C
ATOM	1249	C	THR	311	137.521	31.781	-0.643	1.00	28.67	A	C
ATOM	1250	O	THR	311	136.535	32.173	-0.025	1.00	29.84	A	O
ATOM	1251	N	GLU	312	138.759	32.009	-0.223	1.00	47.89	A	N
ATOM	1252	CA	GLU	312	139.007	32.713	1.029	1.00	46.51	A	C
ATOM	1253	CB	GLU	312	140.506	32.751	1.340	1.00	98.24	A	C
ATOM	1254	CG	GLU	312	141.354	33.411	0.268	1.00	100.00	A	C
ATOM	1255	CD	GLU	312	142.621	34.031	0.825	1.00	99.11	A	C
ATOM	1256	OE1	GLU	312	143.491	34.431	0.024	1.00	102.46	A	O
ATOM	1257	OE2	GLU	312	142.742	34.130	2.065	1.00	99.98	A	O
ATOM	1258	C	GLU	312	138.453	34.134	1.092	1.00	45.13	A	C
ATOM	1259	O	GLU	312	137.997	34.576	2.147	1.00	45.09	A	O
ATOM	1260	N	LYS	313	138.490	34.856	-0.021	1.00	49.11	A	N
ATOM	1261	CA	LYS	313	137.990	36.226	-0.024	1.00	48.31	A	C
ATOM	1262	CB	LYS	313	138.797	37.091	-1.000	1.00	91.02	A	C
ATOM	1263	CG	LYS	313	140.171	37.508	-0.486	1.00	90.90	A	C
ATOM	1264	CD	LYS	313	140.081	38.565	0.620	1.00	87.20	A	C
ATOM	1265	CE	LYS	313	139.966	39.982	0.066	1.00	89.24	A	C
ATOM	1266	NZ	LYS	313	138.804	40.159	-0.842	1.00	93.72	A	N
ATOM	1267	C	LYS	313	136.511	36.307	-0.374	1.00	49.46	A	C
ATOM	1268	O	LYS	313	135.973	37.397	-0.580	1.00	51.78	A	O
ATOM	1269	N	HIS	314	135.849	35.159	-0.427	1.00	27.67	A	N
ATOM	1270	CA	HIS	314	134.437	35.137	-0.775	1.00	28.52	A	C
ATOM	1271	CB	HIS	314	134.274	34.652	-2.212	1.00	32.51	A	C
ATOM	1272	CG	HIS	314	134.872	35.574	-3.224	1.00	29.37	A	C
ATOM	1273	CD2	HIS	314	136.073	35.552	-3.849	1.00	28.84	A	C
ATOM	1274	ND1	HIS	314	134.220	36.697	-3.683	1.00	28.95	A	N
ATOM	1275	CE1	HIS	314	134.992	37.326	-4.551	1.00	28.24	A	C
ATOM	1276	NE2	HIS	314	136.122	36.652	-4.669	1.00	28.63	A	N
ATOM	1277	C	HIS	314	133.587	34.277	0.141	1.00	28.65	A	C
ATOM	1278	O	HIS	314	132.366	34.238	-0.008	1.00	32.05	A	O
ATOM	1279	N	PHE	315	134.230	33.591	1.081	1.00	32.99	A	N
ATOM	1280	CA	PHE	315	133.519	32.723	2.013	1.00	32.79	A	C
ATOM	1281	CB	PHE	315	134.045	31.294	1.878	1.00	35.38	A	C
ATOM	1282	CG	PHE	315	133.476	30.339	2.884	1.00	30.36	A	C
ATOM	1283	CD1	PHE	315	132.123	30.026	2.877	1.00	32.20	A	C
ATOM	1284	CD2	PHE	315	134.298	29.749	3.839	1.00	28.44	A	C
ATOM	1285	CE1	PHE	315	131.592	29.144	3.800	1.00	27.15	A	C
ATOM	1286	CE2	PHE	315	133.783	28.866	4.769	1.00	29.14	A	C
ATOM	1287	CZ	PHE	315	132.421	28.560	4.749	1.00	30.81	A	C
ATOM	1288	C	PHE	315	133.640	33.198	3.466	1.00	33.51	A	C
ATOM	1289	O	PHE	315	134.706	33.643	3.896	1.00	34.91	A	O
ATOM	1290	N	PHE	316	132.539	33.104	4.210	1.00	26.09	A	N
ATOM	1291	CA	PHE	316	132.513	33.516	5.610	1.00	23.14	A	C
ATOM	1292	CB	PHE	316	131.707	34.803	5.780	1.00	27.51	A	C
ATOM	1293	CG	PHE	316	132.343	36.008	5.155	1.00	31.13	A	C
ATOM	1294	CD1	PHE	316	132.125	36.312	3.822	1.00	26.72	A	C
ATOM	1295	CD2	PHE	316	133.182	36.827	5.903	1.00	27.98	A	C
ATOM	1296	CE1	PHE	316	132.737	37.420	3.237	1.00	29.29	A	C
ATOM	1297	CE2	PHE	316	133.799	37.931	5.334	1.00	31.09	A	C
ATOM	1298	CZ	PHE	316	133.577	38.230	3.998	1.00	31.32	A	C
ATOM	1299	C	PHE	316	131.909	32.438	6.497	1.00	21.07	A	C
ATOM	1300	O	PHE	316	130.901	31.831	6.153	1.00	20.31	A	O
ATOM	1301	N	ASN	317	132.533	32.220	7.647	1.00	37.16	A	N
ATOM	1302	CA	ASN	317	132.093	31.214	8.599	1.00	38.38	A	C
ATOM	1303	CB	ASN	317	133.288	30.385	9.047	1.00	74.28	A	C
ATOM	1304	CG	ASN	317	133.055	28.919	8.888	1.00	77.27	A	C
ATOM	1305	OD1	ASN	317	131.954	28.433	9.138	1.00	79.20	A	O
ATOM	1306	ND2	ASN	317	134.088	28.190	8.478	1.00	75.53	A	N
ATOM	1307	C	ASN	317	131.487	31.893	9.817	1.00	39.34	A	C
ATOM	1308	O	ASN	317	132.001	32.902	10.285	1.00	40.20	A	O
ATOM	1309	N	VAL	318	130.398	31.348	10.336	1.00	30.64	A	N
ATOM	1310	CA	VAL	318	129.763	31.924	11.521	1.00	29.27	A	C
ATOM	1311	CB	VAL	318	128.531	32.778	11.144	1.00	70.89	A	C
ATOM	1312	CG1	VAL	318	127.896	33.349	12.386	1.00	71.02	A	C
ATOM	1313	CG2	VAL	318	128.942	33.899	10.223	1.00	70.87	A	C
ATOM	1314	C	VAL	318	129.331	30.808	12.482	1.00	24.42	A	C

Fig. 19: A-19

ATOM	1315	O	VAL	318	128.872	29.744	12.053	1.00	25.09	A	O
ATOM	1316	N	SER	319	129.482	31.045	13.779	1.00	32.47	A	N
ATOM	1317	CA	SER	319	129.108	30.035	14.752	1.00	31.73	A	C
ATOM	1318	CB	SER	319	129.669	30.384	16.134	1.00	29.19	A	C
ATOM	1319	OG	SER	319	129.289	31.687	16.538	1.00	41.14	A	O
ATOM	1320	C	SER	319	127.600	29.840	14.831	1.00	30.33	A	C
ATOM	1321	O	SER	319	127.132	28.716	14.963	1.00	28.40	A	O
ATOM	1322	N	ASP	320	126.839	30.926	14.741	1.00	32.33	A	N
ATOM	1323	CA	ASP	320	125.382	30.846	14.816	1.00	32.31	A	C
ATOM	1324	CB	ASP	320	124.934	30.632	16.275	1.00	63.91	A	C
ATOM	1325	CG	ASP	320	125.369	31.760	17.209	1.00	62.36	A	C
ATOM	1326	OD1	ASP	320	126.586	31.992	17.364	1.00	61.04	A	O
ATOM	1327	OD2	ASP	320	124.486	32.412	17.801	1.00	62.91	A	O
ATOM	1328	C	ASP	320	124.698	32.088	14.237	1.00	30.68	A	C
ATOM	1329	O	ASP	320	125.367	33.072	13.905	1.00	30.46	A	O
ATOM	1330	N	GLU	321	123.371	32.042	14.110	1.00	35.58	A	N
ATOM	1331	CA	GLU	321	122.614	33.173	13.569	1.00	36.56	A	C
ATOM	1332	CB	GLU	321	121.126	33.029	13.889	1.00	84.00	A	C
ATOM	1333	CG	GLU	321	120.285	32.398	12.796	1.00	77.84	A	C
ATOM	1334	CD	GLU	321	120.602	30.938	12.569	1.00	77.59	A	C
ATOM	1335	OE1	GLU	321	120.595	30.164	13.549	1.00	79.02	A	O
ATOM	1336	OE2	GLU	321	120.849	30.565	11.404	1.00	81.63	A	O
ATOM	1337	C	GLU	321	123.101	34.500	14.134	1.00	40.55	A	C
ATOM	1338	O	GLU	321	123.278	35.475	13.397	1.00	37.31	A	O
ATOM	1339	N	LEU	322	123.323	34.519	15.447	1.00	25.97	A	N
ATOM	1340	CA	LEU	322	123.769	35.717	16.155	1.00	28.66	A	C
ATOM	1341	CB	LEU	322	123.925	35.407	17.648	1.00	49.06	A	C
ATOM	1342	CG	LEU	322	122.646	35.281	18.477	1.00	47.69	A	C
ATOM	1343	CD1	LEU	322	121.935	36.625	18.486	1.00	49.43	A	C
ATOM	1344	CD2	LEU	322	121.745	34.194	17.917	1.00	52.74	A	C
ATOM	1345	C	LEU	322	125.052	36.368	15.644	1.00	30.25	A	C
ATOM	1346	O	LEU	322	125.106	37.580	15.459	1.00	33.60	A	O
ATOM	1347	N	ALA	323	126.080	35.558	15.424	1.00	27.12	A	N
ATOM	1348	CA	ALA	323	127.358	36.071	14.965	1.00	27.55	A	C
ATOM	1349	CB	ALA	323	128.420	34.994	15.112	1.00	20.92	A	C
ATOM	1350	C	ALA	323	127.368	36.631	13.539	1.00	27.96	A	C
ATOM	1351	O	ALA	323	128.363	37.227	13.120	1.00	27.98	A	O
ATOM	1352	N	LEU	324	126.280	36.451	12.794	1.00	44.60	A	N
ATOM	1353	CA	LEU	324	126.231	36.961	11.427	1.00	43.08	A	C
ATOM	1354	CB	LEU	324	124.807	36.875	10.867	1.00	12.96	A	C
ATOM	1355	CG	LEU	324	124.398	35.546	10.215	1.00	11.69	A	C
ATOM	1356	CD1	LEU	324	122.900	35.547	9.935	1.00	10.83	A	C
ATOM	1357	CD2	LEU	324	125.197	35.331	8.938	1.00	9.62	A	C
ATOM	1358	C	LEU	324	126.734	38.400	11.346	1.00	46.61	A	C
ATOM	1359	O	LEU	324	127.545	38.735	10.484	1.00	43.15	A	O
ATOM	1360	N	VAL	325	126.257	39.244	12.252	1.00	37.14	A	N
ATOM	1361	CA	VAL	325	126.657	40.645	12.297	1.00	40.67	A	C
ATOM	1362	CB	VAL	325	126.111	41.328	13.549	1.00	15.02	A	C
ATOM	1363	CG1	VAL	325	124.613	41.517	13.425	1.00	15.13	A	C
ATOM	1364	CG2	VAL	325	126.453	40.503	14.773	1.00	18.41	A	C
ATOM	1365	C	VAL	325	128.168	40.840	12.304	1.00	43.49	A	C
ATOM	1366	O	VAL	325	128.706	41.663	11.560	1.00	45.55	A	O
ATOM	1367	N	THR	326	128.844	40.088	13.161	1.00	37.74	A	N
ATOM	1368	CA	THR	326	130.289	40.164	13.286	1.00	39.15	A	C
ATOM	1369	CB	THR	326	130.768	39.218	14.391	1.00	28.63	A	C
ATOM	1370	OG1	THR	326	130.648	37.863	13.944	1.00	30.54	A	O
ATOM	1371	CG2	THR	326	129.911	39.398	15.643	1.00	31.00	A	C
ATOM	1372	C	THR	326	130.996	39.790	11.985	1.00	39.16	A	C
ATOM	1373	O	THR	326	132.105	39.268	12.005	1.00	37.98	A	O
ATOM	1374	N	ILE	327	130.358	40.065	10.854	1.00	29.50	A	N
ATOM	1375	CA	ILE	327	130.922	39.739	9.552	1.00	29.69	A	C
ATOM	1376	CB	ILE	327	130.407	38.343	9.098	1.00	36.77	A	C
ATOM	1377	CG2	ILE	327	129.867	38.372	7.679	1.00	37.54	A	C
ATOM	1378	CG1	ILE	327	131.539	37.335	9.199	1.00	37.13	A	C
ATOM	1379	CD1	ILE	327	131.100	35.928	8.903	1.00	36.80	A	C
ATOM	1380	C	ILE	327	130.572	40.816	8.520	1.00	30.20	A	C
ATOM	1381	O	ILE	327	131.284	41.008	7.530	1.00	30.45	A	O
ATOM	1382	N	VAL	328	129.478	41.527	8.766	1.00	25.26	A	N
ATOM	1383	CA	VAL	328	129.040	42.565	7.851	1.00	27.40	A	C
ATOM	1384	CB	VAL	328	127.851	43.363	8.436	1.00	56.37	A	C
ATOM	1385	CG1	VAL	328	126.752	42.408	8.838	1.00	58.32	A	C
ATOM	1386	CG2	VAL	328	128.301	44.197	9.626	1.00	57.64	A	C
ATOM	1387	C	VAL	328	130.159	43.539	7.485	1.00	27.32	A	C

Fig. 19: A-20

ATOM	1388	O	VAL	328	130.220	44.017	6.355	1.00	26.60	A	O
ATOM	1389	N	LYS	329	131.047	43.837	8.426	1.00	32.39	A	N
ATOM	1390	CA	LYS	329	132.121	44.773	8.124	1.00	31.60	A	C
ATOM	1391	CB	LYS	329	132.949	45.076	9.378	1.00	67.11	A	C
ATOM	1392	CG	LYS	329	133.861	46.291	9.242	1.00	68.66	A	C
ATOM	1393	CD	LYS	329	134.737	46.454	10.474	1.00	70.98	A	C
ATOM	1394	CE	LYS	329	135.540	47.746	10.437	1.00	74.02	A	C
ATOM	1395	NZ	LYS	329	134.660	48.952	10.496	1.00	77.70	A	N
ATOM	1396	C	LYS	329	133.014	44.194	7.036	1.00	29.77	A	C
ATOM	1397	O	LYS	329	133.205	44.802	5.978	1.00	30.98	A	O
ATOM	1398	N	ALA	330	133.551	43.008	7.293	1.00	29.12	A	N
ATOM	1399	CA	ALA	330	134.425	42.365	6.331	1.00	29.15	A	C
ATOM	1400	CB	ALA	330	134.997	41.091	6.922	1.00	30.19	A	C
ATOM	1401	C	ALA	330	133.681	42.056	5.043	1.00	30.30	A	C
ATOM	1402	O	ALA	330	134.207	42.269	3.955	1.00	30.20	A	O
ATOM	1403	N	LEU	331	132.457	41.551	5.168	1.00	22.22	A	N
ATOM	1404	CA	LEU	331	131.661	41.206	3.994	1.00	19.86	A	C
ATOM	1405	CB	LEU	331	130.284	40.667	4.403	1.00	36.97	A	C
ATOM	1406	CG	LEU	331	129.567	39.761	3.389	1.00	33.39	A	C
ATOM	1407	CD1	LEU	331	128.110	39.600	3.787	1.00	35.02	A	C
ATOM	1408	CD2	LEU	331	129.658	40.343	1.996	1.00	29.08	A	C
ATOM	1409	C	LEU	331	131.483	42.467	3.162	1.00	19.89	A	C
ATOM	1410	O	LEU	331	131.741	42.468	1.961	1.00	19.24	A	O
ATOM	1411	N	GLY	332	131.045	43.535	3.830	1.00	15.82	A	N
ATOM	1412	CA	GLY	332	130.824	44.811	3.179	1.00	16.92	A	C
ATOM	1413	C	GLY	332	132.024	45.309	2.402	1.00	17.18	A	C
ATOM	1414	O	GLY	332	131.911	45.651	1.224	1.00	21.05	A	O
ATOM	1415	N	GLU	333	133.185	45.347	3.045	1.00	34.74	A	N
ATOM	1416	CA	GLU	333	134.369	45.831	2.362	1.00	32.80	A	C
ATOM	1417	CB	GLU	333	135.472	46.165	3.371	1.00	75.29	A	C
ATOM	1418	CG	GLU	333	136.139	44.968	4.005	1.00	73.66	A	C
ATOM	1419	CD	GLU	333	137.251	45.363	4.959	1.00	73.68	A	C
ATOM	1420	OE1	GLU	333	137.953	44.459	5.456	1.00	75.73	A	O
ATOM	1421	OE2	GLU	333	137.421	46.575	5.215	1.00	67.80	A	O
ATOM	1422	C	GLU	333	134.888	44.841	1.322	1.00	31.78	A	C
ATOM	1423	O	GLU	333	135.370	45.236	0.261	1.00	31.40	A	O
ATOM	1424	N	ARG	334	134.781	43.552	1.610	1.00	50.02	A	N
ATOM	1425	CA	ARG	334	135.275	42.563	0.669	1.00	53.40	A	C
ATOM	1426	CB	ARG	334	135.064	41.152	1.215	1.00	83.27	A	C
ATOM	1427	CG	ARG	334	136.000	40.123	0.607	1.00	82.56	A	C
ATOM	1428	CD	ARG	334	136.564	39.198	1.677	1.00	81.32	A	C
ATOM	1429	NE	ARG	334	137.441	39.901	2.612	1.00	76.87	A	N
ATOM	1430	CZ	ARG	334	137.888	39.383	3.753	1.00	80.96	A	C
ATOM	1431	NH1	ARG	334	137.537	38.148	4.108	1.00	77.70	A	N
ATOM	1432	NH2	ARG	334	138.686	40.097	4.539	1.00	87.10	A	N
ATOM	1433	C	ARG	334	134.556	42.757	-0.654	1.00	54.70	A	C
ATOM	1434	O	ARG	334	135.170	42.716	-1.716	1.00	51.62	A	O
ATOM	1435	N	ILE	335	133.253	42.988	-0.591	1.00	36.48	A	N
ATOM	1436	CA	ILE	335	132.473	43.214	-1.803	1.00	36.41	A	C
ATOM	1437	CB	ILE	335	130.940	42.967	-1.539	1.00	33.09	A	C
ATOM	1438	CG2	ILE	335	130.524	43.522	-0.203	1.00	35.87	A	C
ATOM	1439	CG1	ILE	335	130.094	43.611	-2.630	1.00	34.31	A	C
ATOM	1440	CD1	ILE	335	128.612	43.520	-2.368	1.00	37.10	A	C
ATOM	1441	C	ILE	335	132.742	44.663	-2.215	1.00	34.70	A	C
ATOM	1442	O	ILE	335	132.421	45.092	-3.326	1.00	37.30	A	O
ATOM	1443	N	PHE	336	133.392	45.377	-1.299	1.00	108.43	A	N
ATOM	1444	CA	PHE	336	133.744	46.789	-1.419	1.00	108.06	A	C
ATOM	1445	CB	PHE	336	135.092	46.989	-2.157	1.00	57.00	A	C
ATOM	1446	CG	PHE	336	135.114	46.540	-3.601	1.00	53.32	A	C
ATOM	1447	CD1	PHE	336	134.135	46.941	-4.508	1.00	52.74	A	C
ATOM	1448	CD2	PHE	336	136.178	45.779	-4.073	1.00	51.27	A	C
ATOM	1449	CE1	PHE	336	134.219	46.589	-5.868	1.00	43.07	A	C
ATOM	1450	CE2	PHE	336	136.271	45.426	-5.422	1.00	45.63	A	C
ATOM	1451	CZ	PHE	336	135.292	45.832	-6.319	1.00	46.09	A	C
ATOM	1452	C	PHE	336	132.662	47.670	-2.020	1.00	108.09	A	C
ATOM	1453	O	PHE	336	131.623	47.131	-2.453	1.00	87.71	A	O
ATOM	1454	OXT	PHE	336	132.864	48.902	-2.024	1.00	40.49	A	O
ATOM	1455	CB	GLU	1	119.537	12.185	27.786	1.00	88.08	H	C
ATOM	1456	CG	GLU	1	118.650	11.120	28.419	1.00	88.08	H	C
ATOM	1457	CD	GLU	1	119.399	10.237	29.409	1.00	88.08	H	C
ATOM	1458	OE1	GLU	1	120.127	10.777	30.271	1.00	88.08	H	O
ATOM	1459	OE2	GLU	1	119.251	8.998	29.324	1.00	88.08	H	O
ATOM	1460	C	GLU	1	118.366	14.360	28.176	1.00	62.78	H	C

Fig. 19: A-21

ATOM	1461	O	GLU	1	117.763	15.033	29.012	1.00	62.78	H	O
ATOM	1462	N	GLU	1	119.687	13.262	30.016	1.00	62.78	H	N
ATOM	1463	CA	GLU	1	119.580	13.515	28.553	1.00	62.78	H	C
ATOM	1464	N	VAL	2	118.019	14.312	26.896	1.00	44.26	H	N
ATOM	1465	CA	VAL	2	116.896	15.064	26.359	1.00	44.26	H	C
ATOM	1466	CB	VAL	2	117.154	15.460	24.909	1.00	15.14	H	C
ATOM	1467	CG1	VAL	2	118.610	15.840	24.732	1.00	15.14	H	C
ATOM	1468	CG2	VAL	2	116.807	14.309	23.997	1.00	15.14	H	C
ATOM	1469	C	VAL	2	115.677	14.174	26.353	1.00	44.26	H	C
ATOM	1470	O	VAL	2	115.803	12.951	26.347	1.00	44.26	H	O
ATOM	1471	N	GLN	3	114.497	14.780	26.340	1.00	25.45	H	N
ATOM	1472	CA	GLN	3	113.280	13.984	26.288	1.00	25.45	H	C
ATOM	1473	CB	GLN	3	113.191	13.046	27.494	1.00	105.15	H	C
ATOM	1474	CG	GLN	3	113.307	13.707	28.841	1.00	105.15	H	C
ATOM	1475	CD	GLN	3	113.015	12.733	29.961	1.00	105.15	H	C
ATOM	1476	OE1	GLN	3	113.554	11.623	29.990	1.00	105.15	H	O
ATOM	1477	NE2	GLN	3	112.157	13.139	30.892	1.00	105.15	H	N
ATOM	1478	C	GLN	3	111.961	14.708	26.119	1.00	25.45	H	C
ATOM	1479	O	GLN	3	111.809	15.887	26.438	1.00	25.45	H	O
ATOM	1480	N	LEU	4	111.009	13.959	25.588	1.00	27.88	H	N
ATOM	1481	CA	LEU	4	109.668	14.446	25.339	1.00	27.88	H	C
ATOM	1482	CB	LEU	4	109.347	14.369	23.842	1.00	33.14	H	C
ATOM	1483	CG	LEU	4	110.367	14.924	22.847	1.00	33.14	H	C
ATOM	1484	CD1	LEU	4	109.821	14.772	21.438	1.00	33.14	H	C
ATOM	1485	CD2	LEU	4	110.646	16.385	23.155	1.00	33.14	H	C
ATOM	1486	C	LEU	4	108.755	13.507	26.095	1.00	27.88	H	C
ATOM	1487	O	LEU	4	108.871	12.282	25.960	1.00	27.88	H	O
ATOM	1488	N	VAL	5	107.858	14.061	26.901	1.00	26.47	H	N
ATOM	1489	CA	VAL	5	106.942	13.215	27.656	1.00	26.47	H	C
ATOM	1490	CB	VAL	5	107.176	13.329	29.197	1.00	25.39	H	C
ATOM	1491	CG1	VAL	5	107.281	14.772	29.606	1.00	25.39	H	C
ATOM	1492	CG2	VAL	5	106.046	12.654	29.947	1.00	25.39	H	C
ATOM	1493	C	VAL	5	105.520	13.578	27.297	1.00	26.47	H	C
ATOM	1494	O	VAL	5	105.031	14.664	27.635	1.00	26.47	H	O
ATOM	1495	N	GLU	6	104.868	12.650	26.601	1.00	23.78	H	N
ATOM	1496	CA	GLU	6	103.495	12.835	26.133	1.00	23.78	H	C
ATOM	1497	CB	GLU	6	103.258	11.995	24.885	1.00	29.58	H	C
ATOM	1498	CG	GLU	6	104.409	12.017	23.933	1.00	29.58	H	C
ATOM	1499	CD	GLU	6	104.188	11.109	22.756	1.00	29.58	H	C
ATOM	1500	OE1	GLU	6	105.194	10.664	22.168	1.00	29.58	H	O
ATOM	1501	OE2	GLU	6	103.013	10.846	22.413	1.00	29.58	H	O
ATOM	1502	C	GLU	6	102.429	12.485	27.155	1.00	23.78	H	C
ATOM	1503	O	GLU	6	102.680	11.740	28.101	1.00	23.78	H	O
ATOM	1504	N	SER	7	101.242	13.047	26.937	1.00	26.30	H	N
ATOM	1505	CA	SER	7	100.061	12.823	27.766	1.00	26.30	H	C
ATOM	1506	CB	SER	7	100.177	13.535	29.102	1.00	32.56	H	C
ATOM	1507	OG	SER	7	100.574	14.871	28.906	1.00	32.56	H	O
ATOM	1508	C	SER	7	98.886	13.381	26.998	1.00	26.30	H	C
ATOM	1509	O	SER	7	99.060	14.248	26.136	1.00	26.30	H	O
ATOM	1510	N	GLY	8	97.693	12.872	27.287	1.00	41.74	H	N
ATOM	1511	CA	GLY	8	96.514	13.360	26.598	1.00	41.74	H	C
ATOM	1512	C	GLY	8	95.807	12.321	25.752	1.00	41.74	H	C
ATOM	1513	O	GLY	8	94.745	12.603	25.201	1.00	41.74	H	O
ATOM	1514	N	GLY	9	96.383	11.127	25.637	1.00	47.50	H	N
ATOM	1515	CA	GLY	9	95.751	10.079	24.851	1.00	47.50	H	C
ATOM	1516	C	GLY	9	94.431	9.601	25.446	1.00	47.50	H	C
ATOM	1517	O	GLY	9	94.038	10.020	26.536	1.00	47.50	H	O
ATOM	1518	N	GLY	10	93.732	8.723	24.735	1.00	16.50	H	N
ATOM	1519	CA	GLY	10	92.469	8.225	25.244	1.00	16.50	H	C
ATOM	1520	C	GLY	10	91.485	7.806	24.169	1.00	16.50	H	C
ATOM	1521	O	GLY	10	91.830	7.701	22.990	1.00	16.50	H	O
ATOM	1522	N	LEU	11	90.251	7.559	24.595	1.00	37.61	H	N
ATOM	1523	CA	LEU	11	89.175	7.137	23.710	1.00	37.61	H	C
ATOM	1524	CB	LEU	11	88.388	6.003	24.365	1.00	18.32	H	C
ATOM	1525	CG	LEU	11	86.959	5.715	23.885	1.00	18.32	H	C
ATOM	1526	CD1	LEU	11	86.962	5.148	22.463	1.00	18.32	H	C
ATOM	1527	CD2	LEU	11	86.313	4.729	24.856	1.00	18.32	H	C
ATOM	1528	C	LEU	11	88.235	8.292	23.436	1.00	37.61	H	C
ATOM	1529	O	LEU	11	87.769	8.943	24.365	1.00	37.61	H	O
ATOM	1530	N	VAL	12	87.961	8.550	22.165	1.00	31.23	H	N
ATOM	1531	CA	VAL	12	87.048	9.624	21.792	1.00	31.23	H	C
ATOM	1532	CB	VAL	12	87.794	10.800	21.144	1.00	52.64	H	C
ATOM	1533	CG1	VAL	12	88.609	11.532	22.192	1.00	52.64	H	C

Fig. 19: A-22

ATOM	1534	CG2	VAL	12	88.699	10.290	20.039	1.00	52.64	H	C
ATOM	1535	C	VAL	12	86.062	9.045	20.794	1.00	31.23	H	C
ATOM	1536	O	VAL	12	86.365	8.057	20.138	1.00	31.23	H	O
ATOM	1537	N	GLN	13	84.882	9.640	20.681	1.00	27.32	H	N
ATOM	1538	CA	GLN	13	83.894	9.126	19.741	1.00	27.32	H	C
ATOM	1539	CB	GLN	13	82.493	9.391	20.270	1.00	92.40	H	C
ATOM	1540	CG	GLN	13	82.206	8.652	21.553	1.00	92.40	H	C
ATOM	1541	CD	GLN	13	80.808	8.906	22.056	1.00	92.40	H	C
ATOM	1542	OE1	GLN	13	79.836	8.766	21.310	1.00	92.40	H	O
ATOM	1543	NE2	GLN	13	80.693	9.276	23.329	1.00	92.40	H	N
ATOM	1544	C	GLN	13	84.063	9.747	18.356	1.00	27.32	H	C
ATOM	1545	O	GLN	13	84.400	10.924	18.227	1.00	27.32	H	O
ATOM	1546	N	PRO	14	83.834	8.955	17.298	1.00	39.48	H	N
ATOM	1547	CD	PRO	14	83.418	7.539	17.302	1.00	31.44	H	C
ATOM	1548	CA	PRO	14	83.971	9.452	15.929	1.00	39.48	H	C
ATOM	1549	CB	PRO	14	83.219	8.406	15.118	1.00	31.44	H	C
ATOM	1550	CG	PRO	14	83.584	7.145	15.837	1.00	31.44	H	C
ATOM	1551	C	PRO	14	83.401	10.849	15.766	1.00	39.48	H	C
ATOM	1552	O	PRO	14	82.235	11.076	16.053	1.00	39.48	H	O
ATOM	1553	N	GLY	15	84.233	11.784	15.319	1.00	28.44	H	N
ATOM	1554	CA	GLY	15	83.788	13.154	15.130	1.00	28.44	H	C
ATOM	1555	C	GLY	15	84.048	14.065	16.323	1.00	28.44	H	C
ATOM	1556	O	GLY	15	83.759	15.265	16.269	1.00	28.44	H	O
ATOM	1557	N	GLY	16	84.588	13.496	17.401	1.00	22.09	H	N
ATOM	1558	CA	GLY	16	84.880	14.266	18.601	1.00	22.09	H	C
ATOM	1559	C	GLY	16	86.286	14.826	18.571	1.00	22.09	H	C
ATOM	1560	O	GLY	16	86.900	14.912	17.507	1.00	22.09	H	O
ATOM	1561	N	SER	17	86.819	15.202	19.726	1.00	31.69	H	N
ATOM	1562	CA	SER	17	88.161	15.762	19.749	1.00	31.69	H	C
ATOM	1563	CB	SER	17	88.085	17.272	19.592	1.00	54.23	H	C
ATOM	1564	OG	SER	17	87.308	17.829	20.625	1.00	54.23	H	O
ATOM	1565	C	SER	17	88.953	15.416	21.000	1.00	31.69	H	C
ATOM	1566	O	SER	17	88.427	14.824	21.944	1.00	31.69	H	O
ATOM	1567	N	LEU	18	90.227	15.794	20.995	1.00	31.76	H	N
ATOM	1568	CA	LEU	18	91.132	15.515	22.105	1.00	31.76	H	C
ATOM	1569	CB	LEU	18	91.452	14.019	22.124	1.00	63.56	H	C
ATOM	1570	CG	LEU	18	92.462	13.465	23.124	1.00	63.56	H	C
ATOM	1571	CD1	LEU	18	92.121	13.932	24.536	1.00	63.56	H	C
ATOM	1572	CD2	LEU	18	92.462	11.942	23.017	1.00	63.56	H	C
ATOM	1573	C	LEU	18	92.407	16.334	21.899	1.00	31.76	H	C
ATOM	1574	O	LEU	18	92.622	16.884	20.815	1.00	31.76	H	O
ATOM	1575	N	ARG	19	93.243	16.443	22.928	1.00	39.26	H	N
ATOM	1576	CA	ARG	19	94.475	17.207	22.781	1.00	39.26	H	C
ATOM	1577	CB	ARG	19	94.303	18.650	23.258	1.00	32.50	H	C
ATOM	1578	CG	ARG	19	95.571	19.474	23.063	1.00	32.50	H	C
ATOM	1579	CD	ARG	19	95.481	20.862	23.667	1.00	32.50	H	C
ATOM	1580	NE	ARG	19	95.387	20.846	25.125	1.00	32.50	H	N
ATOM	1581	CZ	ARG	19	95.262	21.936	25.879	1.00	32.50	H	C
ATOM	1582	NH1	ARG	19	95.220	23.138	25.322	1.00	32.50	H	N
ATOM	1583	NH2	ARG	19	95.162	21.824	27.193	1.00	32.50	H	N
ATOM	1584	C	ARG	19	95.668	16.606	23.500	1.00	39.26	H	C
ATOM	1585	O	ARG	19	95.687	16.469	24.732	1.00	39.26	H	O
ATOM	1586	N	LEU	20	96.677	16.266	22.709	1.00	36.74	H	N
ATOM	1587	CA	LEU	20	97.896	15.695	23.241	1.00	36.74	H	C
ATOM	1588	CB	LEU	20	98.534	14.737	22.222	1.00	31.69	H	C
ATOM	1589	CG	LEU	20	97.601	13.846	21.390	1.00	31.69	H	C
ATOM	1590	CD1	LEU	20	98.426	12.870	20.555	1.00	31.69	H	C
ATOM	1591	CD2	LEU	20	96.659	13.093	22.292	1.00	31.69	H	C
ATOM	1592	C	LEU	20	98.854	16.838	23.533	1.00	36.74	H	C
ATOM	1593	O	LEU	20	98.866	17.856	22.840	1.00	36.74	H	O
ATOM	1594	N	SER	21	99.638	16.664	24.584	1.00	25.68	H	N
ATOM	1595	CA	SER	21	100.635	17.640	24.974	1.00	25.68	H	C
ATOM	1596	CB	SER	21	100.273	18.278	26.307	1.00	13.03	H	C
ATOM	1597	OG	SER	21	99.718	17.320	27.175	1.00	13.03	H	O
ATOM	1598	C	SER	21	101.901	16.838	25.099	1.00	25.68	H	C
ATOM	1599	O	SER	21	101.851	15.635	25.336	1.00	25.68	H	O
ATOM	1600	N	CYS	22	103.036	17.498	24.931	1.00	22.18	H	N
ATOM	1601	CA	CYS	22	104.321	16.822	25.008	1.00	22.18	H	C
ATOM	1602	C	CYS	22	105.255	17.765	25.713	1.00	22.18	H	C
ATOM	1603	O	CYS	22	105.491	18.863	25.229	1.00	22.18	H	O
ATOM	1604	CB	CYS	22	104.804	16.543	23.603	1.00	57.35	H	C
ATOM	1605	SG	CYS	22	106.473	15.867	23.383	1.00	57.35	H	S
ATOM	1606	N	ALA	23	105.769	17.349	26.867	1.00	26.87	H	N

Fig. 19: A-23

ATOM	1607	CA	ALA	23	106.669	18.191	27.654	1.00	26.87	H	C
ATOM	1608	CB	ALA	23	106.470	17.937	29.141	1.00	9.84	H	C
ATOM	1609	C	ALA	23	108.125	17.989	27.284	1.00	26.87	H	C
ATOM	1610	O	ALA	23	108.683	16.899	27.437	1.00	26.87	H	O
ATOM	1611	N	ALA	24	108.738	19.058	26.800	1.00	13.29	H	N
ATOM	1612	CA	ALA	24	110.124	18.988	26.409	1.00	13.29	H	C
ATOM	1613	CB	ALA	24	110.357	19.851	25.183	1.00	45.62	H	C
ATOM	1614	C	ALA	24	111.023	19.432	27.552	1.00	13.29	H	C
ATOM	1615	O	ALA	24	110.664	20.304	28.356	1.00	13.29	H	O
ATOM	1616	N	SER	25	112.194	18.819	27.617	1.00	22.11	H	N
ATOM	1617	CA	SER	25	113.168	19.152	28.634	1.00	22.11	H	C
ATOM	1618	CB	SER	25	112.731	18.582	29.982	1.00	51.20	H	C
ATOM	1619	OG	SER	25	112.401	17.214	29.862	1.00	51.20	H	O
ATOM	1620	C	SER	25	114.526	18.591	28.232	1.00	22.11	H	C
ATOM	1621	O	SER	25	114.614	17.539	27.590	1.00	22.11	H	O
ATOM	1622	N	GLY	26	115.582	19.306	28.591	1.00	10.76	H	N
ATOM	1623	CA	GLY	26	116.914	18.844	28.263	1.00	10.76	H	C
ATOM	1624	C	GLY	26	117.553	19.585	27.107	1.00	10.76	H	C
ATOM	1625	O	GLY	26	118.728	19.367	26.809	1.00	10.76	H	O
ATOM	1626	N	PHE	27	116.794	20.458	26.448	1.00	18.08	H	N
ATOM	1627	CA	PHE	27	117.325	21.207	25.318	1.00	18.08	H	C
ATOM	1628	CB	PHE	27	117.241	20.373	24.031	1.00	16.53	H	C
ATOM	1629	CG	PHE	27	115.842	19.974	23.651	1.00	16.53	H	C
ATOM	1630	CD1	PHE	27	115.089	19.140	24.476	1.00	16.53	H	C
ATOM	1631	CD2	PHE	27	115.269	20.448	22.476	1.00	16.53	H	C
ATOM	1632	CE1	PHE	27	113.770	18.782	24.137	1.00	16.53	H	C
ATOM	1633	CE2	PHE	27	113.958	20.101	22.125	1.00	16.53	H	C
ATOM	1634	CZ	PHE	27	113.203	19.268	22.954	1.00	16.53	H	C
ATOM	1635	C	PHE	27	116.592	22.528	25.135	1.00	18.08	H	C
ATOM	1636	O	PHE	27	115.566	22.780	25.763	1.00	18.08	H	O
ATOM	1637	N	THR	28	117.139	23.377	24.276	1.00	42.88	H	N
ATOM	1638	CA	THR	28	116.544	24.672	24.017	1.00	42.88	H	C
ATOM	1639	CB	THR	28	117.575	25.604	23.381	1.00	53.65	H	C
ATOM	1640	OG1	THR	28	118.841	25.399	24.018	1.00	53.65	H	O
ATOM	1641	CG2	THR	28	117.168	27.056	23.561	1.00	53.65	H	C
ATOM	1642	C	THR	28	115.369	24.463	23.074	1.00	42.88	H	C
ATOM	1643	O	THR	28	115.484	24.666	21.868	1.00	42.88	H	O
ATOM	1644	N	PHE	29	114.239	24.051	23.644	1.00	29.92	H	N
ATOM	1645	CA	PHE	29	113.004	23.772	22.901	1.00	29.92	H	C
ATOM	1646	CB	PHE	29	111.855	23.614	23.906	1.00	3.95	H	C
ATOM	1647	CG	PHE	29	110.503	23.347	23.276	1.00	3.95	H	C
ATOM	1648	CD1	PHE	29	110.208	22.102	22.696	1.00	3.95	H	C
ATOM	1649	CD2	PHE	29	109.504	24.336	23.283	1.00	3.95	H	C
ATOM	1650	CE1	PHE	29	108.939	21.852	22.139	1.00	3.95	H	C
ATOM	1651	CE2	PHE	29	108.234	24.092	22.727	1.00	3.95	H	C
ATOM	1652	CZ	PHE	29	107.953	22.860	22.160	1.00	3.95	H	C
ATOM	1653	C	PHE	29	112.611	24.777	21.797	1.00	29.92	H	C
ATOM	1654	O	PHE	29	112.390	24.389	20.647	1.00	29.92	H	O
ATOM	1655	N	SER	30	112.539	26.058	22.144	1.00	32.50	H	N
ATOM	1656	CA	SER	30	112.139	27.105	21.199	1.00	32.50	H	C
ATOM	1657	CB	SER	30	112.335	28.473	21.852	1.00	67.50	H	C
ATOM	1658	OG	SER	30	113.644	28.591	22.372	1.00	67.50	H	O
ATOM	1659	C	SER	30	112.799	27.107	19.812	1.00	32.50	H	C
ATOM	1660	O	SER	30	112.191	27.504	18.816	1.00	32.50	H	O
ATOM	1661	N	ARG	31	114.037	26.649	19.751	1.00	18.89	H	N
ATOM	1662	CA	ARG	31	114.801	26.636	18.515	1.00	18.89	H	C
ATOM	1663	CB	ARG	31	116.292	26.604	18.886	1.00	48.17	H	C
ATOM	1664	CG	ARG	31	117.217	25.955	17.887	1.00	48.17	H	C
ATOM	1665	CD	ARG	31	118.650	26.425	18.112	1.00	48.17	H	C
ATOM	1666	NE	ARG	31	119.135	26.203	19.476	1.00	48.17	H	N
ATOM	1667	CZ	ARG	31	120.228	26.777	19.980	1.00	48.17	H	C
ATOM	1668	NH1	ARG	31	120.950	27.608	19.238	1.00	48.17	H	N
ATOM	1669	NH2	ARG	31	120.604	26.524	21.226	1.00	48.17	H	N
ATOM	1670	C	ARG	31	114.463	25.523	17.521	1.00	18.89	H	C
ATOM	1671	O	ARG	31	114.520	25.723	16.313	1.00	18.89	H	O
ATOM	1672	N	TYR	32	114.095	24.353	18.027	1.00	15.47	H	N
ATOM	1673	CA	TYR	32	113.791	23.200	17.179	1.00	15.47	H	C
ATOM	1674	CB	TYR	32	113.949	21.922	17.996	1.00	6.03	H	C
ATOM	1675	CG	TYR	32	115.367	21.653	18.426	1.00	6.03	H	C
ATOM	1676	CD1	TYR	32	115.934	22.336	19.500	1.00	6.03	H	C
ATOM	1677	CE1	TYR	32	117.249	22.097	19.889	1.00	6.03	H	C
ATOM	1678	CD2	TYR	32	116.153	20.722	17.747	1.00	6.03	H	C
ATOM	1679	CE2	TYR	32	117.467	20.477	18.122	1.00	6.03	H	C

Fig. 19: A-24

ATOM	1680	CZ	TYR	32	118.013	21.165	19.198	1.00	6.03	H	C
ATOM	1681	OH	TYR	32	119.317	20.907	19.597	1.00	6.03	H	O
ATOM	1682	C	TYR	32	112.426	23.184	16.534	1.00	15.47	H	C
ATOM	1683	O	TYR	32	111.480	23.748	17.058	1.00	15.47	H	O
ATOM	1684	N	THR	33	112.309	22.545	15.382	1.00	10.91	H	N
ATOM	1685	CA	THR	33	110.988	22.451	14.792	1.00	10.91	H	C
ATOM	1686	CB	THR	33	111.032	22.556	13.230	1.00	11.96	H	C
ATOM	1687	OG1	THR	33	111.079	21.259	12.639	1.00	11.96	H	O
ATOM	1688	CG2	THR	33	112.251	23.338	12.786	1.00	11.96	H	C
ATOM	1689	C	THR	33	110.501	21.082	15.303	1.00	10.91	H	C
ATOM	1690	O	THR	33	111.188	20.061	15.157	1.00	10.91	H	O
ATOM	1691	N	MET	34	109.348	21.070	15.960	1.00	21.14	H	N
ATOM	1692	CA	MET	34	108.815	19.835	16.518	1.00	21.14	H	C
ATOM	1693	CB	MET	34	108.188	20.094	17.888	1.00	16.88	H	C
ATOM	1694	CG	MET	34	109.035	20.899	18.847	1.00	16.88	H	C
ATOM	1695	SD	MET	34	110.603	20.131	19.122	1.00	16.88	H	S
ATOM	1696	CE	MET	34	110.155	18.770	20.240	1.00	16.88	H	C
ATOM	1697	C	MET	34	107.760	19.218	15.614	1.00	21.14	H	C
ATOM	1698	O	MET	34	107.160	19.905	14.781	1.00	21.14	H	O
ATOM	1699	N	SER	35	107.519	17.925	15.802	1.00	15.88	H	N
ATOM	1700	CA	SER	35	106.533	17.232	14.997	1.00	15.88	H	C
ATOM	1701	CB	SER	35	107.205	16.581	13.794	1.00	13.53	H	C
ATOM	1702	OG	SER	35	107.895	17.550	13.034	1.00	13.53	H	O
ATOM	1703	C	SER	35	105.767	16.168	15.763	1.00	15.88	H	C
ATOM	1704	O	SER	35	106.058	15.867	16.926	1.00	15.88	H	O
ATOM	1705	N	TRP	36	104.765	15.617	15.087	1.00	13.73	H	N
ATOM	1706	CA	TRP	36	103.948	14.556	15.626	1.00	13.73	H	C
ATOM	1707	CB	TRP	36	102.510	15.023	15.849	1.00	20.04	H	C
ATOM	1708	CG	TRP	36	102.337	15.903	17.039	1.00	20.04	H	C
ATOM	1709	CD2	TRP	36	102.259	15.489	18.406	1.00	20.04	H	C
ATOM	1710	CE2	TRP	36	102.112	16.654	19.186	1.00	20.04	H	C
ATOM	1711	CE3	TRP	36	102.301	14.248	19.046	1.00	20.04	H	C
ATOM	1712	CD1	TRP	36	102.236	17.255	17.045	1.00	20.04	H	C
ATOM	1713	NE1	TRP	36	102.100	17.716	18.329	1.00	20.04	H	N
ATOM	1714	CZ2	TRP	36	102.004	16.622	20.576	1.00	20.04	H	C
ATOM	1715	CZ3	TRP	36	102.192	14.211	20.442	1.00	20.04	H	C
ATOM	1716	CH2	TRP	36	102.044	15.396	21.190	1.00	20.04	H	C
ATOM	1717	C	TRP	36	103.978	13.470	14.565	1.00	13.73	H	C
ATOM	1718	O	TRP	36	103.879	13.769	13.373	1.00	13.73	H	O
ATOM	1719	N	VAL	37	104.138	12.221	15.006	1.00	21.09	H	N
ATOM	1720	CA	VAL	37	104.179	11.054	14.125	1.00	21.09	H	C
ATOM	1721	CB	VAL	37	105.622	10.464	14.053	1.00	6.36	H	C
ATOM	1722	CG1	VAL	37	105.591	9.017	13.642	1.00	6.36	H	C
ATOM	1723	CG2	VAL	37	106.461	11.253	13.057	1.00	6.36	H	C
ATOM	1724	C	VAL	37	103.229	10.041	14.748	1.00	21.09	H	C
ATOM	1725	O	VAL	37	103.144	9.940	15.963	1.00	21.09	H	O
ATOM	1726	N	ARG	38	102.508	9.294	13.929	1.00	17.98	H	N
ATOM	1727	CA	ARG	38	101.562	8.309	14.454	1.00	17.98	H	C
ATOM	1728	CB	ARG	38	100.133	8.697	14.058	1.00	13.99	H	C
ATOM	1729	CG	ARG	38	100.106	9.210	12.633	1.00	13.99	H	C
ATOM	1730	CD	ARG	38	98.899	8.817	11.839	1.00	13.99	H	C
ATOM	1731	NE	ARG	38	97.664	9.434	12.289	1.00	13.99	H	N
ATOM	1732	CZ	ARG	38	96.652	9.707	11.470	1.00	13.99	H	C
ATOM	1733	NH1	ARG	38	96.744	9.432	10.171	1.00	13.99	H	N
ATOM	1734	NH2	ARG	38	95.533	10.224	11.960	1.00	13.99	H	N
ATOM	1735	C	ARG	38	101.856	6.925	13.895	1.00	17.98	H	C
ATOM	1736	O	ARG	38	102.468	6.785	12.840	1.00	17.98	H	O
ATOM	1737	N	GLN	39	101.386	5.909	14.604	1.00	17.63	H	N
ATOM	1738	CA	GLN	39	101.560	4.521	14.200	1.00	17.63	H	C
ATOM	1739	CB	GLN	39	102.659	3.866	15.051	1.00	12.11	H	C
ATOM	1740	CG	GLN	39	102.976	2.424	14.712	1.00	12.11	H	C
ATOM	1741	CD	GLN	39	104.396	2.025	15.134	1.00	12.11	H	C
ATOM	1742	OE1	GLN	39	104.811	2.262	16.272	1.00	12.11	H	O
ATOM	1743	NE2	GLN	39	105.143	1.414	14.212	1.00	12.11	H	N
ATOM	1744	C	GLN	39	100.206	3.847	14.429	1.00	17.63	H	C
ATOM	1745	O	GLN	39	99.712	3.770	15.562	1.00	17.63	H	O
ATOM	1746	N	ALA	40	99.590	3.399	13.344	1.00	55.11	H	N
ATOM	1747	CA	ALA	40	98.300	2.737	13.436	1.00	55.11	H	C
ATOM	1748	CB	ALA	40	97.605	2.754	12.088	1.00	43.12	H	C
ATOM	1749	C	ALA	40	98.536	1.302	13.881	1.00	55.11	H	C
ATOM	1750	O	ALA	40	99.626	0.762	13.687	1.00	55.11	H	O
ATOM	1751	N	PRO	41	97.517	0.670	14.491	1.00	55.83	H	N
ATOM	1752	CD	PRO	41	96.189	1.237	14.782	1.00	86.02	H	C

Fig. 19: A-25

ATOM	1753	CA	PRO	41	97.600	-0.712	14.969	1.00	55.83	H	C
ATOM	1754	CB	PRO	41	96.169	-1.009	15.400	1.00	86.02	H	C
ATOM	1755	CG	PRO	41	95.681	0.315	15.859	1.00	86.02	H	C
ATOM	1756	C	PRO	41	98.057	-1.624	13.838	1.00	55.83	H	C
ATOM	1757	O	PRO	41	97.423	-1.670	12.781	1.00	55.83	H	O
ATOM	1758	N	GLY	42	99.160	-2.335	14.061	1.00	43.01	H	N
ATOM	1759	CA	GLY	42	99.684	-3.227	13.042	1.00	43.01	H	C
ATOM	1760	C	GLY	42	100.227	-2.529	11.800	1.00	43.01	H	C
ATOM	1761	O	GLY	42	100.480	-3.175	10.775	1.00	43.01	H	O
ATOM	1762	N	LYS	43	100.415	-1.212	11.882	1.00	46.16	H	N
ATOM	1763	CA	LYS	43	100.922	-0.446	10.750	1.00	46.16	H	C
ATOM	1764	CB	LYS	43	99.896	0.612	10.334	1.00	59.60	H	C
ATOM	1765	CG	LYS	43	98.800	0.081	9.421	1.00	59.60	H	C
ATOM	1766	CD	LYS	43	98.003	-1.023	10.079	1.00	59.60	H	C
ATOM	1767	CE	LYS	43	97.230	-1.831	9.047	1.00	59.60	H	C
ATOM	1768	NZ	LYS	43	98.125	-2.590	8.124	1.00	59.60	H	N
ATOM	1769	C	LYS	43	102.278	0.215	10.994	1.00	46.16	H	C
ATOM	1770	O	LYS	43	102.889	0.060	12.063	1.00	46.16	H	O
ATOM	1771	N	GLY	44	102.742	0.942	9.976	1.00	50.42	H	N
ATOM	1772	CA	GLY	44	104.016	1.631	10.054	1.00	50.42	H	C
ATOM	1773	C	GLY	44	103.916	3.004	10.691	1.00	50.42	H	C
ATOM	1774	O	GLY	44	103.001	3.281	11.462	1.00	50.42	H	O
ATOM	1775	N	LEU	45	104.862	3.870	10.347	1.00	25.59	H	N
ATOM	1776	CA	LEU	45	104.933	5.229	10.883	1.00	25.59	H	C
ATOM	1777	CB	LEU	45	106.387	5.544	11.224	1.00	8.94	H	C
ATOM	1778	CG	LEU	45	107.011	4.480	12.118	1.00	8.94	H	C
ATOM	1779	CD1	LEU	45	108.520	4.578	12.054	1.00	8.94	H	C
ATOM	1780	CD2	LEU	45	106.481	4.638	13.541	1.00	8.94	H	C
ATOM	1781	C	LEU	45	104.394	6.259	9.893	1.00	25.59	H	C
ATOM	1782	O	LEU	45	104.613	6.142	8.684	1.00	25.59	H	O
ATOM	1783	N	GLU	46	103.698	7.268	10.411	1.00	28.67	H	N
ATOM	1784	CA	GLU	46	103.111	8.308	9.569	1.00	28.67	H	C
ATOM	1785	CB	GLU	46	101.617	8.045	9.370	1.00	21.38	H	C
ATOM	1786	CG	GLU	46	100.977	8.902	8.304	1.00	21.38	H	C
ATOM	1787	CD	GLU	46	99.555	8.471	7.972	1.00	21.38	H	C
ATOM	1788	OE1	GLU	46	98.711	8.399	8.903	1.00	21.38	H	O
ATOM	1789	OE2	GLU	46	99.283	8.214	6.776	1.00	21.38	H	O
ATOM	1790	C	GLU	46	103.304	9.698	10.152	1.00	28.67	H	C
ATOM	1791	O	GLU	46	102.942	9.962	11.301	1.00	28.67	H	O
ATOM	1792	N	TRP	47	103.887	10.579	9.347	1.00	2.61	H	N
ATOM	1793	CA	TRP	47	104.132	11.944	9.758	1.00	2.61	H	C
ATOM	1794	CB	TRP	47	105.055	12.618	8.757	1.00	14.19	H	C
ATOM	1795	CG	TRP	47	105.068	14.095	8.904	1.00	14.19	H	C
ATOM	1796	CD2	TRP	47	104.446	15.035	8.036	1.00	14.19	H	C
ATOM	1797	CE2	TRP	47	104.681	16.323	8.578	1.00	14.19	H	C
ATOM	1798	CE3	TRP	47	103.709	14.919	6.852	1.00	14.19	H	C
ATOM	1799	CD1	TRP	47	105.644	14.824	9.914	1.00	14.19	H	C
ATOM	1800	NE1	TRP	47	105.418	16.161	9.723	1.00	14.19	H	N
ATOM	1801	CZ2	TRP	47	104.201	17.490	7.969	1.00	14.19	H	C
ATOM	1802	CZ3	TRP	47	103.233	16.074	6.248	1.00	14.19	H	C
ATOM	1803	CH2	TRP	47	103.480	17.344	6.808	1.00	14.19	H	C
ATOM	1804	C	TRP	47	102.791	12.673	9.802	1.00	2.61	H	C
ATOM	1805	O	TRP	47	102.083	12.752	8.796	1.00	2.61	H	O
ATOM	1806	N	VAL	48	102.443	13.215	10.962	1.00	34.26	H	N
ATOM	1807	CA	VAL	48	101.165	13.895	11.114	1.00	34.26	H	C
ATOM	1808	CB	VAL	48	100.576	13.639	12.523	1.00	16.29	H	C
ATOM	1809	CG1	VAL	48	99.137	14.148	12.623	1.00	16.29	H	C
ATOM	1810	CG2	VAL	48	100.624	12.187	12.812	1.00	16.29	H	C
ATOM	1811	C	VAL	48	101.246	15.393	10.884	1.00	34.26	H	C
ATOM	1812	O	VAL	48	100.563	15.932	10.015	1.00	34.26	H	O
ATOM	1813	N	ALA	49	102.078	16.068	11.665	1.00	19.79	H	N
ATOM	1814	CA	ALA	49	102.198	17.505	11.533	1.00	19.79	H	C
ATOM	1815	CB	ALA	49	101.052	18.193	12.288	1.00	1.87	H	C
ATOM	1816	C	ALA	49	103.542	17.994	12.041	1.00	19.79	H	C
ATOM	1817	O	ALA	49	104.295	17.244	12.645	1.00	19.79	H	O
ATOM	1818	N	THR	50	103.816	19.271	11.795	1.00	29.76	H	N
ATOM	1819	CA	THR	50	105.067	19.906	12.184	1.00	29.76	H	C
ATOM	1820	CB	THR	50	106.142	19.637	11.127	1.00	20.69	H	C
ATOM	1821	OG1	THR	50	106.390	18.232	11.065	1.00	20.69	H	O
ATOM	1822	CG2	THR	50	107.422	20.357	11.460	1.00	20.69	H	C
ATOM	1823	C	THR	50	104.897	21.416	12.327	1.00	29.76	H	C
ATOM	1824	O	THR	50	104.113	22.035	11.616	1.00	29.76	H	O
ATOM	1825	N	ILE	51	105.649	21.994	13.258	1.00	20.54	H	N

Fig. 19: A-26

ATOM	1826	CA	ILE	51	105.626	23.424	13.530	1.00	20.54	H	C
ATOM	1827	CB	ILE	51	104.824	23.714	14.816	1.00	27.11	H	C
ATOM	1828	CG2	ILE	51	105.430	22.955	15.975	1.00	27.11	H	C
ATOM	1829	CG1	ILE	51	104.805	25.217	15.108	1.00	27.11	H	C
ATOM	1830	CD1	ILE	51	104.073	25.593	16.389	1.00	27.11	H	C
ATOM	1831	C	ILE	51	107.090	23.813	13.723	1.00	20.54	H	C
ATOM	1832	O	ILE	51	107.781	23.208	14.533	1.00	20.54	H	O
ATOM	1833	N	SER	52	107.565	24.803	12.970	1.00	28.49	H	N
ATOM	1834	CA	SER	52	108.962	25.234	13.047	1.00	28.49	H	C
ATOM	1835	CB	SER	52	109.356	26.018	11.797	1.00	35.37	H	C
ATOM	1836	OG	SER	52	108.819	27.332	11.832	1.00	35.37	H	O
ATOM	1837	C	SER	52	109.236	26.105	14.256	1.00	28.49	H	C
ATOM	1838	O	SER	52	108.316	26.461	14.994	1.00	28.49	H	O
ATOM	1839	N	GLY	53	110.509	26.452	14.451	1.00	16.74	H	N
ATOM	1840	CA	GLY	53	110.864	27.295	15.568	1.00	16.74	H	C
ATOM	1841	C	GLY	53	110.203	28.651	15.410	1.00	16.74	H	C
ATOM	1842	O	GLY	53	110.093	29.412	16.369	1.00	16.74	H	O
ATOM	1843	N	GLY	54	109.746	28.939	14.192	1.00	26.55	H	N
ATOM	1844	CA	GLY	54	109.120	30.218	13.907	1.00	26.55	H	C
ATOM	1845	C	GLY	54	107.605	30.253	13.815	1.00	26.55	H	C
ATOM	1846	O	GLY	54	107.020	31.317	13.607	1.00	26.55	H	O
ATOM	1847	N	GLY	55	106.953	29.105	13.948	1.00	34.83	H	N
ATOM	1848	CA	GLY	55	105.505	29.105	13.889	1.00	34.83	H	C
ATOM	1849	C	GLY	55	104.878	28.610	12.604	1.00	34.83	H	C
ATOM	1850	O	GLY	55	103.657	28.663	12.458	1.00	34.83	H	O
ATOM	1851	N	HIS	56	105.683	28.149	11.655	1.00	20.17	H	N
ATOM	1852	CA	HIS	56	105.091	27.643	10.426	1.00	20.17	H	C
ATOM	1853	CB	HIS	56	106.117	27.522	9.302	1.00	75.35	H	C
ATOM	1854	CG	HIS	56	106.829	28.797	8.996	1.00	75.35	H	C
ATOM	1855	CD2	HIS	56	106.561	29.773	8.096	1.00	75.35	H	C
ATOM	1856	ND1	HIS	56	107.959	29.201	9.677	1.00	75.35	H	N
ATOM	1857	CE1	HIS	56	108.356	30.370	9.209	1.00	75.35	H	C
ATOM	1858	NE2	HIS	56	107.525	30.739	8.250	1.00	75.35	H	N
ATOM	1859	C	HIS	56	104.585	26.266	10.774	1.00	20.17	H	C
ATOM	1860	O	HIS	56	105.309	25.465	11.350	1.00	20.17	H	O
ATOM	1861	N	THR	57	103.331	25.994	10.458	1.00	9.30	H	N
ATOM	1862	CA	THR	57	102.793	24.676	10.728	1.00	9.30	H	C
ATOM	1863	CB	THR	57	101.437	24.766	11.475	1.00	25.93	H	C
ATOM	1864	OG1	THR	57	100.483	25.493	10.691	1.00	25.93	H	O
ATOM	1865	CG2	THR	57	101.624	25.460	12.821	1.00	25.93	H	C
ATOM	1866	C	THR	57	102.657	23.911	9.403	1.00	9.30	H	C
ATOM	1867	O	THR	57	102.437	24.503	8.348	1.00	9.30	H	O
ATOM	1868	N	TYR	58	102.849	22.598	9.463	1.00	10.35	H	N
ATOM	1869	CA	TYR	58	102.739	21.729	8.293	1.00	10.35	H	C
ATOM	1870	CB	TYR	58	104.115	21.217	7.912	1.00	22.31	H	C
ATOM	1871	CG	TYR	58	105.023	22.324	7.485	1.00	22.31	H	C
ATOM	1872	CD1	TYR	58	105.051	22.744	6.167	1.00	22.31	H	C
ATOM	1873	CE1	TYR	58	105.871	23.765	5.768	1.00	22.31	H	C
ATOM	1874	CD2	TYR	58	105.843	22.967	8.399	1.00	22.31	H	C
ATOM	1875	CE2	TYR	58	106.667	23.997	8.007	1.00	22.31	H	C
ATOM	1876	CZ	TYR	58	106.674	24.388	6.689	1.00	22.31	H	C
ATOM	1877	OH	TYR	58	107.478	25.419	6.279	1.00	22.31	H	O
ATOM	1878	C	TYR	58	101.812	20.565	8.635	1.00	10.35	H	C
ATOM	1879	O	TYR	58	101.699	20.164	9.801	1.00	10.35	H	O
ATOM	1880	N	TYR	59	101.147	20.007	7.634	1.00	15.64	H	N
ATOM	1881	CA	TYR	59	100.219	18.936	7.931	1.00	15.64	H	C
ATOM	1882	CB	TYR	59	98.843	19.542	8.203	1.00	11.32	H	C
ATOM	1883	CG	TYR	59	98.803	20.511	9.360	1.00	11.32	H	C
ATOM	1884	CD1	TYR	59	98.625	20.058	10.661	1.00	11.32	H	C
ATOM	1885	CE1	TYR	59	98.540	20.942	11.731	1.00	11.32	H	C
ATOM	1886	CD2	TYR	59	98.912	21.886	9.148	1.00	11.32	H	C
ATOM	1887	CE2	TYR	59	98.835	22.783	10.208	1.00	11.32	H	C
ATOM	1888	CZ	TYR	59	98.640	22.302	11.502	1.00	11.32	H	C
ATOM	1889	OH	TYR	59	98.498	23.177	12.557	1.00	11.32	H	O
ATOM	1890	C	TYR	59	100.071	17.883	6.856	1.00	15.64	H	C
ATOM	1891	O	TYR	59	100.150	18.182	5.666	1.00	15.64	H	O
ATOM	1892	N	LEU	60	99.854	16.644	7.286	1.00	33.81	H	N
ATOM	1893	CA	LEU	60	99.616	15.539	6.366	1.00	33.81	H	C
ATOM	1894	CB	LEU	60	99.625	14.217	7.135	1.00	13.27	H	C
ATOM	1895	CG	LEU	60	99.371	12.896	6.406	1.00	13.27	H	C
ATOM	1896	CD1	LEU	60	100.681	12.371	5.800	1.00	13.27	H	C
ATOM	1897	CD2	LEU	60	98.804	11.882	7.397	1.00	13.27	H	C
ATOM	1898	C	LEU	60	98.198	15.861	5.869	1.00	33.81	H	C

Fig. 19: A-27

ATOM	1899	O	LEU	60	97.329	16.255	6.659	1.00	33.81	H	O
ATOM	1900	N	ASP	61	97.962	15.710	4.573	1.00	24.56	H	N
ATOM	1901	CA	ASP	61	96.659	16.028	3.991	1.00	24.56	H	C
ATOM	1902	CB	ASP	61	96.639	15.579	2.530	1.00	55.35	H	C
ATOM	1903	CG	ASP	61	97.719	16.260	1.708	1.00	55.35	H	C
ATOM	1904	OD1	ASP	61	98.919	16.083	2.023	1.00	55.35	H	O
ATOM	1905	OD2	ASP	61	97.374	16.981	0.754	1.00	55.35	H	O
ATOM	1906	C	ASP	61	95.436	15.495	4.731	1.00	24.56	H	C
ATOM	1907	O	ASP	61	94.515	16.254	5.043	1.00	24.56	H	O
ATOM	1908	N	SER	62	95.432	14.198	5.024	1.00	20.78	H	N
ATOM	1909	CA	SER	62	94.317	13.567	5.717	1.00	20.78	H	C
ATOM	1910	CB	SER	62	94.630	12.085	5.955	1.00	31.68	H	C
ATOM	1911	OG	SER	62	95.820	11.902	6.708	1.00	31.68	H	O
ATOM	1912	C	SER	62	93.882	14.216	7.044	1.00	20.78	H	C
ATOM	1913	O	SER	62	92.732	14.053	7.475	1.00	20.78	H	O
ATOM	1914	N	VAL	63	94.779	14.949	7.695	1.00	24.27	H	N
ATOM	1915	CA	VAL	63	94.439	15.567	8.968	1.00	24.27	H	C
ATOM	1916	CB	VAL	63	95.478	15.202	10.049	1.00	45.54	H	C
ATOM	1917	CG1	VAL	63	95.642	13.698	10.110	1.00	45.54	H	C
ATOM	1918	CG2	VAL	63	96.812	15.873	9.752	1.00	45.54	H	C
ATOM	1919	C	VAL	63	94.374	17.083	8.839	1.00	24.27	H	C
ATOM	1920	O	VAL	63	94.112	17.812	9.823	1.00	24.27	H	O
ATOM	1921	N	LYS	64	94.611	17.556	7.618	1.00	38.99	H	N
ATOM	1922	CA	LYS	64	94.611	18.985	7.348	1.00	38.99	H	C
ATOM	1923	CB	LYS	64	94.983	19.235	5.889	1.00	39.16	H	C
ATOM	1924	CG	LYS	64	95.736	20.528	5.671	1.00	39.16	H	C
ATOM	1925	CD	LYS	64	96.417	20.521	4.309	1.00	39.16	H	C
ATOM	1926	CE	LYS	64	97.432	19.380	4.176	1.00	39.16	H	C
ATOM	1927	NZ	LYS	64	98.011	19.296	2.803	1.00	39.16	H	N
ATOM	1928	C	LYS	64	93.262	19.607	7.667	1.00	38.99	H	C
ATOM	1929	O	LYS	64	92.240	19.212	7.121	1.00	38.99	H	O
ATOM	1930	N	GLY	65	93.263	20.577	8.567	1.00	28.42	H	N
ATOM	1931	CA	GLY	65	92.019	21.219	8.918	1.00	28.42	H	C
ATOM	1932	C	GLY	65	91.277	20.501	10.021	1.00	28.42	H	C
ATOM	1933	O	GLY	65	90.271	21.005	10.509	1.00	28.42	H	O
ATOM	1934	N	ARG	66	91.751	19.324	10.414	1.00	48.07	H	N
ATOM	1935	CA	ARG	66	91.098	18.588	11.488	1.00	48.07	H	C
ATOM	1936	CB	ARG	66	90.783	17.154	11.064	1.00	36.61	H	C
ATOM	1937	CG	ARG	66	89.845	17.052	9.887	1.00	36.61	H	C
ATOM	1938	CD	ARG	66	89.484	15.608	9.571	1.00	36.61	H	C
ATOM	1939	NE	ARG	66	90.654	14.750	9.346	1.00	36.61	H	N
ATOM	1940	CZ	ARG	66	91.133	13.877	10.236	1.00	36.61	H	C
ATOM	1941	NH1	ARG	66	90.545	13.739	11.421	1.00	36.61	H	N
ATOM	1942	NH2	ARG	66	92.203	13.144	9.944	1.00	36.61	H	N
ATOM	1943	C	ARG	66	92.018	18.568	12.687	1.00	48.07	H	C
ATOM	1944	O	ARG	66	91.584	18.312	13.808	1.00	48.07	H	O
ATOM	1945	N	PHE	67	93.296	18.839	12.438	1.00	31.81	H	N
ATOM	1946	CA	PHE	67	94.304	18.854	13.490	1.00	31.81	H	C
ATOM	1947	CB	PHE	67	95.372	17.802	13.211	1.00	34.94	H	C
ATOM	1948	CG	PHE	67	94.937	16.394	13.444	1.00	34.94	H	C
ATOM	1949	CD1	PHE	67	93.763	15.907	12.902	1.00	34.94	H	C
ATOM	1950	CD2	PHE	67	95.748	15.530	14.158	1.00	34.94	H	C
ATOM	1951	CE1	PHE	67	93.400	14.564	13.063	1.00	34.94	H	C
ATOM	1952	CE2	PHE	67	95.400	14.192	14.326	1.00	34.94	H	C
ATOM	1953	CZ	PHE	67	94.222	13.706	13.777	1.00	34.94	H	C
ATOM	1954	C	PHE	67	94.989	20.209	13.520	1.00	31.81	H	C
ATOM	1955	O	PHE	67	95.054	20.899	12.501	1.00	31.81	H	O
ATOM	1956	N	THR	68	95.511	20.587	14.683	1.00	27.20	H	N
ATOM	1957	CA	THR	68	96.233	21.851	14.804	1.00	27.20	H	C
ATOM	1958	CB	THR	68	95.344	22.998	15.384	1.00	14.56	H	C
ATOM	1959	OG1	THR	68	94.400	23.434	14.399	1.00	14.56	H	O
ATOM	1960	CG2	THR	68	96.196	24.192	15.758	1.00	14.56	H	C
ATOM	1961	C	THR	68	97.466	21.680	15.689	1.00	27.20	H	C
ATOM	1962	O	THR	68	97.355	21.393	16.882	1.00	27.20	H	O
ATOM	1963	N	ILE	69	98.643	21.847	15.099	1.00	22.74	H	N
ATOM	1964	CA	ILE	69	99.869	21.718	15.861	1.00	22.74	H	C
ATOM	1965	CB	ILE	69	100.991	21.084	15.020	1.00	13.28	H	C
ATOM	1966	CG2	ILE	69	101.417	22.022	13.933	1.00	13.28	H	C
ATOM	1967	CG1	ILE	69	102.188	20.736	15.908	1.00	13.28	H	C
ATOM	1968	CD1	ILE	69	103.226	19.848	15.206	1.00	13.28	H	C
ATOM	1969	C	ILE	69	100.287	23.096	16.336	1.00	22.74	H	C
ATOM	1970	O	ILE	69	100.282	24.065	15.578	1.00	22.74	H	O
ATOM	1971	N	SER	70	100.632	23.188	17.608	1.00	15.22	H	N

Fig. 19: A-28

ATOM	1972	CA	SER	70	101.032	24.460	18.183	1.00	15.22	H	C
ATOM	1973	CB	SER	70	99.834	25.147	18.851	1.00	3.12	H	C
ATOM	1974	OG	SER	70	99.588	24.606	20.144	1.00	3.12	H	O
ATOM	1975	C	SER	70	102.088	24.203	19.235	1.00	15.22	H	C
ATOM	1976	O	SER	70	102.392	23.053	19.557	1.00	15.22	H	O
ATOM	1977	N	ARG	71	102.636	25.281	19.780	1.00	42.13	H	N
ATOM	1978	CA	ARG	71	103.640	25.158	20.813	1.00	42.13	H	C
ATOM	1979	CB	ARG	71	105.039	25.089	20.210	1.00	12.52	H	C
ATOM	1980	CG	ARG	71	105.417	26.296	19.388	1.00	12.52	H	C
ATOM	1981	CD	ARG	71	106.906	26.507	19.436	1.00	12.52	H	C
ATOM	1982	NE	ARG	71	107.644	25.627	18.540	1.00	12.52	H	N
ATOM	1983	CZ	ARG	71	108.844	25.114	18.816	1.00	12.52	H	C
ATOM	1984	NH1	ARG	71	109.444	25.380	19.970	1.00	12.52	H	N
ATOM	1985	NH2	ARG	71	109.456	24.354	17.924	1.00	12.52	H	N
ATOM	1986	C	ARG	71	103.568	26.341	21.739	1.00	42.13	H	C
ATOM	1987	O	ARG	71	103.115	27.416	21.352	1.00	42.13	H	O
ATOM	1988	N	ASP	72	104.003	26.131	22.973	1.00	26.38	H	N
ATOM	1989	CA	ASP	72	104.034	27.197	23.954	1.00	26.38	H	C
ATOM	1990	CB	ASP	72	102.949	27.026	25.007	1.00	47.03	H	C
ATOM	1991	CG	ASP	72	103.003	28.108	26.050	1.00	47.03	H	C
ATOM	1992	OD1	ASP	72	102.157	28.112	26.964	1.00	47.03	H	O
ATOM	1993	OD2	ASP	72	103.907	28.959	25.953	1.00	47.03	H	O
ATOM	1994	C	ASP	72	105.402	27.159	24.607	1.00	26.38	H	C
ATOM	1995	O	ASP	72	105.618	26.508	25.633	1.00	26.38	H	O
ATOM	1996	N	ASN	73	106.325	27.868	23.979	1.00	50.64	H	N
ATOM	1997	CA	ASN	73	107.692	27.939	24.441	1.00	50.64	H	C
ATOM	1998	CB	ASN	73	108.522	28.747	23.446	1.00	30.24	H	C
ATOM	1999	CG	ASN	73	108.584	28.091	22.086	1.00	30.24	H	C
ATOM	2000	OD1	ASN	73	109.170	28.625	21.149	1.00	30.24	H	O
ATOM	2001	ND2	ASN	73	107.984	26.917	21.974	1.00	30.24	H	N
ATOM	2002	C	ASN	73	107.827	28.516	25.841	1.00	50.64	H	C
ATOM	2003	O	ASN	73	108.898	28.436	26.438	1.00	50.64	H	O
ATOM	2004	N	SER	74	106.758	29.097	26.376	1.00	33.75	H	N
ATOM	2005	CA	SER	74	106.848	29.644	27.723	1.00	33.75	H	C
ATOM	2006	CB	SER	74	105.593	30.429	28.093	1.00	48.57	H	C
ATOM	2007	OG	SER	74	104.534	29.556	28.444	1.00	48.57	H	O
ATOM	2008	C	SER	74	106.979	28.456	28.653	1.00	33.75	H	C
ATOM	2009	O	SER	74	107.681	28.530	29.660	1.00	33.75	H	O
ATOM	2010	N	LYS	75	106.312	27.354	28.302	1.00	39.57	H	N
ATOM	2011	CA	LYS	75	106.352	26.142	29.119	1.00	39.57	H	C
ATOM	2012	CB	LYS	75	104.973	25.889	29.732	1.00	42.48	H	C
ATOM	2013	CG	LYS	75	103.842	25.924	28.731	1.00	42.48	H	C
ATOM	2014	CD	LYS	75	102.482	25.985	29.418	1.00	42.48	H	C
ATOM	2015	CE	LYS	75	102.156	27.393	29.918	1.00	42.48	H	C
ATOM	2016	NZ	LYS	75	103.090	27.928	30.963	1.00	42.48	H	N
ATOM	2017	C	LYS	75	106.843	24.894	28.380	1.00	39.57	H	C
ATOM	2018	O	LYS	75	106.497	23.767	28.744	1.00	39.57	H	O
ATOM	2019	N	ASN	76	107.660	25.110	27.353	1.00	44.84	H	N
ATOM	2020	CA	ASN	76	108.245	24.043	26.539	1.00	44.84	H	C
ATOM	2021	CB	ASN	76	109.572	23.608	27.139	1.00	31.30	H	C
ATOM	2022	CG	ASN	76	110.528	24.766	27.312	1.00	31.30	H	C
ATOM	2023	OD1	ASN	76	111.666	24.593	27.739	1.00	31.30	H	O
ATOM	2024	ND2	ASN	76	110.067	25.965	26.979	1.00	31.30	H	N
ATOM	2025	C	ASN	76	107.362	22.827	26.322	1.00	44.84	H	C
ATOM	2026	O	ASN	76	107.793	21.681	26.479	1.00	44.84	H	O
ATOM	2027	N	THR	77	106.121	23.090	25.941	1.00	30.42	H	N
ATOM	2028	CA	THR	77	105.181	22.032	25.686	1.00	30.42	H	C
ATOM	2029	CB	THR	77	103.989	22.131	26.628	1.00	46.49	H	C
ATOM	2030	OG1	THR	77	104.446	21.977	27.974	1.00	46.49	H	O
ATOM	2031	CG2	THR	77	102.975	21.045	26.319	1.00	46.49	H	C
ATOM	2032	C	THR	77	104.708	22.182	24.254	1.00	30.42	H	C
ATOM	2033	O	THR	77	104.488	23.291	23.786	1.00	30.42	H	O
ATOM	2034	N	LEU	78	104.583	21.056	23.563	1.00	20.66	H	N
ATOM	2035	CA	LEU	78	104.135	21.017	22.185	1.00	20.66	H	C
ATOM	2036	CB	LEU	78	104.978	20.024	21.394	1.00	19.59	H	C
ATOM	2037	CG	LEU	78	104.550	19.758	19.953	1.00	19.59	H	C
ATOM	2038	CD1	LEU	78	104.575	21.055	19.166	1.00	19.59	H	C
ATOM	2039	CD2	LEU	78	105.470	18.731	19.320	1.00	19.59	H	C
ATOM	2040	C	LEU	78	102.716	20.520	22.298	1.00	20.66	H	C
ATOM	2041	O	LEU	78	102.368	19.921	23.312	1.00	20.66	H	O
ATOM	2042	N	TYR	79	101.902	20.753	21.271	1.00	30.75	H	N
ATOM	2043	CA	TYR	79	100.498	20.333	21.294	1.00	30.75	H	C
ATOM	2044	CB	TYR	79	99.591	21.494	21.728	1.00	47.95	H	C

Fig. 19: A-29

ATOM	2045	CG	TYR	79	99.809	22.008	23.119	1.00	47.95	H	C
ATOM	2046	CD1	TYR	79	99.166	21.430	24.205	1.00	47.95	H	C
ATOM	2047	CE1	TYR	79	99.357	21.916	25.491	1.00	47.95	H	C
ATOM	2048	CD2	TYR	79	100.655	23.085	23.349	1.00	47.95	H	C
ATOM	2049	CE2	TYR	79	100.857	23.579	24.628	1.00	47.95	H	C
ATOM	2050	CZ	TYR	79	100.204	22.991	25.695	1.00	47.95	H	C
ATOM	2051	OH	TYR	79	100.404	23.493	26.958	1.00	47.95	H	O
ATOM	2052	C	TYR	79	99.966	19.863	19.950	1.00	30.75	H	C
ATOM	2053	O	TYR	79	100.418	20.316	18.898	1.00	30.75	H	O
ATOM	2054	N	LEU	80	98.981	18.969	20.003	1.00	19.83	H	N
ATOM	2055	CA	LEU	80	98.308	18.472	18.811	1.00	19.83	H	C
ATOM	2056	CB	LEU	80	98.776	17.070	18.397	1.00	5.08	H	C
ATOM	2057	CG	LEU	80	98.132	16.598	17.076	1.00	5.08	H	C
ATOM	2058	CD1	LEU	80	98.706	17.386	15.914	1.00	5.08	H	C
ATOM	2059	CD2	LEU	80	98.352	15.111	16.874	1.00	5.08	H	C
ATOM	2060	C	LEU	80	96.838	18.411	19.182	1.00	19.83	H	C
ATOM	2061	O	LEU	80	96.398	17.503	19.879	1.00	19.83	H	O
ATOM	2062	N	GLN	81	96.091	19.412	18.742	1.00	24.43	H	N
ATOM	2063	CA	GLN	81	94.671	19.463	19.004	1.00	24.43	H	C
ATOM	2064	CB	GLN	81	94.169	20.911	18.966	1.00	60.73	H	C
ATOM	2065	CG	GLN	81	92.710	21.093	19.399	1.00	60.73	H	C
ATOM	2066	CD	GLN	81	92.505	20.974	20.911	1.00	60.73	H	C
ATOM	2067	OE1	GLN	81	92.981	21.810	21.691	1.00	60.73	H	O
ATOM	2068	NE2	GLN	81	91.787	19.935	21.328	1.00	60.73	H	N
ATOM	2069	C	GLN	81	94.064	18.672	17.867	1.00	24.43	H	C
ATOM	2070	O	GLN	81	94.376	18.921	16.698	1.00	24.43	H	O
ATOM	2071	N	MET	82	93.205	17.718	18.210	1.00	35.69	H	N
ATOM	2072	CA	MET	82	92.559	16.878	17.211	1.00	35.69	H	C
ATOM	2073	CB	MET	82	92.989	15.424	17.383	1.00	24.95	H	C
ATOM	2074	CG	MET	82	94.481	15.209	17.363	1.00	24.95	H	C
ATOM	2075	SD	MET	82	94.896	13.491	17.609	1.00	24.95	H	S
ATOM	2076	CE	MET	82	94.985	13.427	19.373	1.00	24.95	H	C
ATOM	2077	C	MET	82	91.051	16.957	17.316	1.00	35.69	H	C
ATOM	2078	O	MET	82	90.479	16.599	18.338	1.00	35.69	H	O
ATOM	2079	N	ASN	83	90.414	17.416	16.247	1.00	28.29	H	N
ATOM	2080	CA	ASN	83	88.968	17.536	16.204	1.00	28.29	H	C
ATOM	2081	CB	ASN	83	88.550	18.989	15.985	1.00	66.28	H	C
ATOM	2082	CG	ASN	83	89.274	19.943	16.899	1.00	66.28	H	C
ATOM	2083	OD1	ASN	83	89.213	19.819	18.121	1.00	66.28	H	O
ATOM	2084	ND2	ASN	83	89.970	20.910	16.309	1.00	66.28	H	N
ATOM	2085	C	ASN	83	88.502	16.728	15.025	1.00	28.29	H	C
ATOM	2086	O	ASN	83	89.306	16.348	14.185	1.00	28.29	H	O
ATOM	2087	N	SER	84	87.199	16.486	14.954	1.00	57.41	H	N
ATOM	2088	CA	SER	84	86.618	15.739	13.847	1.00	57.41	H	C
ATOM	2089	CB	SER	84	86.648	16.584	12.574	1.00	29.12	H	C
ATOM	2090	OG	SER	84	86.027	17.836	12.786	1.00	29.12	H	O
ATOM	2091	C	SER	84	87.374	14.450	13.603	1.00	57.41	H	C
ATOM	2092	O	SER	84	87.642	14.085	12.456	1.00	57.41	H	O
ATOM	2093	N	LEU	85	87.725	13.769	14.687	1.00	32.34	H	N
ATOM	2094	CA	LEU	85	88.452	12.513	14.595	1.00	32.34	H	C
ATOM	2095	CB	LEU	85	88.818	12.009	15.990	1.00	15.22	H	C
ATOM	2096	CG	LEU	85	89.913	12.880	16.600	1.00	15.22	H	C
ATOM	2097	CD1	LEU	85	90.082	12.594	18.078	1.00	15.22	H	C
ATOM	2098	CD2	LEU	85	91.204	12.636	15.828	1.00	15.22	H	C
ATOM	2099	C	LEU	85	87.641	11.460	13.877	1.00	32.34	H	C
ATOM	2100	O	LEU	85	86.434	11.369	14.050	1.00	32.34	H	O
ATOM	2101	N	ARG	86	88.319	10.680	13.049	1.00	24.27	H	N
ATOM	2102	CA	ARG	86	87.686	9.604	12.316	1.00	24.27	H	C
ATOM	2103	CB	ARG	86	87.858	9.801	10.815	1.00	51.87	H	C
ATOM	2104	CG	ARG	86	87.146	11.026	10.286	1.00	51.87	H	C
ATOM	2105	CD	ARG	86	86.864	10.887	8.808	1.00	51.87	H	C
ATOM	2106	NE	ARG	86	87.237	12.088	8.076	1.00	51.87	H	N
ATOM	2107	CZ	ARG	86	88.470	12.581	8.043	1.00	51.87	H	C
ATOM	2108	NH1	ARG	86	89.444	11.967	8.707	1.00	51.87	H	N
ATOM	2109	NH2	ARG	86	88.733	13.676	7.334	1.00	51.87	H	N
ATOM	2110	C	ARG	86	88.387	8.343	12.769	1.00	24.27	H	C
ATOM	2111	O	ARG	86	89.367	8.416	13.514	1.00	24.27	H	O
ATOM	2112	N	ALA	87	87.894	7.191	12.335	1.00	40.98	H	N
ATOM	2113	CA	ALA	87	88.499	5.928	12.733	1.00	40.98	H	C
ATOM	2114	CB	ALA	87	87.678	4.763	12.196	1.00	28.01	H	C
ATOM	2115	C	ALA	87	89.937	5.833	12.242	1.00	40.98	H	C
ATOM	2116	O	ALA	87	90.824	5.425	12.989	1.00	40.98	H	O
ATOM	2117	N	GLU	88	90.169	6.222	10.993	1.00	32.24	H	N

Fig. 19: A-30

ATOM	2118	CA	GLU	88	91.511	6.157	10.433	1.00	32.24	H	C
ATOM	2119	CB	GLU	88	91.583	6.890	9.094	1.00	72.38	H	C
ATOM	2120	CG	GLU	88	90.432	6.614	8.169	1.00	72.38	H	C
ATOM	2121	CD	GLU	88	89.327	7.623	8.336	1.00	72.38	H	C
ATOM	2122	OE1	GLU	88	89.529	8.792	7.937	1.00	72.38	H	O
ATOM	2123	OE2	GLU	88	88.265	7.246	8.874	1.00	72.38	H	O
ATOM	2124	C	GLU	88	92.529	6.780	11.372	1.00	32.24	H	C
ATOM	2125	O	GLU	88	93.691	6.370	11.417	1.00	32.24	H	O
ATOM	2126	N	ASP	89	92.080	7.772	12.128	1.00	18.63	H	N
ATOM	2127	CA	ASP	89	92.935	8.497	13.054	1.00	18.63	H	C
ATOM	2128	CB	ASP	89	92.212	9.764	13.507	1.00	29.25	H	C
ATOM	2129	CG	ASP	89	92.073	10.775	12.392	1.00	29.25	H	C
ATOM	2130	OD1	ASP	89	91.297	11.732	12.553	1.00	29.25	H	O
ATOM	2131	OD2	ASP	89	92.748	10.622	11.355	1.00	29.25	H	O
ATOM	2132	C	ASP	89	93.434	7.724	14.268	1.00	18.63	H	C
ATOM	2133	O	ASP	89	94.391	8.149	14.922	1.00	18.63	H	O
ATOM	2134	N	THR	90	92.817	6.588	14.575	1.00	29.66	H	N
ATOM	2135	CA	THR	90	93.261	5.845	15.749	1.00	29.66	H	C
ATOM	2136	CB	THR	90	92.303	4.668	16.113	1.00	30.61	H	C
ATOM	2137	OG1	THR	90	92.601	3.537	15.293	1.00	30.61	H	O
ATOM	2138	CG2	THR	90	90.828	5.072	15.903	1.00	30.61	H	C
ATOM	2139	C	THR	90	94.664	5.311	15.527	1.00	29.66	H	C
ATOM	2140	O	THR	90	94.961	4.727	14.492	1.00	29.66	H	O
ATOM	2141	N	ALA	91	95.532	5.553	16.499	1.00	11.25	H	N
ATOM	2142	CA	ALA	91	96.918	5.094	16.451	1.00	11.25	H	C
ATOM	2143	CB	ALA	91	97.629	5.690	15.259	1.00	1.87	H	C
ATOM	2144	C	ALA	91	97.611	5.536	17.729	1.00	11.25	H	C
ATOM	2145	O	ALA	91	96.972	6.044	18.646	1.00	11.25	H	O
ATOM	2146	N	VAL	92	98.915	5.312	17.797	1.00	22.44	H	N
ATOM	2147	CA	VAL	92	99.694	5.755	18.947	1.00	22.44	H	C
ATOM	2148	CB	VAL	92	100.654	4.665	19.465	1.00	21.44	H	C
ATOM	2149	CG1	VAL	92	101.306	3.966	18.298	1.00	21.44	H	C
ATOM	2150	CG2	VAL	92	101.716	5.284	20.346	1.00	21.44	H	C
ATOM	2151	C	VAL	92	100.482	6.913	18.363	1.00	22.44	H	C
ATOM	2152	O	VAL	92	101.107	6.771	17.310	1.00	22.44	H	O
ATOM	2153	N	TYR	93	100.413	8.066	19.019	1.00	21.58	H	N
ATOM	2154	CA	TYR	93	101.105	9.261	18.538	1.00	21.58	H	C
ATOM	2155	CB	TYR	93	100.161	10.470	18.585	1.00	12.38	H	C
ATOM	2156	CG	TYR	93	99.000	10.385	17.624	1.00	12.38	H	C
ATOM	2157	CD1	TYR	93	98.023	9.399	17.759	1.00	12.38	H	C
ATOM	2158	CE1	TYR	93	96.975	9.287	16.836	1.00	12.38	H	C
ATOM	2159	CD2	TYR	93	98.899	11.264	16.553	1.00	12.38	H	C
ATOM	2160	CE2	TYR	93	97.863	11.165	15.634	1.00	12.38	H	C
ATOM	2161	CZ	TYR	93	96.908	10.173	15.773	1.00	12.38	H	C
ATOM	2162	OH	TYR	93	95.915	10.043	14.827	1.00	12.38	H	O
ATOM	2163	C	TYR	93	102.384	9.577	19.312	1.00	21.58	H	C
ATOM	2164	O	TYR	93	102.466	9.401	20.531	1.00	21.58	H	O
ATOM	2165	N	TYR	94	103.381	10.049	18.579	1.00	19.04	H	N
ATOM	2166	CA	TYR	94	104.668	10.409	19.151	1.00	19.04	H	C
ATOM	2167	CB	TYR	94	105.789	9.576	18.533	1.00	29.80	H	C
ATOM	2168	CG	TYR	94	105.548	8.101	18.431	1.00	29.80	H	C
ATOM	2169	CD1	TYR	94	105.948	7.237	19.454	1.00	29.80	H	C
ATOM	2170	CE1	TYR	94	105.768	5.876	19.345	1.00	29.80	H	C
ATOM	2171	CD2	TYR	94	104.958	7.563	17.298	1.00	29.80	H	C
ATOM	2172	CE2	TYR	94	104.773	6.204	17.177	1.00	29.80	H	C
ATOM	2173	CZ	TYR	94	105.179	5.363	18.202	1.00	29.80	H	C
ATOM	2174	OH	TYR	94	104.996	4.007	18.071	1.00	29.80	H	O
ATOM	2175	C	TYR	94	104.991	11.853	18.805	1.00	19.04	H	C
ATOM	2176	O	TYR	94	104.867	12.244	17.642	1.00	19.04	H	O
ATOM	2177	N	CYS	95	105.383	12.654	19.791	1.00	25.07	H	N
ATOM	2178	CA	CYS	95	105.806	14.000	19.466	1.00	25.07	H	C
ATOM	2179	C	CYS	95	107.228	13.689	19.096	1.00	25.07	H	C
ATOM	2180	O	CYS	95	107.716	12.584	19.342	1.00	25.07	H	O
ATOM	2181	CB	CYS	95	105.784	14.942	20.647	1.00	46.53	H	C
ATOM	2182	SG	CYS	95	106.112	14.206	22.267	1.00	46.53	H	S
ATOM	2183	N	THR	96	107.931	14.657	18.549	1.00	31.61	H	N
ATOM	2184	CA	THR	96	109.253	14.331	18.115	1.00	31.61	H	C
ATOM	2185	CB	THR	96	109.088	13.445	16.861	1.00	32.15	H	C
ATOM	2186	OG1	THR	96	110.331	12.862	16.494	1.00	32.15	H	O
ATOM	2187	CG2	THR	96	108.554	14.260	15.708	1.00	32.15	H	C
ATOM	2188	C	THR	96	110.045	15.591	17.830	1.00	31.61	H	C
ATOM	2189	O	THR	96	109.530	16.548	17.260	1.00	31.61	H	O
ATOM	2190	N	ARG	97	111.292	15.610	18.270	1.00	26.02	H	N

Fig. 19: A-31

ATOM	2191	CA	ARG	97	112.135	16.759	17.996	1.00	26.02	H	C
ATOM	2192	CB	ARG	97	113.220	16.959	19.053	1.00	22.53	H	C
ATOM	2193	CG	ARG	97	114.076	18.184	18.766	1.00	22.53	H	C
ATOM	2194	CD	ARG	97	115.204	18.345	19.764	1.00	22.53	H	C
ATOM	2195	NE	ARG	97	116.357	17.532	19.411	1.00	22.53	H	N
ATOM	2196	CZ	ARG	97	117.494	17.509	20.099	1.00	22.53	H	C
ATOM	2197	NH1	ARG	97	117.635	18.257	21.183	1.00	22.53	H	N
ATOM	2198	NH2	ARG	97	118.494	16.739	19.704	1.00	22.53	H	N
ATOM	2199	C	ARG	97	112.799	16.473	16.665	1.00	26.02	H	C
ATOM	2200	O	ARG	97	113.145	15.322	16.357	1.00	26.02	H	O
ATOM	2201	N	GLY	98	112.980	17.528	15.882	1.00	13.43	H	N
ATOM	2202	CA	GLY	98	113.586	17.367	14.582	1.00	13.43	H	C
ATOM	2203	C	GLY	98	114.947	17.995	14.496	1.00	13.43	H	C
ATOM	2204	O	GLY	98	115.308	18.850	15.281	1.00	13.43	H	O
ATOM	2205	N	PHE	99	115.719	17.537	13.534	1.00	20.13	H	N
ATOM	2206	CA	PHE	99	117.038	18.065	13.315	1.00	20.13	H	C
ATOM	2207	CB	PHE	99	118.018	16.902	13.211	1.00	25.23	H	C
ATOM	2208	CG	PHE	99	119.338	17.271	12.628	1.00	25.23	H	C
ATOM	2209	CD1	PHE	99	119.587	17.079	11.279	1.00	25.23	H	C
ATOM	2210	CD2	PHE	99	120.326	17.828	13.420	1.00	25.23	H	C
ATOM	2211	CE1	PHE	99	120.804	17.437	10.721	1.00	25.23	H	C
ATOM	2212	CE2	PHE	99	121.543	18.191	12.875	1.00	25.23	H	C
ATOM	2213	CZ	PHE	99	121.784	17.994	11.517	1.00	25.23	H	C
ATOM	2214	C	PHE	99	116.887	18.819	11.996	1.00	20.13	H	C
ATOM	2215	O	PHE	99	115.950	18.551	11.241	1.00	20.13	H	O
ATOM	2216	N	GLY	100	117.768	19.774	11.719	1.00	15.08	H	N
ATOM	2217	CA	GLY	100	117.655	20.513	10.469	1.00	15.08	H	C
ATOM	2218	C	GLY	100	116.285	21.139	10.274	1.00	15.08	H	C
ATOM	2219	O	GLY	100	115.682	21.636	11.216	1.00	15.08	H	O
ATOM	2220	N	ASP	101	115.779	21.128	9.050	1.00	7.89	H	N
ATOM	2221	CA	ASP	101	114.462	21.692	8.812	1.00	7.89	H	C
ATOM	2222	CB	ASP	101	114.195	21.848	7.302	1.00	13.13	H	C
ATOM	2223	CG	ASP	101	115.328	22.587	6.564	1.00	13.13	H	C
ATOM	2224	OD1	ASP	101	115.921	23.558	7.105	1.00	13.13	H	O
ATOM	2225	OD2	ASP	101	115.616	22.190	5.417	1.00	13.13	H	O
ATOM	2226	C	ASP	101	113.406	20.785	9.460	1.00	7.89	H	C
ATOM	2227	O	ASP	101	112.222	20.844	9.124	1.00	7.89	H	O
ATOM	2228	N	GLY	102	113.854	19.924	10.374	1.00	22.31	H	N
ATOM	2229	CA	GLY	102	112.952	19.043	11.100	1.00	22.31	H	C
ATOM	2230	C	GLY	102	112.588	17.674	10.562	1.00	22.31	H	C
ATOM	2231	O	GLY	102	111.927	16.915	11.263	1.00	22.31	H	O
ATOM	2232	N	GLY	103	113.001	17.347	9.343	1.00	25.09	H	N
ATOM	2233	CA	GLY	103	112.662	16.054	8.772	1.00	25.09	H	C
ATOM	2234	C	GLY	103	113.342	14.844	9.403	1.00	25.09	H	C
ATOM	2235	O	GLY	103	112.948	13.703	9.156	1.00	25.09	H	O
ATOM	2236	N	TYR	104	114.376	15.071	10.202	1.00	22.52	H	N
ATOM	2237	CA	TYR	104	115.070	13.961	10.844	1.00	22.52	H	C
ATOM	2238	CB	TYR	104	116.578	14.114	10.715	1.00	15.87	H	C
ATOM	2239	CG	TYR	104	117.342	13.175	11.599	1.00	15.87	H	C
ATOM	2240	CD1	TYR	104	118.507	13.600	12.233	1.00	15.87	H	C
ATOM	2241	CE1	TYR	104	119.198	12.776	13.100	1.00	15.87	H	C
ATOM	2242	CD2	TYR	104	116.884	11.880	11.844	1.00	15.87	H	C
ATOM	2243	CE2	TYR	104	117.575	11.034	12.713	1.00	15.87	H	C
ATOM	2244	CZ	TYR	104	118.734	11.498	13.343	1.00	15.87	H	C
ATOM	2245	OH	TYR	104	119.417	10.713	14.239	1.00	15.87	H	O
ATOM	2246	C	TYR	104	114.665	13.991	12.296	1.00	22.52	H	C
ATOM	2247	O	TYR	104	114.933	14.956	13.001	1.00	22.52	H	O
ATOM	2248	N	PHE	105	114.036	12.909	12.733	1.00	16.00	H	N
ATOM	2249	CA	PHE	105	113.501	12.806	14.073	1.00	16.00	H	C
ATOM	2250	CB	PHE	105	112.292	11.890	14.031	1.00	16.01	H	C
ATOM	2251	CG	PHE	105	111.269	12.327	13.020	1.00	16.01	H	C
ATOM	2252	CD1	PHE	105	110.782	13.627	13.038	1.00	16.01	H	C
ATOM	2253	CD2	PHE	105	110.827	11.459	12.023	1.00	16.01	H	C
ATOM	2254	CE1	PHE	105	109.880	14.059	12.091	1.00	16.01	H	C
ATOM	2255	CE2	PHE	105	109.918	11.885	11.067	1.00	16.01	H	C
ATOM	2256	CZ	PHE	105	109.443	13.190	11.101	1.00	16.01	H	C
ATOM	2257	C	PHE	105	114.442	12.433	15.179	1.00	16.00	H	C
ATOM	2258	O	PHE	105	114.543	11.283	15.595	1.00	16.00	H	O
ATOM	2259	N	ASP	106	115.105	13.481	15.642	1.00	29.40	H	N
ATOM	2260	CA	ASP	106	116.089	13.519	16.714	1.00	29.40	H	C
ATOM	2261	CB	ASP	106	116.251	14.976	17.117	1.00	39.43	H	C
ATOM	2262	CG	ASP	106	117.656	15.400	17.133	1.00	39.43	H	C
ATOM	2263	OD1	ASP	106	118.492	14.528	17.433	1.00	39.43	H	O

Fig. 19: A-32

ATOM	2264	OD2	ASP	106	117.922	16.591	16.859	1.00	39.43	H	O
ATOM	2265	C	ASP	106	115.797	12.728	17.993	1.00	29.40	H	C
ATOM	2266	O	ASP	106	116.567	11.861	18.396	1.00	29.40	H	O
ATOM	2267	N	VAL	107	114.687	13.094	18.635	1.00	7.69	H	N
ATOM	2268	CA	VAL	107	114.248	12.533	19.906	1.00	7.69	H	C
ATOM	2269	CB	VAL	107	114.402	13.600	21.026	1.00	10.61	H	C
ATOM	2270	CG1	VAL	107	113.985	13.045	22.374	1.00	10.61	H	C
ATOM	2271	CG2	VAL	107	115.838	14.116	21.048	1.00	10.61	H	C
ATOM	2272	C	VAL	107	112.778	12.199	19.765	1.00	7.69	H	C
ATOM	2273	O	VAL	107	112.107	12.835	18.970	1.00	7.69	H	O
ATOM	2274	N	TRP	108	112.285	11.224	20.540	1.00	26.84	H	N
ATOM	2275	CA	TRP	108	110.871	10.795	20.510	1.00	26.84	H	C
ATOM	2276	CB	TRP	108	110.729	9.405	19.868	1.00	1.87	H	C
ATOM	2277	CG	TRP	108	111.201	9.329	18.468	1.00	1.87	H	C
ATOM	2278	CD2	TRP	108	110.431	8.950	17.328	1.00	1.87	H	C
ATOM	2279	CE2	TRP	108	111.287	9.020	16.201	1.00	1.87	H	C
ATOM	2280	CE3	TRP	108	109.102	8.557	17.142	1.00	1.87	H	C
ATOM	2281	CD1	TRP	108	112.460	9.606	18.008	1.00	1.87	H	C
ATOM	2282	NE1	TRP	108	112.520	9.422	16.648	1.00	1.87	H	N
ATOM	2283	CZ2	TRP	108	110.854	8.710	14.904	1.00	1.87	H	C
ATOM	2284	CZ3	TRP	108	108.667	8.244	15.836	1.00	1.87	H	C
ATOM	2285	CH2	TRP	108	109.547	8.325	14.742	1.00	1.87	H	C
ATOM	2286	C	TRP	108	110.204	10.724	21.881	1.00	26.84	H	C
ATOM	2287	O	TRP	108	110.859	10.503	22.899	1.00	26.84	H	O
ATOM	2288	N	GLY	109	108.889	10.907	21.889	1.00	15.55	H	N
ATOM	2289	CA	GLY	109	108.134	10.811	23.125	1.00	15.55	H	C
ATOM	2290	C	GLY	109	107.896	9.331	23.386	1.00	15.55	H	C
ATOM	2291	O	GLY	109	108.170	8.502	22.511	1.00	15.55	H	O
ATOM	2292	N	GLN	110	107.393	8.971	24.563	1.00	21.92	H	N
ATOM	2293	CA	GLN	110	107.161	7.554	24.852	1.00	21.92	H	C
ATOM	2294	CB	GLN	110	106.800	7.338	26.325	1.00	44.26	H	C
ATOM	2295	CG	GLN	110	105.404	7.798	26.703	1.00	44.26	H	C
ATOM	2296	CD	GLN	110	105.321	9.283	26.957	1.00	44.26	H	C
ATOM	2297	OE1	GLN	110	105.573	10.102	26.071	1.00	44.26	H	O
ATOM	2298	NE2	GLN	110	104.967	9.642	28.181	1.00	44.26	H	N
ATOM	2299	C	GLN	110	106.051	6.979	23.973	1.00	21.92	H	C
ATOM	2300	O	GLN	110	106.054	5.798	23.651	1.00	21.92	H	O
ATOM	2301	N	GLY	111	105.114	7.824	23.574	1.00	22.63	H	N
ATOM	2302	CA	GLY	111	104.014	7.361	22.761	1.00	22.63	H	C
ATOM	2303	C	GLY	111	102.758	7.463	23.597	1.00	22.63	H	C
ATOM	2304	O	GLY	111	102.834	7.414	24.827	1.00	22.63	H	O
ATOM	2305	N	THR	112	101.611	7.619	22.938	1.00	17.52	H	N
ATOM	2306	CA	THR	112	100.333	7.740	23.630	1.00	17.52	H	C
ATOM	2307	CB	THR	112	100.058	9.211	24.030	1.00	34.98	H	C
ATOM	2308	OG1	THR	112	98.958	9.261	24.939	1.00	34.98	H	O
ATOM	2309	CG2	THR	112	99.734	10.055	22.809	1.00	34.98	H	C
ATOM	2310	C	THR	112	99.228	7.203	22.717	1.00	17.52	H	C
ATOM	2311	O	THR	112	99.133	7.559	21.533	1.00	17.52	H	O
ATOM	2312	N	LEU	113	98.396	6.340	23.292	1.00	32.82	H	N
ATOM	2313	CA	LEU	113	97.318	5.668	22.576	1.00	32.82	H	C
ATOM	2314	CB	LEU	113	96.953	4.374	23.328	1.00	26.98	H	C
ATOM	2315	CG	LEU	113	95.842	3.431	22.856	1.00	26.98	H	C
ATOM	2316	CD1	LEU	113	94.455	4.057	23.105	1.00	26.98	H	C
ATOM	2317	CD2	LEU	113	96.055	3.115	21.392	1.00	26.98	H	C
ATOM	2318	C	LEU	113	96.073	6.498	22.354	1.00	32.82	H	C
ATOM	2319	O	LEU	113	95.448	6.964	23.299	1.00	32.82	H	O
ATOM	2320	N	VAL	114	95.708	6.671	21.094	1.00	38.48	H	N
ATOM	2321	CA	VAL	114	94.506	7.419	20.767	1.00	38.48	H	C
ATOM	2322	CB	VAL	114	94.809	8.658	19.870	1.00	53.69	H	C
ATOM	2323	CG1	VAL	114	93.518	9.420	19.571	1.00	53.69	H	C
ATOM	2324	CG2	VAL	114	95.798	9.575	20.562	1.00	53.69	H	C
ATOM	2325	C	VAL	114	93.557	6.484	20.022	1.00	38.48	H	C
ATOM	2326	O	VAL	114	93.859	6.003	18.928	1.00	38.48	H	O
ATOM	2327	N	THR	115	92.411	6.216	20.629	1.00	29.76	H	N
ATOM	2328	CA	THR	115	91.414	5.356	20.012	1.00	29.76	H	C
ATOM	2329	CB	THR	115	91.081	4.125	20.916	1.00	30.84	H	C
ATOM	2330	OG1	THR	115	92.292	3.453	21.300	1.00	30.84	H	O
ATOM	2331	CG2	THR	115	90.180	3.151	20.170	1.00	30.84	H	C
ATOM	2332	C	THR	115	90.133	6.164	19.803	1.00	29.76	H	C
ATOM	2333	O	THR	115	89.700	6.905	20.694	1.00	29.76	H	O
ATOM	2334	N	VAL	116	89.543	6.056	18.619	1.00	38.29	H	N
ATOM	2335	CA	VAL	116	88.289	6.747	18.371	1.00	38.29	H	C
ATOM	2336	CB	VAL	116	88.395	7.822	17.240	1.00	10.28	H	C

Fig. 19: A-33

ATOM	2337	CG1	VAL	116	89.861	8.088	16.922	1.00	10.28	H	C
ATOM	2338	CG2	VAL	116	87.575	7.415	15.994	1.00	10.28	H	C
ATOM	2339	C	VAL	116	87.303	5.656	17.996	1.00	38.29	H	C
ATOM	2340	O	VAL	116	87.545	4.888	17.063	1.00	38.29	H	O
ATOM	2341	N	SER	117	86.207	5.579	18.746	1.00	41.53	H	N
ATOM	2342	CA	SER	117	85.193	4.565	18.517	1.00	41.53	H	C
ATOM	2343	CB	SER	117	85.768	3.182	18.851	1.00	61.62	H	C
ATOM	2344	OG	SER	117	84.788	2.165	18.751	1.00	61.62	H	O
ATOM	2345	C	SER	117	83.959	4.815	19.366	1.00	41.53	H	C
ATOM	2346	O	SER	117	84.049	5.336	20.482	1.00	41.53	H	O
ATOM	2347	N	SER	118	82.808	4.431	18.828	1.00	36.79	H	N
ATOM	2348	CA	SER	118	81.538	4.581	19.525	1.00	36.79	H	C
ATOM	2349	CB	SER	118	80.401	4.226	18.579	1.00	49.30	H	C
ATOM	2350	OG	SER	118	80.598	2.919	18.069	1.00	49.30	H	O
ATOM	2351	C	SER	118	81.510	3.649	20.740	1.00	36.79	H	C
ATOM	2352	O	SER	118	80.753	3.853	21.685	1.00	35.84	H	O
ATOM	2353	N	ALA	119	82.339	2.616	20.707	1.00	26.31	H	N
ATOM	2354	CA	ALA	119	82.412	1.679	21.815	1.00	26.31	H	C
ATOM	2355	CB	ALA	119	83.569	0.707	21.617	1.00	20.55	H	C
ATOM	2356	C	ALA	119	82.611	2.461	23.100	1.00	26.31	H	C
ATOM	2357	O	ALA	119	83.319	3.477	23.124	1.00	26.31	H	O
ATOM	2358	N	SER	120	81.988	1.975	24.166	1.00	39.08	H	N
ATOM	2359	CA	SER	120	82.074	2.621	25.462	1.00	39.08	H	C
ATOM	2360	CB	SER	120	80.711	2.597	26.151	1.00	57.76	H	C
ATOM	2361	OG	SER	120	79.720	3.179	25.329	1.00	57.76	H	O
ATOM	2362	C	SER	120	83.086	1.938	26.353	1.00	39.08	H	C
ATOM	2363	O	SER	120	83.194	0.715	26.362	1.00	39.08	H	O
ATOM	2364	N	THR	121	83.837	2.734	27.100	1.00	26.62	H	N
ATOM	2365	CA	THR	121	84.813	2.188	28.023	1.00	25.63	H	C
ATOM	2366	CB	THR	121	85.274	3.267	29.002	1.00	27.79	H	C
ATOM	2367	OG1	THR	121	85.860	4.353	28.268	1.00	32.58	H	O
ATOM	2368	CG2	THR	121	86.273	2.691	30.007	1.00	25.52	H	C
ATOM	2369	C	THR	121	84.108	1.078	28.801	1.00	26.35	H	C
ATOM	2370	O	THR	121	82.919	1.189	29.098	1.00	29.95	H	O
ATOM	2371	N	LYS	122	84.828	0.007	29.116	1.00	53.26	H	N
ATOM	2372	CA	LYS	122	84.243	-1.102	29.864	1.00	50.64	H	C
ATOM	2373	CB	LYS	122	83.333	-1.930	28.947	1.00	42.70	H	C
ATOM	2374	CG	LYS	122	83.009	-3.347	29.437	1.00	44.07	H	C
ATOM	2375	CD	LYS	122	82.469	-3.373	30.864	1.00	47.16	H	C
ATOM	2376	CE	LYS	122	82.216	-4.805	31.337	1.00	51.36	H	C
ATOM	2377	NZ	LYS	122	81.986	-4.880	32.809	1.00	50.23	H	N
ATOM	2378	C	LYS	122	85.301	-1.991	30.496	1.00	52.40	H	C
ATOM	2379	O	LYS	122	86.154	-2.548	29.809	1.00	54.02	H	O
ATOM	2380	N	GLY	123	85.240	-2.114	31.817	1.00	42.56	H	N
ATOM	2381	CA	GLY	123	86.188	-2.952	32.530	1.00	42.89	H	C
ATOM	2382	C	GLY	123	86.213	-4.396	32.035	1.00	44.35	H	C
ATOM	2383	O	GLY	123	85.222	-4.907	31.503	1.00	40.33	H	O
ATOM	2384	N	PRO	124	87.346	-5.090	32.198	1.00	44.81	H	N
ATOM	2385	CD	PRO	124	88.680	-4.632	32.633	1.00	21.78	H	C
ATOM	2386	CA	PRO	124	87.397	-6.472	31.731	1.00	46.19	H	C
ATOM	2387	CB	PRO	124	88.868	-6.668	31.439	1.00	22.93	H	C
ATOM	2388	CG	PRO	124	89.504	-5.905	32.561	1.00	22.69	H	C
ATOM	2389	C	PRO	124	86.899	-7.461	32.764	1.00	45.69	H	C
ATOM	2390	O	PRO	124	86.854	-7.170	33.961	1.00	46.94	H	O
ATOM	2391	N	SER	125	86.507	-8.631	32.287	1.00	43.49	H	N
ATOM	2392	CA	SER	125	86.053	-9.678	33.176	1.00	38.23	H	C
ATOM	2393	CB	SER	125	84.858	-10.416	32.579	1.00	23.34	H	C
ATOM	2394	OG	SER	125	83.756	-9.544	32.402	1.00	25.34	H	O
ATOM	2395	C	SER	125	87.262	-10.576	33.200	1.00	33.52	H	C
ATOM	2396	O	SER	125	87.738	-10.972	32.139	1.00	32.91	H	O
ATOM	2397	N	VAL	126	87.787	-10.873	34.386	1.00	23.96	H	N
ATOM	2398	CA	VAL	126	88.962	-11.727	34.452	1.00	20.86	H	C
ATOM	2399	CB	VAL	126	90.135	-11.003	35.174	1.00	22.19	H	C
ATOM	2400	CG1	VAL	126	89.894	-9.504	35.113	1.00	17.46	H	C
ATOM	2401	CG2	VAL	126	90.331	-11.507	36.597	1.00	22.90	H	C
ATOM	2402	C	VAL	126	88.666	-13.091	35.065	1.00	20.51	H	C
ATOM	2403	O	VAL	126	88.382	-13.227	36.256	1.00	24.79	H	O
ATOM	2404	N	PHE	127	88.713	-14.105	34.213	1.00	27.15	H	N
ATOM	2405	CA	PHE	127	88.443	-15.464	34.625	1.00	29.56	H	C
ATOM	2406	CB	PHE	127	87.628	-16.167	33.544	1.00	16.06	H	C
ATOM	2407	CG	PHE	127	86.392	-15.419	33.141	1.00	12.41	H	C
ATOM	2408	CD1	PHE	127	85.380	-15.167	34.071	1.00	11.21	H	C
ATOM	2409	CD2	PHE	127	86.255	-14.922	31.840	1.00	10.06	H	C

Fig. 19: A-34

ATOM	2410	CE1	PHE	127	84.254	-14.428	33.721	1.00	12.93	H	C
ATOM	2411	CE2	PHE	127	85.126	-14.174	31.470	1.00	6.89	H	C
ATOM	2412	CZ	PHE	127	84.125	-13.925	32.413	1.00	6.94	H	C
ATOM	2413	C	PHE	127	89.763	-16.183	34.825	1.00	31.37	H	C
ATOM	2414	O	PHE	127	90.806	-15.733	34.351	1.00	34.05	H	O
ATOM	2415	N	PRO	128	89.743	-17.310	35.540	1.00	21.35	H	N
ATOM	2416	CD	PRO	128	88.681	-17.812	36.434	1.00	32.37	H	C
ATOM	2417	CA	PRO	128	90.996	-18.039	35.752	1.00	22.25	H	C
ATOM	2418	CB	PRO	128	90.823	-18.577	37.161	1.00	34.03	H	C
ATOM	2419	CG	PRO	128	89.358	-18.983	37.130	1.00	33.18	H	C
ATOM	2420	C	PRO	128	91.198	-19.176	34.739	1.00	21.65	H	C
ATOM	2421	O	PRO	128	90.235	-19.770	34.244	1.00	21.29	H	O
ATOM	2422	N	LEU	129	92.457	-19.457	34.432	1.00	17.17	H	N
ATOM	2423	CA	LEU	129	92.811	-20.557	33.545	1.00	19.61	H	C
ATOM	2424	CB	LEU	129	93.683	-20.061	32.396	1.00	18.81	H	C
ATOM	2425	CG	LEU	129	93.086	-18.872	31.635	1.00	18.17	H	C
ATOM	2426	CD1	LEU	129	94.115	-18.254	30.696	1.00	16.12	H	C
ATOM	2427	CD2	LEU	129	91.886	-19.341	30.870	1.00	11.94	H	C
ATOM	2428	C	LEU	129	93.601	-21.457	34.497	1.00	23.45	H	C
ATOM	2429	O	LEU	129	94.824	-21.481	34.499	1.00	25.82	H	O
ATOM	2430	N	ALA	130	92.870	-22.179	35.332	1.00	16.93	H	N
ATOM	2431	CA	ALA	130	93.455	-23.046	36.341	1.00	18.97	H	C
ATOM	2432	CB	ALA	130	92.363	-23.561	37.256	1.00	49.82	H	C
ATOM	2433	C	ALA	130	94.280	-24.219	35.846	1.00	18.88	H	C
ATOM	2434	O	ALA	130	93.928	-24.876	34.869	1.00	20.61	H	O
ATOM	2435	N	PRO	131	95.401	-24.490	36.534	1.00	29.98	H	N
ATOM	2436	CD	PRO	131	95.929	-23.703	37.665	1.00	16.68	H	C
ATOM	2437	CA	PRO	131	96.301	-25.595	36.198	1.00	27.20	H	C
ATOM	2438	CB	PRO	131	97.453	-25.424	37.196	1.00	12.88	H	C
ATOM	2439	CG	PRO	131	96.815	-24.691	38.354	1.00	15.86	H	C
ATOM	2440	C	PRO	131	95.534	-26.897	36.405	1.00	26.68	H	C
ATOM	2441	O	PRO	131	94.666	-26.978	37.274	1.00	27.16	H	O
ATOM	2442	N	SER	132	95.838	-27.912	35.607	1.00	64.88	H	N
ATOM	2443	CA	SER	132	95.138	-29.187	35.720	1.00	67.56	H	C
ATOM	2444	CB	SER	132	93.745	-29.075	35.086	1.00	44.77	H	C
ATOM	2445	OG	SER	132	93.824	-28.747	33.704	1.00	46.53	H	O
ATOM	2446	C	SER	132	95.918	-30.284	35.020	1.00	69.15	H	C
ATOM	2447	O	SER	132	97.107	-30.139	34.757	1.00	69.80	H	O
ATOM	2448	N	SER	133	95.247	-31.391	34.732	1.00	58.75	H	N
ATOM	2449	CA	SER	133	95.894	-32.483	34.024	1.00	61.13	H	C
ATOM	2450	CB	SER	133	95.007	-33.738	34.068	1.00	91.14	H	C
ATOM	2451	OG	SER	133	93.668	-33.456	33.684	1.00	100.88	H	O
ATOM	2452	C	SER	133	96.121	-32.017	32.576	1.00	60.76	H	C
ATOM	2453	O	SER	133	97.091	-32.413	31.927	1.00	61.01	H	O
ATOM	2454	N	LYS	134	95.220	-31.156	32.095	1.00	101.65	H	N
ATOM	2455	CA	LYS	134	95.285	-30.605	30.739	1.00	102.79	H	C
ATOM	2456	CB	LYS	134	93.951	-29.962	30.341	1.00	44.82	H	C
ATOM	2457	CG	LYS	134	92.703	-30.784	30.609	1.00	52.94	H	C
ATOM	2458	CD	LYS	134	92.058	-30.452	31.959	1.00	55.86	H	C
ATOM	2459	CE	LYS	134	90.686	-31.127	32.091	1.00	53.71	H	C
ATOM	2460	NZ	LYS	134	89.988	-30.792	33.367	1.00	52.28	H	N
ATOM	2461	C	LYS	134	96.364	-29.531	30.655	1.00	102.96	H	C
ATOM	2462	O	LYS	134	96.932	-29.284	29.589	1.00	104.03	H	O
ATOM	2463	N	SER	135	96.619	-28.885	31.791	1.00	77.03	H	N
ATOM	2464	CA	SER	135	97.611	-27.818	31.896	1.00	76.76	H	C
ATOM	2465	CB	SER	135	97.069	-26.698	32.784	1.00	81.66	H	C
ATOM	2466	OG	SER	135	95.726	-26.390	32.443	1.00	81.07	H	O
ATOM	2467	C	SER	135	98.911	-28.358	32.488	1.00	71.98	H	C
ATOM	2468	O	SER	135	99.733	-27.601	33.006	1.00	72.29	H	O
ATOM	2469	N	THR	136	99.075	-29.676	32.418	1.00	86.02	H	N
ATOM	2470	CA	THR	136	100.262	-30.351	32.932	1.00	86.44	H	C
ATOM	2471	CB	THR	136	99.897	-31.391	34.036	1.00	47.16	H	C
ATOM	2472	OG1	THR	136	99.491	-30.715	35.237	1.00	47.25	H	O
ATOM	2473	CG2	THR	136	101.096	-32.281	34.354	1.00	50.70	H	C
ATOM	2474	C	THR	136	100.977	-31.072	31.788	1.00	86.90	H	C
ATOM	2475	O	THR	136	100.334	-31.615	30.885	1.00	85.81	H	O
ATOM	2476	N	SER	137	102.309	-31.059	31.836	1.00	82.54	H	N
ATOM	2477	CA	SER	137	103.164	-31.700	30.834	1.00	82.34	H	C
ATOM	2478	CB	SER	137	103.113	-30.942	29.495	1.00	65.40	H	C
ATOM	2479	OG	SER	137	101.863	-31.097	28.841	1.00	66.87	H	O
ATOM	2480	C	SER	137	104.600	-31.715	31.352	1.00	82.68	H	C
ATOM	2481	O	SER	137	105.321	-30.722	31.244	1.00	84.11	H	O
ATOM	2482	N	GLY	138	105.016	-32.845	31.911	1.00	62.73	H	N

Fig. 19: A-35

ATOM	2483	CA	GLY	138	106.361	-32.941	32.438	1.00	62.79	H	C
ATOM	2484	C	GLY	138	106.394	-32.371	33.840	1.00	65.01	H	C
ATOM	2485	O	GLY	138	105.392	-32.410	34.555	1.00	65.52	H	O
ATOM	2486	N	GLY	139	107.537	-31.827	34.237	1.00	45.62	H	N
ATOM	2487	CA	GLY	139	107.645	-31.267	35.570	1.00	45.97	H	C
ATOM	2488	C	GLY	139	107.037	-29.884	35.680	1.00	46.52	H	C
ATOM	2489	O	GLY	139	107.020	-29.297	36.762	1.00	50.66	H	O
ATOM	2490	N	THR	140	106.527	-29.365	34.568	1.00	41.37	H	N
ATOM	2491	CA	THR	140	105.941	-28.030	34.571	1.00	35.80	H	C
ATOM	2492	CB	THR	140	106.626	-27.108	33.533	1.00	32.97	H	C
ATOM	2493	OG1	THR	140	105.886	-27.138	32.311	1.00	30.01	H	O
ATOM	2494	CG2	THR	140	108.052	-27.574	33.250	1.00	33.92	H	C
ATOM	2495	C	THR	140	104.434	-27.993	34.299	1.00	32.68	H	C
ATOM	2496	O	THR	140	103.884	-28.820	33.560	1.00	31.27	H	O
ATOM	2497	N	ALA	141	103.777	-27.013	34.914	1.00	23.19	H	N
ATOM	2498	CA	ALA	141	102.350	-26.817	34.752	1.00	23.90	H	C
ATOM	2499	CB	ALA	141	101.647	-26.986	36.087	1.00	31.87	H	C
ATOM	2500	C	ALA	141	102.121	-25.408	34.206	1.00	24.06	H	C
ATOM	2501	O	ALA	141	102.930	-24.498	34.415	1.00	28.34	H	O
ATOM	2502	N	ALA	142	101.022	-25.239	33.487	1.00	36.28	H	N
ATOM	2503	CA	ALA	142	100.685	-23.948	32.924	1.00	31.12	H	C
ATOM	2504	CB	ALA	142	100.507	-24.062	31.419	1.00	1.87	H	C
ATOM	2505	C	ALA	142	99.389	-23.519	33.588	1.00	29.11	H	C
ATOM	2506	O	ALA	142	98.565	-24.359	33.961	1.00	33.50	H	O
ATOM	2507	N	LEU	143	99.233	-22.211	33.751	1.00	27.06	H	N
ATOM	2508	CA	LEU	143	98.054	-21.611	34.372	1.00	31.22	H	C
ATOM	2509	CB	LEU	143	98.154	-21.670	35.900	1.00	28.24	H	C
ATOM	2510	CG	LEU	143	99.269	-20.865	36.582	1.00	30.55	H	C
ATOM	2511	CD1	LEU	143	98.702	-19.526	36.991	1.00	23.14	H	C
ATOM	2512	CD2	LEU	143	99.817	-21.596	37.809	1.00	37.29	H	C
ATOM	2513	C	LEU	143	98.068	-20.169	33.913	1.00	34.46	H	C
ATOM	2514	O	LEU	143	99.069	-19.700	33.364	1.00	32.14	H	O
ATOM	2515	N	GLY	144	96.970	-19.458	34.128	1.00	25.78	H	N
ATOM	2516	CA	GLY	144	96.922	-18.074	33.694	1.00	28.57	H	C
ATOM	2517	C	GLY	144	95.578	-17.425	33.896	1.00	31.81	H	C
ATOM	2518	O	GLY	144	94.693	-17.985	34.543	1.00	35.57	H	O
ATOM	2519	N	CYS	145	95.420	-16.235	33.335	1.00	24.76	H	N
ATOM	2520	CA	CYS	145	94.177	-15.501	33.471	1.00	23.67	H	C
ATOM	2521	C	CYS	145	93.665	-15.071	32.122	1.00	21.65	H	C
ATOM	2522	O	CYS	145	94.437	-14.868	31.188	1.00	22.23	H	O
ATOM	2523	CB	CYS	145	94.385	-14.273	34.363	1.00	28.67	H	C
ATOM	2524	SG	CYS	145	94.354	-14.658	36.141	1.00	36.96	H	S
ATOM	2525	N	LEU	146	92.351	-14.940	32.024	1.00	43.52	H	N
ATOM	2526	CA	LEU	146	91.712	-14.512	30.792	1.00	43.76	H	C
ATOM	2527	CB	LEU	146	90.715	-15.580	30.314	1.00	38.89	H	C
ATOM	2528	CG	LEU	146	89.754	-15.245	29.164	1.00	28.77	H	C
ATOM	2529	CD1	LEU	146	90.519	-14.669	27.982	1.00	25.69	H	C
ATOM	2530	CD2	LEU	146	88.989	-16.489	28.755	1.00	35.84	H	C
ATOM	2531	C	LEU	146	90.997	-13.188	31.055	1.00	45.61	H	C
ATOM	2532	O	LEU	146	89.943	-13.160	31.690	1.00	45.79	H	O
ATOM	2533	N	VAL	147	91.609	-12.098	30.593	1.00	12.91	H	N
ATOM	2534	CA	VAL	147	91.069	-10.732	30.716	1.00	12.94	H	C
ATOM	2535	CB	VAL	147	92.231	-9.696	30.638	1.00	24.21	H	C
ATOM	2536	CG1	VAL	147	91.703	-8.291	30.722	1.00	25.32	H	C
ATOM	2537	CG2	VAL	147	93.212	-9.947	31.778	1.00	13.52	H	C
ATOM	2538	C	VAL	147	90.101	-10.563	29.532	1.00	18.31	H	C
ATOM	2539	O	VAL	147	90.532	-10.460	28.381	1.00	18.59	H	O
ATOM	2540	N	LYS	148	88.798	-10.519	29.806	1.00	25.16	H	N
ATOM	2541	CA	LYS	148	87.835	-10.467	28.709	1.00	29.22	H	C
ATOM	2542	CB	LYS	148	87.140	-11.827	28.609	1.00	15.56	H	C
ATOM	2543	CG	LYS	148	86.353	-12.032	27.348	1.00	22.92	H	C
ATOM	2544	CD	LYS	148	85.731	-13.405	27.355	1.00	22.16	H	C
ATOM	2545	CE	LYS	148	84.795	-13.570	26.190	1.00	24.54	H	C
ATOM	2546	NZ	LYS	148	85.514	-13.308	24.928	1.00	22.92	H	N
ATOM	2547	C	LYS	148	86.777	-9.372	28.646	1.00	32.79	H	C
ATOM	2548	O	LYS	148	86.332	-8.844	29.664	1.00	33.18	H	O
ATOM	2549	N	ASP	149	86.387	-9.069	27.409	1.00	55.13	H	N
ATOM	2550	CA	ASP	149	85.381	-8.070	27.078	1.00	53.92	H	C
ATOM	2551	CB	ASP	149	83.993	-8.595	27.429	1.00	38.49	H	C
ATOM	2552	CG	ASP	149	83.635	-9.853	26.661	1.00	42.52	H	C
ATOM	2553	OD1	ASP	149	83.797	-9.882	25.421	1.00	46.52	H	O
ATOM	2554	OD2	ASP	149	83.181	-10.817	27.305	1.00	41.08	H	O
ATOM	2555	C	ASP	149	85.585	-6.690	27.698	1.00	56.06	H	C

Fig. 19: A-36

ATOM	2556	O	ASP	149	84.720	-6.175	28.415	1.00	57.30	H	O
ATOM	2557	N	TYR	150	86.734	-6.091	27.399	1.00	33.00	H	N
ATOM	2558	CA	TYR	150	87.072	-4.770	27.897	1.00	33.34	H	C
ATOM	2559	CB	TYR	150	88.306	-4.844	28.797	1.00	39.19	H	C
ATOM	2560	CG	TYR	150	89.622	-5.155	28.097	1.00	44.75	H	C
ATOM	2561	CD1	TYR	150	90.405	-4.137	27.556	1.00	44.06	H	C
ATOM	2562	CE1	TYR	150	91.653	-4.401	26.994	1.00	46.40	H	C
ATOM	2563	CD2	TYR	150	90.121	-6.457	28.046	1.00	44.23	H	C
ATOM	2564	CE2	TYR	150	91.369	-6.730	27.483	1.00	43.19	H	C
ATOM	2565	CZ	TYR	150	92.130	-5.694	26.963	1.00	45.07	H	C
ATOM	2566	OH	TYR	150	93.376	-5.942	26.431	1.00	42.66	H	O
ATOM	2567	C	TYR	150	87.331	-3.838	26.723	1.00	34.19	H	C
ATOM	2568	O	TYR	150	87.420	-4.275	25.569	1.00	36.79	H	O
ATOM	2569	N	PHE	151	87.450	-2.549	27.034	1.00	53.36	H	N
ATOM	2570	CA	PHE	151	87.686	-1.522	26.034	1.00	51.06	H	C
ATOM	2571	CB	PHE	151	86.520	-1.506	25.038	1.00	22.52	H	C
ATOM	2572	CG	PHE	151	86.663	-0.500	23.923	1.00	22.34	H	C
ATOM	2573	CD1	PHE	151	86.509	0.865	24.164	1.00	21.58	H	C
ATOM	2574	CD2	PHE	151	86.896	-0.923	22.616	1.00	24.08	H	C
ATOM	2575	CE1	PHE	151	86.576	1.789	23.117	1.00	22.62	H	C
ATOM	2576	CE2	PHE	151	86.968	-0.003	21.558	1.00	25.39	H	C
ATOM	2577	CZ	PHE	151	86.805	1.351	21.809	1.00	25.56	H	C
ATOM	2578	C	PHE	151	87.819	-0.175	26.734	1.00	48.17	H	C
ATOM	2579	O	PHE	151	87.161	0.084	27.737	1.00	47.45	H	O
ATOM	2580	N	PRO	152	88.712	0.685	26.232	1.00	46.09	H	N
ATOM	2581	CD	PRO	152	88.959	2.055	26.730	1.00	7.14	H	C
ATOM	2582	CA	PRO	152	89.554	0.388	25.065	1.00	47.66	H	C
ATOM	2583	CB	PRO	152	89.773	1.765	24.464	1.00	12.39	H	C
ATOM	2584	CG	PRO	152	90.017	2.594	25.730	1.00	9.55	H	C
ATOM	2585	C	PRO	152	90.835	-0.199	25.636	1.00	47.42	H	C
ATOM	2586	O	PRO	152	90.826	-0.716	26.748	1.00	49.63	H	O
ATOM	2587	N	GLU	153	91.933	-0.128	24.894	1.00	48.37	H	N
ATOM	2588	CA	GLU	153	93.200	-0.620	25.422	1.00	45.01	H	C
ATOM	2589	CB	GLU	153	94.232	-0.788	24.308	1.00	35.76	H	C
ATOM	2590	CG	GLU	153	93.983	-1.951	23.370	1.00	41.71	H	C
ATOM	2591	CD	GLU	153	94.465	-3.279	23.920	1.00	49.73	H	C
ATOM	2592	OE1	GLU	153	94.329	-4.276	23.191	1.00	53.96	H	O
ATOM	2593	OE2	GLU	153	94.979	-3.337	25.062	1.00	49.06	H	O
ATOM	2594	C	GLU	153	93.667	0.487	26.355	1.00	40.62	H	C
ATOM	2595	O	GLU	153	93.160	1.611	26.288	1.00	43.09	H	O
ATOM	2596	N	PRO	154	94.626	0.193	27.242	1.00	31.67	H	N
ATOM	2597	CD	PRO	154	95.605	1.250	27.562	1.00	24.24	H	C
ATOM	2598	CA	PRO	154	95.266	-1.107	27.404	1.00	32.01	H	C
ATOM	2599	CB	PRO	154	96.707	-0.803	27.072	1.00	23.56	H	C
ATOM	2600	CG	PRO	154	96.899	0.447	27.855	1.00	23.31	H	C
ATOM	2601	C	PRO	154	95.127	-1.577	28.846	1.00	37.33	H	C
ATOM	2602	O	PRO	154	94.929	-0.788	29.770	1.00	40.93	H	O
ATOM	2603	N	VAL	155	95.270	-2.874	29.029	1.00	27.89	H	N
ATOM	2604	CA	VAL	155	95.171	-3.468	30.339	1.00	28.93	H	C
ATOM	2605	CB	VAL	155	94.167	-4.647	30.309	1.00	32.63	H	C
ATOM	2606	CG1	VAL	155	94.624	-5.699	29.306	1.00	39.44	H	C
ATOM	2607	CG2	VAL	155	94.030	-5.243	31.690	1.00	38.09	H	C
ATOM	2608	C	VAL	155	96.561	-3.969	30.715	1.00	29.75	H	C
ATOM	2609	O	VAL	155	97.319	-4.427	29.856	1.00	34.58	H	O
ATOM	2610	N	THR	156	96.898	-3.864	31.995	1.00	30.47	H	N
ATOM	2611	CA	THR	156	98.195	-4.322	32.482	1.00	30.67	H	C
ATOM	2612	CB	THR	156	98.855	-3.316	33.458	1.00	37.06	H	C
ATOM	2613	OG1	THR	156	98.554	-3.699	34.810	1.00	41.96	H	O
ATOM	2614	CG2	THR	156	98.346	-1.895	33.213	1.00	35.30	H	C
ATOM	2615	C	THR	156	97.956	-5.589	33.276	1.00	28.26	H	C
ATOM	2616	O	THR	156	96.915	-5.736	33.906	1.00	24.33	H	O
ATOM	2617	N	VAL	157	98.914	-6.501	33.250	1.00	20.40	H	N
ATOM	2618	CA	VAL	157	98.784	-7.731	34.014	1.00	23.86	H	C
ATOM	2619	CB	VAL	157	98.263	-8.918	33.149	1.00	6.55	H	C
ATOM	2620	CG1	VAL	157	98.307	-10.191	33.970	1.00	2.70	H	C
ATOM	2621	CG2	VAL	157	96.817	-8.649	32.662	1.00	8.40	H	C
ATOM	2622	C	VAL	157	100.122	-8.142	34.618	1.00	25.91	H	C
ATOM	2623	O	VAL	157	101.130	-8.220	33.918	1.00	28.24	H	O
ATOM	2624	N	SER	158	100.127	-8.401	35.918	1.00	37.92	H	N
ATOM	2625	CA	SER	158	101.333	-8.840	36.606	1.00	38.42	H	C
ATOM	2626	CB	SER	158	101.852	-7.738	37.521	1.00	26.79	H	C
ATOM	2627	OG	SER	158	101.008	-7.591	38.648	1.00	29.78	H	O
ATOM	2628	C	SER	158	100.947	-10.064	37.439	1.00	37.35	H	C

Fig. 19: A-37

ATOM	2629	O	SER	158	99.765	-10.366	37.583	1.00	35.45	H	O
ATOM	2630	N	TRP	159	101.926	-10.772	37.989	1.00	38.23	H	N
ATOM	2631	CA	TRP	159	101.604	-11.945	38.790	1.00	38.96	H	C
ATOM	2632	CB	TRP	159	102.060	-13.224	38.074	1.00	33.06	H	C
ATOM	2633	CG	TRP	159	101.197	-13.555	36.899	1.00	30.80	H	C
ATOM	2634	CD2	TRP	159	100.089	-14.463	36.879	1.00	31.04	H	C
ATOM	2635	CE2	TRP	159	99.540	-14.423	35.577	1.00	29.21	H	C
ATOM	2636	CE3	TRP	159	99.507	-15.307	37.836	1.00	31.84	H	C
ATOM	2637	CD1	TRP	159	101.271	-13.015	35.649	1.00	26.46	H	C
ATOM	2638	NE1	TRP	159	100.280	-13.531	34.848	1.00	30.17	H	N
ATOM	2639	CZ2	TRP	159	98.439	-15.196	35.204	1.00	33.73	H	C
ATOM	2640	CZ3	TRP	159	98.407	-16.079	37.465	1.00	33.56	H	C
ATOM	2641	CH2	TRP	159	97.887	-16.018	36.158	1.00	34.95	H	C
ATOM	2642	C	TRP	159	102.166	-11.908	40.203	1.00	41.53	H	C
ATOM	2643	O	TRP	159	103.355	-11.670	40.412	1.00	40.45	H	O
ATOM	2644	N	ASN	160	101.295	-12.163	41.170	1.00	50.63	H	N
ATOM	2645	CA	ASN	160	101.699	-12.153	42.557	1.00	51.18	H	C
ATOM	2646	CB	ASN	160	102.753	-13.230	42.814	1.00	31.23	H	C
ATOM	2647	CG	ASN	160	102.145	-14.619	42.946	1.00	28.65	H	C
ATOM	2648	OD1	ASN	160	100.924	-14.784	42.911	1.00	22.55	H	O
ATOM	2649	ND2	ASN	160	103.000	-15.630	43.107	1.00	28.71	H	N
ATOM	2650	C	ASN	160	102.245	-10.777	42.891	1.00	53.56	H	C
ATOM	2651	O	ASN	160	103.277	-10.637	43.554	1.00	51.84	H	O
ATOM	2652	N	SER	161	101.548	-9.758	42.397	1.00	57.36	H	N
ATOM	2653	CA	SER	161	101.915	-8.372	42.651	1.00	58.07	H	C
ATOM	2654	CB	SER	161	101.833	-8.106	44.161	1.00	44.49	H	C
ATOM	2655	OG	SER	161	100.611	-8.586	44.713	1.00	48.26	H	O
ATOM	2656	C	SER	161	103.305	-7.997	42.118	1.00	57.98	H	C
ATOM	2657	O	SER	161	103.779	-6.883	42.329	1.00	58.91	H	O
ATOM	2658	N	GLY	162	103.957	-8.927	41.431	1.00	43.40	H	N
ATOM	2659	CA	GLY	162	105.271	-8.641	40.886	1.00	41.61	H	C
ATOM	2660	C	GLY	162	106.343	-9.670	41.195	1.00	41.13	H	C
ATOM	2661	O	GLY	162	107.340	-9.756	40.475	1.00	41.89	H	O
ATOM	2662	N	ALA	163	106.144	-10.460	42.248	1.00	32.79	H	N
ATOM	2663	CA	ALA	163	107.135	-11.462	42.644	1.00	33.15	H	C
ATOM	2664	CB	ALA	163	106.845	-11.956	44.065	1.00	7.75	H	C
ATOM	2665	C	ALA	163	107.265	-12.651	41.702	1.00	33.69	H	C
ATOM	2666	O	ALA	163	108.154	-13.473	41.868	1.00	36.52	H	O
ATOM	2667	N	LEU	164	106.378	-12.750	40.722	1.00	33.04	H	N
ATOM	2668	CA	LEU	164	106.412	-13.847	39.755	1.00	28.09	H	C
ATOM	2669	CB	LEU	164	105.146	-14.701	39.869	1.00	29.67	H	C
ATOM	2670	CG	LEU	164	105.008	-15.851	38.870	1.00	27.43	H	C
ATOM	2671	CD1	LEU	164	105.976	-16.963	39.215	1.00	24.01	H	C
ATOM	2672	CD2	LEU	164	103.605	-16.370	38.903	1.00	22.28	H	C
ATOM	2673	C	LEU	164	106.483	-13.227	38.370	1.00	26.00	H	C
ATOM	2674	O	LEU	164	105.492	-12.663	37.893	1.00	20.06	H	O
ATOM	2675	N	THR	165	107.656	-13.326	37.740	1.00	28.49	H	N
ATOM	2676	CA	THR	165	107.893	-12.758	36.410	1.00	32.54	H	C
ATOM	2677	CB	THR	165	108.927	-11.613	36.462	1.00	18.33	H	C
ATOM	2678	OG1	THR	165	110.114	-12.057	37.139	1.00	21.15	H	O
ATOM	2679	CG2	THR	165	108.348	-10.419	37.184	1.00	20.86	H	C
ATOM	2680	C	THR	165	108.394	-13.770	35.397	1.00	33.42	H	C
ATOM	2681	O	THR	165	108.028	-13.717	34.227	1.00	34.44	H	O
ATOM	2682	N	SER	166	109.244	-14.683	35.849	1.00	63.46	H	N
ATOM	2683	CA	SER	166	109.804	-15.702	34.973	1.00	62.93	H	C
ATOM	2684	CB	SER	166	110.901	-16.472	35.710	1.00	37.10	H	C
ATOM	2685	OG	SER	166	111.503	-17.442	34.870	1.00	42.11	H	O
ATOM	2686	C	SER	166	108.748	-16.678	34.458	1.00	60.85	H	C
ATOM	2687	O	SER	166	107.955	-17.226	35.227	1.00	60.31	H	O
ATOM	2688	N	GLY	167	108.744	-16.895	33.148	1.00	58.61	H	N
ATOM	2689	CA	GLY	167	107.784	-17.812	32.566	1.00	55.44	H	C
ATOM	2690	C	GLY	167	106.425	-17.181	32.332	1.00	49.55	H	C
ATOM	2691	O	GLY	167	105.462	-17.878	32.010	1.00	51.52	H	O
ATOM	2692	N	VAL	168	106.340	-15.864	32.491	1.00	12.32	H	N
ATOM	2693	CA	VAL	168	105.081	-15.183	32.280	1.00	12.04	H	C
ATOM	2694	CB	VAL	168	104.933	-13.970	33.190	1.00	2.74	H	C
ATOM	2695	CG1	VAL	168	103.590	-13.273	32.906	1.00	2.74	H	C
ATOM	2696	CG2	VAL	168	105.070	-14.398	34.630	1.00	2.83	H	C
ATOM	2697	C	VAL	168	104.965	-14.687	30.852	1.00	11.82	H	C
ATOM	2698	O	VAL	168	105.894	-14.087	30.319	1.00	11.28	H	O
ATOM	2699	N	HIS	169	103.807	-14.931	30.253	1.00	28.24	H	N
ATOM	2700	CA	HIS	169	103.518	-14.512	28.891	1.00	24.96	H	C
ATOM	2701	CB	HIS	169	103.566	-15.695	27.924	1.00	1.87	H	C

Fig. 19: A-38

ATOM	2702	CG	HIS	169	104.935	-16.209	27.634	1.00	1.87	H	C
ATOM	2703	CD2	HIS	169	105.456	-17.452	27.739	1.00	10.72	H	C
ATOM	2704	ND1	HIS	169	105.935	-15.415	27.114	1.00	4.04	H	N
ATOM	2705	CE1	HIS	169	107.015	-16.147	26.912	1.00	11.56	H	C
ATOM	2706	NE2	HIS	169	106.750	-17.387	27.282	1.00	3.03	H	N
ATOM	2707	C	HIS	169	102.106	-13.934	28.818	1.00	26.88	H	C
ATOM	2708	O	HIS	169	101.143	-14.679	28.610	1.00	27.44	H	O
ATOM	2709	N	THR	170	101.960	-12.628	28.995	1.00	15.52	H	N
ATOM	2710	CA	THR	170	100.637	-12.030	28.885	1.00	14.61	H	C
ATOM	2711	CB	THR	170	100.472	-10.872	29.894	1.00	20.19	H	C
ATOM	2712	OG1	THR	170	99.403	-10.021	29.470	1.00	14.32	H	O
ATOM	2713	CG2	THR	170	101.760	-10.096	30.042	1.00	25.14	H	C
ATOM	2714	C	THR	170	100.487	-11.553	27.433	1.00	15.32	H	C
ATOM	2715	O	THR	170	101.023	-10.532	27.053	1.00	11.65	H	O
ATOM	2716	N	PHE	171	99.762	-12.324	26.630	1.00	23.28	H	N
ATOM	2717	CA	PHE	171	99.587	-12.046	25.206	1.00	17.85	H	C
ATOM	2718	CB	PHE	171	98.695	-13.110	24.554	1.00	15.23	H	C
ATOM	2719	CG	PHE	171	99.138	-14.521	24.806	1.00	7.97	H	C
ATOM	2720	CD1	PHE	171	98.731	-15.195	25.955	1.00	8.65	H	C
ATOM	2721	CD2	PHE	171	99.978	-15.174	23.903	1.00	7.84	H	C
ATOM	2722	CE1	PHE	171	99.153	-16.492	26.202	1.00	17.36	H	C
ATOM	2723	CE2	PHE	171	100.407	-16.473	24.144	1.00	15.22	H	C
ATOM	2724	CZ	PHE	171	99.993	-17.133	25.295	1.00	16.34	H	C
ATOM	2725	C	PHE	171	99.032	-10.692	24.793	1.00	18.20	H	C
ATOM	2726	O	PHE	171	98.344	-10.015	25.552	1.00	23.73	H	O
ATOM	2727	N	PRO	172	99.341	-10.278	23.557	1.00	21.77	H	N
ATOM	2728	CD	PRO	172	100.227	-10.890	22.550	1.00	20.32	H	C
ATOM	2729	CA	PRO	172	98.827	-8.999	23.088	1.00	23.20	H	C
ATOM	2730	CB	PRO	172	99.595	-8.775	21.782	1.00	20.71	H	C
ATOM	2731	CG	PRO	172	99.834	-10.148	21.287	1.00	18.82	H	C
ATOM	2732	C	PRO	172	97.339	-9.235	22.876	1.00	25.11	H	C
ATOM	2733	O	PRO	172	96.916	-10.364	22.645	1.00	23.46	H	O
ATOM	2734	N	ALA	173	96.551	-8.172	22.960	1.00	24.67	H	N
ATOM	2735	CA	ALA	173	95.104	-8.267	22.815	1.00	27.18	H	C
ATOM	2736	CB	ALA	173	94.439	-7.079	23.498	1.00	1.87	H	C
ATOM	2737	C	ALA	173	94.604	-8.379	21.391	1.00	30.18	H	C
ATOM	2738	O	ALA	173	95.304	-8.080	20.426	1.00	32.13	H	O
ATOM	2739	N	VAL	174	93.365	-8.820	21.277	1.00	21.72	H	N
ATOM	2740	CA	VAL	174	92.753	-8.964	19.984	1.00	23.16	H	C
ATOM	2741	CB	VAL	174	92.841	-10.406	19.511	1.00	28.95	H	C
ATOM	2742	CG1	VAL	174	92.103	-10.566	18.201	1.00	32.21	H	C
ATOM	2743	CG2	VAL	174	94.305	-10.797	19.356	1.00	26.32	H	C
ATOM	2744	C	VAL	174	91.302	-8.508	20.058	1.00	25.36	H	C
ATOM	2745	O	VAL	174	90.611	-8.718	21.069	1.00	25.35	H	O
ATOM	2746	N	LEU	175	90.860	-7.856	18.987	1.00	41.55	H	N
ATOM	2747	CA	LEU	175	89.504	-7.338	18.890	1.00	40.23	H	C
ATOM	2748	CB	LEU	175	89.443	-6.276	17.787	1.00	23.29	H	C
ATOM	2749	CG	LEU	175	88.728	-4.928	17.990	1.00	20.94	H	C
ATOM	2750	CD1	LEU	175	88.634	-4.511	19.463	1.00	21.45	H	C
ATOM	2751	CD2	LEU	175	89.518	-3.900	17.186	1.00	22.78	H	C
ATOM	2752	C	LEU	175	88.539	-8.474	18.588	1.00	42.85	H	C
ATOM	2753	O	LEU	175	88.738	-9.233	17.638	1.00	45.50	H	O
ATOM	2754	N	GLN	176	87.500	-8.592	19.407	1.00	41.11	H	N
ATOM	2755	CA	GLN	176	86.514	-9.645	19.228	1.00	42.33	H	C
ATOM	2756	CB	GLN	176	85.852	-9.990	20.564	1.00	38.15	H	C
ATOM	2757	CG	GLN	176	86.817	-10.276	21.703	1.00	37.93	H	C
ATOM	2758	CD	GLN	176	86.109	-10.801	22.939	1.00	36.82	H	C
ATOM	2759	OE1	GLN	176	85.562	-11.899	22.923	1.00	36.67	H	O
ATOM	2760	NE2	GLN	176	86.108	-10.014	24.011	1.00	33.13	H	N
ATOM	2761	C	GLN	176	85.439	-9.207	18.245	1.00	44.39	H	C
ATOM	2762	O	GLN	176	85.274	-8.018	17.969	1.00	34.09	H	O
ATOM	2763	N	SER	177	84.708	-10.182	17.718	1.00	59.83	H	N
ATOM	2764	CA	SER	177	83.624	-9.902	16.790	1.00	58.61	H	C
ATOM	2765	CB	SER	177	82.804	-11.177	16.558	1.00	104.21	H	C
ATOM	2766	OG	SER	177	81.708	-10.945	15.689	1.00	104.01	H	O
ATOM	2767	C	SER	177	82.759	-8.832	17.448	1.00	60.09	H	C
ATOM	2768	O	SER	177	82.169	-7.985	16.778	1.00	62.26	H	O
ATOM	2769	N	SER	178	82.722	-8.877	18.778	1.00	34.26	H	N
ATOM	2770	CA	SER	178	81.942	-7.952	19.596	1.00	32.97	H	C
ATOM	2771	CB	SER	178	81.798	-8.510	21.019	1.00	67.89	H	C
ATOM	2772	OG	SER	178	83.057	-8.636	21.663	1.00	66.22	H	O
ATOM	2773	C	SER	178	82.538	-6.554	19.671	1.00	32.95	H	C
ATOM	2774	O	SER	178	81.921	-5.640	20.210	1.00	35.05	H	O

Fig. 19: A-39

ATOM	2775	N	GLY	179	83.738	-6.382	19.135	1.00	43.45	H	N
ATOM	2776	CA	GLY	179	84.357	-5.072	19.191	1.00	46.81	H	C
ATOM	2777	C	GLY	179	84.972	-4.821	20.552	1.00	50.21	H	C
ATOM	2778	O	GLY	179	85.380	-3.707	20.869	1.00	50.30	H	O
ATOM	2779	N	LEU	180	85.020	-5.862	21.369	1.00	30.24	H	N
ATOM	2780	CA	LEU	180	85.620	-5.749	22.686	1.00	32.27	H	C
ATOM	2781	CB	LEU	180	84.706	-6.380	23.730	1.00	33.41	H	C
ATOM	2782	CG	LEU	180	83.485	-5.524	24.054	1.00	32.78	H	C
ATOM	2783	CD1	LEU	180	82.513	-6.292	24.902	1.00	27.00	H	C
ATOM	2784	CD2	LEU	180	83.943	-4.278	24.781	1.00	32.58	H	C
ATOM	2785	C	LEU	180	86.974	-6.442	22.672	1.00	32.86	H	C
ATOM	2786	O	LEU	180	87.135	-7.488	22.054	1.00	36.18	H	O
ATOM	2787	N	TYR	181	87.952	-5.843	23.336	1.00	31.41	H	N
ATOM	2788	CA	TYR	181	89.293	-6.409	23.387	1.00	32.68	H	C
ATOM	2789	CB	TYR	181	90.297	-5.323	23.792	1.00	57.58	H	C
ATOM	2790	CG	TYR	181	90.773	-4.445	22.651	1.00	56.39	H	C
ATOM	2791	CD1	TYR	181	91.591	-4.961	21.647	1.00	57.58	H	C
ATOM	2792	CE1	TYR	181	92.063	-4.155	20.605	1.00	57.08	H	C
ATOM	2793	CD2	TYR	181	90.430	-3.092	22.585	1.00	56.67	H	C
ATOM	2794	CE2	TYR	181	90.899	-2.273	21.543	1.00	57.48	H	C
ATOM	2795	CZ	TYR	181	91.717	-2.816	20.559	1.00	58.33	H	C
ATOM	2796	OH	TYR	181	92.202	-2.033	19.533	1.00	62.35	H	O
ATOM	2797	C	TYR	181	89.361	-7.573	24.375	1.00	31.73	H	C
ATOM	2798	O	TYR	181	88.581	-7.638	25.324	1.00	32.08	H	O
ATOM	2799	N	SER	182	90.287	-8.499	24.149	1.00	35.13	H	N
ATOM	2800	CA	SER	182	90.446	-9.642	25.045	1.00	32.04	H	C
ATOM	2801	CB	SER	182	89.439	-10.741	24.700	1.00	65.40	H	C
ATOM	2802	OG	SER	182	89.612	-11.868	25.543	1.00	59.63	H	O
ATOM	2803	C	SER	182	91.860	-10.209	24.970	1.00	33.65	H	C
ATOM	2804	O	SER	182	92.494	-10.187	23.906	1.00	37.13	H	O
ATOM	2805	N	LEU	183	92.351	-10.713	26.101	1.00	28.98	H	N
ATOM	2806	CA	LEU	183	93.689	-11.290	26.152	1.00	24.91	H	C
ATOM	2807	CB	LEU	183	94.753	-10.179	26.189	1.00	31.36	H	C
ATOM	2808	CG	LEU	183	94.913	-9.263	27.414	1.00	23.12	H	C
ATOM	2809	CD1	LEU	183	95.475	-10.014	28.625	1.00	27.02	H	C
ATOM	2810	CD2	LEU	183	95.849	-8.148	27.036	1.00	19.84	H	C
ATOM	2811	C	LEU	183	93.898	-12.209	27.342	1.00	24.58	H	C
ATOM	2812	O	LEU	183	93.179	-12.135	28.326	1.00	18.76	H	O
ATOM	2813	N	SER	184	94.894	-13.077	27.250	1.00	26.13	H	N
ATOM	2814	CA	SER	184	95.205	-13.967	28.357	1.00	26.65	H	C
ATOM	2815	CB	SER	184	95.000	-15.445	27.968	1.00	16.60	H	C
ATOM	2816	OG	SER	184	93.638	-15.750	27.710	1.00	22.49	H	O
ATOM	2817	C	SER	184	96.660	-13.752	28.784	1.00	22.47	H	C
ATOM	2818	O	SER	184	97.546	-13.511	27.953	1.00	21.27	H	O
ATOM	2819	N	SER	185	96.896	-13.786	30.087	1.00	27.49	H	N
ATOM	2820	CA	SER	185	98.251	-13.670	30.575	1.00	25.55	H	C
ATOM	2821	CB	SER	185	98.389	-12.634	31.678	1.00	27.24	H	C
ATOM	2822	OG	SER	185	99.760	-12.516	32.031	1.00	25.68	H	O
ATOM	2823	C	SER	185	98.460	-15.060	31.123	1.00	23.97	H	C
ATOM	2824	O	SER	185	97.652	-15.551	31.912	1.00	25.28	H	O
ATOM	2825	N	VAL	186	99.533	-15.699	30.679	1.00	29.81	H	N
ATOM	2826	CA	VAL	186	99.830	-17.060	31.064	1.00	29.28	H	C
ATOM	2827	CB	VAL	186	99.717	-17.966	29.831	1.00	20.56	H	C
ATOM	2828	CG1	VAL	186	100.305	-19.306	30.112	1.00	20.80	H	C
ATOM	2829	CG2	VAL	186	98.253	-18.121	29.446	1.00	19.74	H	C
ATOM	2830	C	VAL	186	101.204	-17.193	31.664	1.00	30.42	H	C
ATOM	2831	O	VAL	186	102.097	-16.416	31.357	1.00	31.20	H	O
ATOM	2832	N	VAL	187	101.359	-18.179	32.540	1.00	29.47	H	N
ATOM	2833	CA	VAL	187	102.645	-18.457	33.178	1.00	26.42	H	C
ATOM	2834	CB	VAL	187	102.739	-17.797	34.586	1.00	27.93	H	C
ATOM	2835	CG1	VAL	187	101.681	-18.385	35.507	1.00	26.86	H	C
ATOM	2836	CG2	VAL	187	104.134	-17.994	35.180	1.00	26.29	H	C
ATOM	2837	C	VAL	187	102.842	-19.975	33.309	1.00	20.75	H	C
ATOM	2838	O	VAL	187	101.882	-20.743	33.316	1.00	22.47	H	O
ATOM	2839	N	THR	188	104.098	-20.397	33.377	1.00	5.29	H	N
ATOM	2840	CA	THR	188	104.441	-21.807	33.539	1.00	7.86	H	C
ATOM	2841	CB	THR	188	105.280	-22.327	32.366	1.00	35.20	H	C
ATOM	2842	OG1	THR	188	106.425	-21.487	32.194	1.00	33.26	H	O
ATOM	2843	CG2	THR	188	104.453	-22.337	31.078	1.00	39.96	H	C
ATOM	2844	C	THR	188	105.270	-21.870	34.802	1.00	13.86	H	C
ATOM	2845	O	THR	188	106.194	-21.077	34.975	1.00	18.45	H	O
ATOM	2846	N	VAL	189	104.921	-22.799	35.688	1.00	28.00	H	N
ATOM	2847	CA	VAL	189	105.613	-22.963	36.965	1.00	25.42	H	C

Fig. 19: A-40

ATOM	2848	CB	VAL	189	104.755	-22.412	38.137	1.00	24.28	H	C
ATOM	2849	CG1	VAL	189	104.399	-20.951	37.904	1.00	17.23	H	C
ATOM	2850	CG2	VAL	189	103.478	-23.234	38.270	1.00	17.84	H	C
ATOM	2851	C	VAL	189	105.875	-24.439	37.242	1.00	32.15	H	C
ATOM	2852	O	VAL	189	105.386	-25.309	36.523	1.00	35.18	H	O
ATOM	2853	N	PRO	190	106.671	-24.738	38.280	1.00	50.39	H	N
ATOM	2854	CD	PRO	190	107.545	-23.823	39.036	1.00	32.03	H	C
ATOM	2855	CA	PRO	190	106.962	-26.133	38.624	1.00	50.40	H	C
ATOM	2856	CB	PRO	190	107.911	-26.001	39.814	1.00	29.50	H	C
ATOM	2857	CG	PRO	190	108.651	-24.746	39.514	1.00	29.72	H	C
ATOM	2858	C	PRO	190	105.650	-26.801	39.018	1.00	50.46	H	C
ATOM	2859	O	PRO	190	104.899	-26.267	39.834	1.00	48.43	H	O
ATOM	2860	N	SER	191	105.357	-27.953	38.436	1.00	54.29	H	N
ATOM	2861	CA	SER	191	104.122	-28.638	38.774	1.00	60.79	H	C
ATOM	2862	CB	SER	191	104.111	-30.036	38.157	1.00	30.49	H	C
ATOM	2863	OG	SER	191	104.076	-29.980	36.740	1.00	31.07	H	O
ATOM	2864	C	SER	191	104.009	-28.730	40.297	1.00	63.91	H	C
ATOM	2865	O	SER	191	102.986	-28.361	40.882	1.00	66.82	H	O
ATOM	2866	N	SER	192	105.084	-29.201	40.924	1.00	39.50	H	N
ATOM	2867	CA	SER	192	105.177	-29.374	42.376	1.00	40.99	H	C
ATOM	2868	CB	SER	192	106.602	-29.776	42.739	1.00	41.75	H	C
ATOM	2869	OG	SER	192	107.475	-28.675	42.565	1.00	41.65	H	O
ATOM	2870	C	SER	192	104.795	-28.150	43.220	1.00	42.26	H	C
ATOM	2871	O	SER	192	104.403	-28.286	44.381	1.00	48.17	H	O
ATOM	2872	N	SER	193	104.923	-26.960	42.645	1.00	20.64	H	N
ATOM	2873	CA	SER	193	104.601	-25.733	43.365	1.00	22.36	H	C
ATOM	2874	CB	SER	193	105.396	-24.567	42.771	1.00	39.90	H	C
ATOM	2875	OG	SER	193	104.973	-24.284	41.447	1.00	36.65	H	O
ATOM	2876	C	SER	193	103.097	-25.380	43.392	1.00	22.92	H	C
ATOM	2877	O	SER	193	102.697	-24.363	43.963	1.00	25.84	H	O
ATOM	2878	N	LEU	194	102.268	-26.218	42.776	1.00	41.78	H	N
ATOM	2879	CA	LEU	194	100.827	-25.974	42.741	1.00	45.87	H	C
ATOM	2880	CB	LEU	194	100.172	-26.850	41.677	1.00	23.80	H	C
ATOM	2881	CG	LEU	194	100.533	-26.605	40.216	1.00	21.31	H	C
ATOM	2882	CD1	LEU	194	99.975	-27.739	39.377	1.00	19.27	H	C
ATOM	2883	CD2	LEU	194	99.973	-25.246	39.757	1.00	15.31	H	C
ATOM	2884	C	LEU	194	100.177	-26.276	44.080	1.00	49.01	H	C
ATOM	2885	O	LEU	194	99.209	-25.623	44.478	1.00	48.38	H	O
ATOM	2886	N	GLY	195	100.718	-27.272	44.770	1.00	65.65	H	N
ATOM	2887	CA	GLY	195	100.160	-27.676	46.043	1.00	68.76	H	C
ATOM	2888	C	GLY	195	100.625	-26.877	47.235	1.00	66.22	H	C
ATOM	2889	O	GLY	195	100.051	-26.992	48.314	1.00	68.30	H	O
ATOM	2890	N	THR	196	101.659	-26.067	47.053	1.00	33.26	H	N
ATOM	2891	CA	THR	196	102.175	-25.265	48.155	1.00	32.73	H	C
ATOM	2892	CB	THR	196	103.575	-25.763	48.585	1.00	30.77	H	C
ATOM	2893	OG1	THR	196	104.489	-25.676	47.478	1.00	28.63	H	O
ATOM	2894	CG2	THR	196	103.488	-27.213	49.071	1.00	27.23	H	C
ATOM	2895	C	THR	196	102.251	-23.786	47.813	1.00	35.97	H	C
ATOM	2896	O	THR	196	102.179	-22.933	48.695	1.00	36.72	H	O
ATOM	2897	N	GLN	197	102.389	-23.488	46.527	1.00	53.90	H	N
ATOM	2898	CA	GLN	197	102.478	-22.110	46.060	1.00	54.25	H	C
ATOM	2899	CB	GLN	197	103.480	-22.031	44.906	1.00	42.12	H	C
ATOM	2900	CG	GLN	197	104.561	-20.975	45.045	1.00	45.66	H	C
ATOM	2901	CD	GLN	197	104.051	-19.587	44.765	1.00	49.49	H	C
ATOM	2902	OE1	GLN	197	103.257	-19.032	45.528	1.00	50.05	H	O
ATOM	2903	NE2	GLN	197	104.500	-19.013	43.656	1.00	49.01	H	N
ATOM	2904	C	GLN	197	101.105	-21.617	45.604	1.00	52.98	H	C
ATOM	2905	O	GLN	197	100.314	-22.382	45.050	1.00	55.53	H	O
ATOM	2906	N	THR	198	100.829	-20.338	45.847	1.00	30.38	H	N
ATOM	2907	CA	THR	198	99.559	-19.719	45.470	1.00	29.29	H	C
ATOM	2908	CB	THR	198	98.922	-18.970	46.677	1.00	45.77	H	C
ATOM	2909	OG1	THR	198	97.546	-18.682	46.404	1.00	43.55	H	O
ATOM	2910	CG2	THR	198	99.643	-17.644	46.929	1.00	47.95	H	C
ATOM	2911	C	THR	198	99.811	-18.719	44.338	1.00	27.94	H	C
ATOM	2912	O	THR	198	100.722	-17.891	44.413	1.00	31.22	H	O
ATOM	2913	N	TYR	199	99.008	-18.789	43.285	1.00	40.84	H	N
ATOM	2914	CA	TYR	199	99.191	-17.874	42.168	1.00	31.26	H	C
ATOM	2915	CB	TYR	199	99.402	-18.681	40.880	1.00	39.46	H	C
ATOM	2916	CG	TYR	199	100.677	-19.496	40.904	1.00	33.83	H	C
ATOM	2917	CD1	TYR	199	101.911	-18.901	40.630	1.00	31.63	H	C
ATOM	2918	CE1	TYR	199	103.107	-19.626	40.735	1.00	31.28	H	C
ATOM	2919	CD2	TYR	199	100.662	-20.847	41.282	1.00	32.94	H	C
ATOM	2920	CE2	TYR	199	101.850	-21.590	41.392	1.00	33.91	H	C

Fig. 19: A-41

ATOM	2921	CZ	TYR	199	103.069	-20.972	41.118	1.00	33.40	H	C
ATOM	2922	OH	TYR	199	104.244	-21.685	41.223	1.00	37.29	H	O
ATOM	2923	C	TYR	199	98.029	-16.897	42.014	1.00	31.50	H	C
ATOM	2924	O	TYR	199	96.876	-17.302	41.913	1.00	32.18	H	O
ATOM	2925	N	ILE	200	98.342	-15.605	42.026	1.00	38.61	H	N
ATOM	2926	CA	ILE	200	97.329	-14.566	41.858	1.00	39.11	H	C
ATOM	2927	CB	ILE	200	97.265	-13.574	43.051	1.00	27.10	H	C
ATOM	2928	CG2	ILE	200	96.185	-12.540	42.793	1.00	26.36	H	C
ATOM	2929	CG1	ILE	200	96.978	-14.301	44.363	1.00	30.59	H	C
ATOM	2930	CD1	ILE	200	98.119	-15.184	44.842	1.00	36.15	H	C
ATOM	2931	C	ILE	200	97.730	-13.736	40.649	1.00	41.59	H	C
ATOM	2932	O	ILE	200	98.916	-13.517	40.415	1.00	45.01	H	O
ATOM	2933	N	CYS	201	96.758	-13.283	39.867	1.00	30.01	H	N
ATOM	2934	CA	CYS	201	97.092	-12.434	38.735	1.00	27.23	H	C
ATOM	2935	C	CYS	201	96.476	-11.075	39.011	1.00	24.60	H	C
ATOM	2936	O	CYS	201	95.307	-10.967	39.386	1.00	22.36	H	O
ATOM	2937	CB	CYS	201	96.577	-12.997	37.394	1.00	42.80	H	C
ATOM	2938	SG	CYS	201	94.784	-12.909	37.090	1.00	39.16	H	S
ATOM	2939	N	ASN	202	97.282	-10.035	38.849	1.00	26.40	H	N
ATOM	2940	CA	ASN	202	96.819	-8.683	39.080	1.00	32.39	H	C
ATOM	2941	CB	ASN	202	97.884	-7.902	39.846	1.00	36.85	H	C
ATOM	2942	CG	ASN	202	98.507	-8.720	40.954	1.00	39.80	H	C
ATOM	2943	OD1	ASN	202	99.570	-9.314	40.779	1.00	38.11	H	O
ATOM	2944	ND2	ASN	202	97.837	-8.776	42.097	1.00	41.02	H	N
ATOM	2945	C	ASN	202	96.530	-8.025	37.743	1.00	36.08	H	C
ATOM	2946	O	ASN	202	97.419	-7.867	36.911	1.00	40.34	H	O
ATOM	2947	N	VAL	203	95.273	-7.668	37.533	1.00	28.99	H	N
ATOM	2948	CA	VAL	203	94.868	-7.017	36.295	1.00	29.18	H	C
ATOM	2949	CB	VAL	203	93.691	-7.781	35.624	1.00	21.70	H	C
ATOM	2950	CG1	VAL	203	93.321	-7.134	34.274	1.00	17.35	H	C
ATOM	2951	CG2	VAL	203	94.067	-9.236	35.450	1.00	25.16	H	C
ATOM	2952	C	VAL	203	94.443	-5.580	36.615	1.00	32.31	H	C
ATOM	2953	O	VAL	203	93.808	-5.320	37.643	1.00	27.84	H	O
ATOM	2954	N	ASN	204	94.799	-4.648	35.741	1.00	45.86	H	N
ATOM	2955	CA	ASN	204	94.442	-3.266	35.979	1.00	50.50	H	C
ATOM	2956	CB	ASN	204	95.565	-2.570	36.739	1.00	59.79	H	C
ATOM	2957	CG	ASN	204	95.186	-1.176	37.164	1.00	65.34	H	C
ATOM	2958	OD1	ASN	204	94.801	-0.347	36.338	1.00	69.10	H	O
ATOM	2959	ND2	ASN	204	95.287	-0.906	38.459	1.00	65.59	H	N
ATOM	2960	C	ASN	204	94.109	-2.486	34.709	1.00	51.54	H	C
ATOM	2961	O	ASN	204	94.985	-2.164	33.905	1.00	51.77	H	O
ATOM	2962	N	HIS	205	92.828	-2.176	34.550	1.00	30.40	H	N
ATOM	2963	CA	HIS	205	92.338	-1.431	33.396	1.00	29.10	H	C
ATOM	2964	CB	HIS	205	90.994	-1.998	32.957	1.00	20.87	H	C
ATOM	2965	CG	HIS	205	90.444	-1.371	31.718	1.00	25.68	H	C
ATOM	2966	CD2	HIS	205	89.209	-0.889	31.437	1.00	28.69	H	C
ATOM	2967	ND1	HIS	205	91.165	-1.282	30.548	1.00	23.44	H	N
ATOM	2968	CE1	HIS	205	90.396	-0.780	29.597	1.00	25.19	H	C
ATOM	2969	NE2	HIS	205	89.203	-0.534	30.110	1.00	28.16	H	N
ATOM	2970	C	HIS	205	92.157	0.022	33.793	1.00	30.12	H	C
ATOM	2971	O	HIS	205	91.057	0.429	34.173	1.00	28.02	H	O
ATOM	2972	N	LYS	206	93.228	0.805	33.714	1.00	50.94	H	N
ATOM	2973	CA	LYS	206	93.138	2.209	34.084	1.00	49.11	H	C
ATOM	2974	CB	LYS	206	94.486	2.906	33.867	1.00	50.82	H	C
ATOM	2975	CG	LYS	206	95.536	2.476	34.895	1.00	57.82	H	C
ATOM	2976	CD	LYS	206	96.809	3.325	34.857	1.00	61.64	H	C
ATOM	2977	CE	LYS	206	97.793	2.906	35.959	1.00	63.00	H	C
ATOM	2978	NZ	LYS	206	99.049	3.715	35.960	1.00	66.30	H	N
ATOM	2979	C	LYS	206	92.017	2.949	33.353	1.00	47.68	H	C
ATOM	2980	O	LYS	206	91.318	3.765	33.955	1.00	46.73	H	O
ATOM	2981	N	PRO	207	91.810	2.650	32.057	1.00	33.42	H	N
ATOM	2982	CD	PRO	207	92.613	1.722	31.239	1.00	21.52	H	C
ATOM	2983	CA	PRO	207	90.770	3.285	31.241	1.00	34.06	H	C
ATOM	2984	CB	PRO	207	90.831	2.501	29.936	1.00	21.18	H	C
ATOM	2985	CG	PRO	207	92.286	2.156	29.831	1.00	24.69	H	C
ATOM	2986	C	PRO	207	89.366	3.280	31.846	1.00	34.36	H	C
ATOM	2987	O	PRO	207	88.452	3.927	31.311	1.00	32.31	H	O
ATOM	2988	N	SER	208	89.190	2.545	32.944	1.00	25.18	H	N
ATOM	2989	CA	SER	208	87.893	2.481	33.628	1.00	28.11	H	C
ATOM	2990	CB	SER	208	87.055	1.320	33.094	1.00	29.27	H	C
ATOM	2991	OG	SER	208	87.724	0.096	33.315	1.00	27.44	H	O
ATOM	2992	C	SER	208	88.120	2.314	35.126	1.00	31.08	H	C
ATOM	2993	O	SER	208	87.266	1.789	35.846	1.00	34.78	H	O

Fig. 19: A-42

ATOM	2994	N	ASN	209	89.284	2.777	35.573	1.00	68.02	H	N
ATOM	2995	CA	ASN	209	89.678	2.701	36.970	1.00	70.18	H	C
ATOM	2996	CB	ASN	209	89.073	3.879	37.741	1.00	49.77	H	C
ATOM	2997	CG	ASN	209	89.673	4.044	39.125	1.00	56.50	H	C
ATOM	2998	OD1	ASN	209	90.885	3.963	39.301	1.00	62.08	H	O
ATOM	2999	ND2	ASN	209	88.824	4.290	40.114	1.00	57.03	H	N
ATOM	3000	C	ASN	209	89.267	1.360	37.593	1.00	68.80	H	C
ATOM	3001	O	ASN	209	88.708	1.304	38.690	1.00	68.05	H	O
ATOM	3002	N	THR	210	89.555	0.282	36.871	1.00	35.45	H	N
ATOM	3003	CA	THR	210	89.246	-1.061	37.322	1.00	37.08	H	C
ATOM	3004	CB	THR	210	88.640	-1.883	36.201	1.00	55.80	H	C
ATOM	3005	OG1	THR	210	87.416	-1.273	35.787	1.00	56.14	H	O
ATOM	3006	CG2	THR	210	88.367	-3.303	36.668	1.00	57.05	H	C
ATOM	3007	C	THR	210	90.538	-1.719	37.762	1.00	36.35	H	C
ATOM	3008	O	THR	210	91.613	-1.388	37.266	1.00	34.79	H	O
ATOM	3009	N	LYS	211	90.426	-2.655	38.692	1.00	33.96	H	N
ATOM	3010	CA	LYS	211	91.588	-3.352	39.207	1.00	34.09	H	C
ATOM	3011	CB	LYS	211	92.366	-2.422	40.154	1.00	52.60	H	C
ATOM	3012	CG	LYS	211	93.360	-3.095	41.117	1.00	57.40	H	C
ATOM	3013	CD	LYS	211	94.338	-4.040	40.416	1.00	62.07	H	C
ATOM	3014	CE	LYS	211	95.636	-4.228	41.216	1.00	64.56	H	C
ATOM	3015	NZ	LYS	211	95.432	-4.548	42.660	1.00	65.70	H	N
ATOM	3016	C	LYS	211	91.147	-4.609	39.935	1.00	32.12	H	C
ATOM	3017	O	LYS	211	90.611	-4.525	41.036	1.00	32.03	H	O
ATOM	3018	N	VAL	212	91.357	-5.772	39.322	1.00	43.02	H	N
ATOM	3019	CA	VAL	212	90.971	-7.017	39.973	1.00	37.80	H	C
ATOM	3020	CB	VAL	212	89.728	-7.685	39.308	1.00	28.95	H	C
ATOM	3021	CG1	VAL	212	88.671	-6.639	39.021	1.00	26.33	H	C
ATOM	3022	CG2	VAL	212	90.125	-8.431	38.059	1.00	26.83	H	C
ATOM	3023	C	VAL	212	92.086	-8.042	40.020	1.00	39.84	H	C
ATOM	3024	O	VAL	212	92.832	-8.224	39.057	1.00	39.92	H	O
ATOM	3025	N	ASP	213	92.184	-8.709	41.162	1.00	52.39	H	N
ATOM	3026	CA	ASP	213	93.177	-9.743	41.376	1.00	49.02	H	C
ATOM	3027	CB	ASP	213	93.900	-9.493	42.692	1.00	46.86	H	C
ATOM	3028	CG	ASP	213	94.548	-8.128	42.740	1.00	52.80	H	C
ATOM	3029	OD1	ASP	213	95.420	-7.852	41.887	1.00	56.11	H	O
ATOM	3030	OD2	ASP	213	94.182	-7.329	43.626	1.00	57.38	H	O
ATOM	3031	C	ASP	213	92.433	-11.067	41.423	1.00	46.03	H	C
ATOM	3032	O	ASP	213	91.537	-11.248	42.236	1.00	45.16	H	O
ATOM	3033	N	LYS	214	92.796	-11.993	40.548	1.00	33.42	H	N
ATOM	3034	CA	LYS	214	92.124	-13.282	40.502	1.00	29.46	H	C
ATOM	3035	CB	LYS	214	91.732	-13.602	39.055	0.00	52.86	H	C
ATOM	3036	CG	LYS	214	90.422	-14.370	38.875	0.00	47.62	H	C
ATOM	3037	CD	LYS	214	90.398	-15.699	39.614	0.00	43.68	H	C
ATOM	3038	CE	LYS	214	89.852	-15.541	41.024	0.00	41.24	H	C
ATOM	3039	NZ	LYS	214	88.452	-15.037	41.021	0.00	39.27	H	N
ATOM	3040	C	LYS	214	93.027	-14.377	41.047	1.00	29.68	H	C
ATOM	3041	O	LYS	214	94.160	-14.549	40.585	1.00	27.06	H	O
ATOM	3042	N	LYS	215	92.533	-15.103	42.045	1.00	38.49	H	N
ATOM	3043	CA	LYS	215	93.289	-16.207	42.617	1.00	34.59	H	C
ATOM	3044	CB	LYS	215	92.788	-16.531	44.032	0.00	48.10	H	C
ATOM	3045	CG	LYS	215	92.812	-15.343	44.987	0.00	42.43	H	C
ATOM	3046	CD	LYS	215	92.403	-15.737	46.401	0.00	38.17	H	C
ATOM	3047	CE	LYS	215	93.458	-16.597	47.089	0.00	35.48	H	C
ATOM	3048	NZ	LYS	215	93.695	-17.895	46.397	0.00	33.32	H	N
ATOM	3049	C	LYS	215	93.042	-17.391	41.675	1.00	36.50	H	C
ATOM	3050	O	LYS	215	91.901	-17.770	41.413	1.00	38.63	H	O
ATOM	3051	N	VAL	216	94.113	-17.939	41.122	1.00	32.15	H	N
ATOM	3052	CA	VAL	216	93.996	-19.081	40.224	1.00	32.08	H	C
ATOM	3053	CB	VAL	216	94.801	-18.850	38.923	1.00	21.03	H	C
ATOM	3054	CG1	VAL	216	94.435	-19.912	37.880	1.00	20.14	H	C
ATOM	3055	CG2	VAL	216	94.482	-17.480	38.375	1.00	18.92	H	C
ATOM	3056	C	VAL	216	94.504	-20.334	40.948	1.00	33.21	H	C
ATOM	3057	O	VAL	216	95.696	-20.441	41.248	1.00	33.32	H	O
ATOM	3058	N	GLU	217	93.586	-21.269	41.219	1.00	45.06	H	N
ATOM	3059	CA	GLU	217	93.871	-22.508	41.949	1.00	48.19	H	C
ATOM	3060	CB	GLU	217	93.065	-22.532	43.250	1.00	91.11	H	C
ATOM	3061	CG	GLU	217	93.114	-21.248	44.065	1.00	95.99	H	C
ATOM	3062	CD	GLU	217	91.872	-21.005	44.901	1.00	101.94	H	C
ATOM	3063	OE1	GLU	217	90.757	-21.353	44.453	1.00	105.02	H	O
ATOM	3064	OE2	GLU	217	92.013	-20.475	46.029	1.00	105.37	H	O
ATOM	3065	C	GLU	217	93.426	-23.720	41.109	1.00	48.96	H	C
ATOM	3066	O	GLU	217	92.500	-23.643	40.332	1.00	51.24	H	O

Fig. 19: A-43

ATOM	3067	N	PRO	218	94.078	-24.870	41.265	1.00	42.53	H	N
ATOM	3068	CD	PRO	218	95.339	-25.074	41.993	1.00	48.02	H	C
ATOM	3069	CA	PRO	218	93.711	-26.079	40.509	1.00	40.69	H	C
ATOM	3070	CB	PRO	218	94.962	-26.924	40.609	1.00	42.70	H	C
ATOM	3071	CG	PRO	218	95.482	-26.557	41.957	1.00	44.19	H	C
ATOM	3072	C	PRO	218	92.544	-26.782	41.183	1.00	41.85	H	C
ATOM	3073	O	PRO	218	92.513	-26.844	42.403	1.00	45.36	H	O
ATOM	3074	N	LYS	219	91.638	-27.354	40.396	1.00	112.06	H	N
ATOM	3075	CA	LYS	219	90.475	-28.045	40.934	1.00	111.92	H	C
ATOM	3076	CB	LYS	219	89.635	-28.618	39.794	0.00	52.93	H	C
ATOM	3077	CG	LYS	219	89.522	-27.658	38.654	0.00	47.21	H	C
ATOM	3078	CD	LYS	219	88.205	-27.801	37.948	0.00	42.71	H	C
ATOM	3079	CE	LYS	219	88.174	-26.793	36.845	0.00	39.84	H	C
ATOM	3080	NZ	LYS	219	86.847	-26.599	36.249	0.00	37.57	H	N
ATOM	3081	C	LYS	219	90.867	-29.169	41.892	1.00	116.73	H	C
ATOM	3082	O	LYS	219	90.330	-29.223	43.021	1.00	116.18	H	O
ATOM	3083	OXT	LYS	219	91.705	-30.007	41.503	1.00	36.39	H	O
ATOM	3084	CB	ILE	2	109.298	10.543	-2.157	1.00	31.85	L	C
ATOM	3085	CG2	ILE	2	110.285	9.382	-2.130	1.00	31.85	L	C
ATOM	3086	CG1	ILE	2	109.803	11.664	-3.069	1.00	31.85	L	C
ATOM	3087	CD1	ILE	2	111.143	12.240	-2.656	1.00	31.85	L	C
ATOM	3088	C	ILE	2	107.518	8.858	-1.778	1.00	41.66	L	C
ATOM	3089	O	ILE	2	107.155	9.019	-0.613	1.00	41.66	L	O
ATOM	3090	N	ILE	2	106.898	11.133	-2.646	1.00	41.66	L	N
ATOM	3091	CA	ILE	2	107.922	10.043	-2.648	1.00	41.66	L	C
ATOM	3092	N	GLN	3	107.597	7.665	-2.361	1.00	28.81	L	N
ATOM	3093	CA	GLN	3	107.244	6.433	-1.669	1.00	28.81	L	C
ATOM	3094	CB	GLN	3	106.206	5.677	-2.484	1.00	56.92	L	C
ATOM	3095	CG	GLN	3	105.708	4.412	-1.837	1.00	56.92	L	C
ATOM	3096	CD	GLN	3	104.579	3.778	-2.622	1.00	56.92	L	C
ATOM	3097	OE1	GLN	3	104.124	2.681	-2.298	1.00	56.92	L	O
ATOM	3098	NE2	GLN	3	104.116	4.469	-3.661	1.00	56.92	L	N
ATOM	3099	C	GLN	3	108.482	5.557	-1.428	1.00	28.81	L	C
ATOM	3100	O	GLN	3	109.297	5.322	-2.327	1.00	28.81	L	O
ATOM	3101	N	LEU	4	108.615	5.088	-0.195	1.00	39.62	L	N
ATOM	3102	CA	LEU	4	109.744	4.260	0.198	1.00	39.62	L	C
ATOM	3103	CB	LEU	4	110.377	4.820	1.469	1.00	19.64	L	C
ATOM	3104	CG	LEU	4	111.546	5.792	1.348	1.00	19.64	L	C
ATOM	3105	CD1	LEU	4	111.407	6.643	0.092	1.00	19.64	L	C
ATOM	3106	CD2	LEU	4	111.614	6.640	2.617	1.00	19.64	L	C
ATOM	3107	C	LEU	4	109.323	2.823	0.445	1.00	39.62	L	C
ATOM	3108	O	LEU	4	108.470	2.548	1.289	1.00	39.62	L	O
ATOM	3109	N	THR	5	109.935	1.903	-0.289	1.00	16.92	L	N
ATOM	3110	CA	THR	5	109.634	0.485	-0.152	1.00	16.92	L	C
ATOM	3111	CB	THR	5	108.945	-0.038	-1.437	1.00	21.45	L	C
ATOM	3112	OG1	THR	5	109.307	-1.402	-1.651	1.00	21.45	L	O
ATOM	3113	CG2	THR	5	109.324	0.802	-2.641	1.00	21.45	L	C
ATOM	3114	C	THR	5	110.908	-0.312	0.186	1.00	16.92	L	C
ATOM	3115	O	THR	5	111.849	-0.382	-0.601	1.00	16.92	L	O
ATOM	3116	N	GLN	6	110.919	-0.880	1.391	1.00	17.69	L	N
ATOM	3117	CA	GLN	6	112.040	-1.661	1.933	1.00	17.69	L	C
ATOM	3118	CB	GLN	6	112.078	-1.544	3.468	1.00	15.96	L	C
ATOM	3119	CG	GLN	6	111.898	-0.138	4.014	1.00	15.96	L	C
ATOM	3120	CD	GLN	6	112.007	-0.060	5.535	1.00	15.96	L	C
ATOM	3121	OE1	GLN	6	111.626	0.944	6.139	1.00	15.96	L	O
ATOM	3122	NE2	GLN	6	112.541	-1.115	6.158	1.00	15.96	L	N
ATOM	3123	C	GLN	6	111.962	-3.143	1.588	1.00	17.69	L	C
ATOM	3124	O	GLN	6	110.882	-3.675	1.352	1.00	17.69	L	O
ATOM	3125	N	SER	7	113.107	-3.814	1.595	1.00	44.56	L	N
ATOM	3126	CA	SER	7	113.148	-5.238	1.293	1.00	44.56	L	C
ATOM	3127	CB	SER	7	113.109	-5.470	-0.214	1.00	33.18	L	C
ATOM	3128	OG	SER	7	114.194	-4.813	-0.837	1.00	33.18	L	O
ATOM	3129	C	SER	7	114.394	-5.898	1.855	1.00	44.56	L	C
ATOM	3130	O	SER	7	115.480	-5.328	1.811	1.00	44.56	L	O
ATOM	3131	N	PRO	8	114.246	-7.107	2.415	1.00	19.10	L	N
ATOM	3132	CD	PRO	8	115.292	-7.921	3.063	1.00	16.76	L	C
ATOM	3133	CA	PRO	8	112.945	-7.771	2.494	1.00	19.10	L	C
ATOM	3134	CB	PRO	8	113.303	-9.161	3.004	1.00	16.76	L	C
ATOM	3135	CG	PRO	8	114.481	-8.882	3.905	1.00	16.76	L	C
ATOM	3136	C	PRO	8	112.068	-7.023	3.479	1.00	19.10	L	C
ATOM	3137	O	PRO	8	112.517	-6.069	4.125	1.00	19.10	L	O
ATOM	3138	N	SER	9	110.822	-7.460	3.589	1.00	12.41	L	N
ATOM	3139	CA	SER	9	109.885	-6.851	4.516	1.00	12.41	L	C

Fig. 19: A-44

ATOM	3140	CB	SER	9	108.466	-7.059	4.023	1.00	25.43	L	C
ATOM	3141	OG	SER	9	108.345	-6.555	2.707	1.00	25.43	L	O
ATOM	3142	C	SER	9	110.083	-7.558	5.837	1.00	12.41	L	C
ATOM	3143	O	SER	9	109.904	-6.983	6.904	1.00	12.41	L	O
ATOM	3144	N	SER	10	110.492	-8.817	5.745	1.00	33.63	L	N
ATOM	3145	CA	SER	10	110.720	-9.645	6.910	1.00	33.63	L	C
ATOM	3146	CB	SER	10	109.490	-10.517	7.144	1.00	43.13	L	C
ATOM	3147	OG	SER	10	109.614	-11.248	8.338	1.00	43.13	L	O
ATOM	3148	C	SER	10	111.942	-10.504	6.624	1.00	33.63	L	C
ATOM	3149	O	SER	10	112.226	-10.814	5.470	1.00	33.63	L	O
ATOM	3150	N	LEU	11	112.677	-10.880	7.666	1.00	38.19	L	N
ATOM	3151	CA	LEU	11	113.867	-11.709	7.484	1.00	38.19	L	C
ATOM	3152	CB	LEU	11	115.020	-10.880	6.894	1.00	33.64	L	C
ATOM	3153	CG	LEU	11	115.721	-9.849	7.793	1.00	33.64	L	C
ATOM	3154	CD1	LEU	11	116.757	-10.532	8.667	1.00	33.64	L	C
ATOM	3155	CD2	LEU	11	116.401	-8.807	6.927	1.00	33.64	L	C
ATOM	3156	C	LEU	11	114.319	-12.335	8.792	1.00	38.19	L	C
ATOM	3157	O	LEU	11	114.365	-11.672	9.829	1.00	38.19	L	O
ATOM	3158	N	SER	12	114.661	-13.616	8.736	1.00	42.98	L	N
ATOM	3159	CA	SER	12	115.128	-14.320	9.916	1.00	42.98	L	C
ATOM	3160	CB	SER	12	114.334	-15.612	10.103	1.00	67.78	L	C
ATOM	3161	OG	SER	12	114.474	-16.092	11.426	1.00	67.78	L	O
ATOM	3162	C	SER	12	116.611	-14.628	9.738	1.00	42.98	L	C
ATOM	3163	O	SER	12	117.031	-15.118	8.697	1.00	42.98	L	O
ATOM	3164	N	ALA	13	117.407	-14.320	10.749	1.00	25.03	L	N
ATOM	3165	CA	ALA	13	118.836	-14.575	10.667	1.00	25.03	L	C
ATOM	3166	CB	ALA	13	119.556	-13.340	10.124	1.00	41.64	L	C
ATOM	3167	C	ALA	13	119.390	-14.952	12.037	1.00	25.03	L	C
ATOM	3168	O	ALA	13	118.829	-14.571	13.067	1.00	25.03	L	O
ATOM	3169	N	SER	14	120.493	-15.701	12.045	1.00	32.48	L	N
ATOM	3170	CA	SER	14	121.111	-16.132	13.294	1.00	32.48	L	C
ATOM	3171	CB	SER	14	121.594	-17.569	13.160	1.00	77.12	L	C
ATOM	3172	OG	SER	14	122.348	-17.721	11.975	1.00	77.12	L	O
ATOM	3173	C	SER	14	122.269	-15.231	13.691	1.00	32.48	L	C
ATOM	3174	O	SER	14	122.893	-14.595	12.841	1.00	32.48	L	O
ATOM	3175	N	VAL	15	122.545	-15.166	14.988	1.00	47.29	L	N
ATOM	3176	CA	VAL	15	123.637	-14.336	15.470	1.00	47.29	L	C
ATOM	3177	CB	VAL	15	123.996	-14.657	16.937	1.00	53.16	L	C
ATOM	3178	CG1	VAL	15	123.121	-13.847	17.881	1.00	53.16	L	C
ATOM	3179	CG2	VAL	15	123.808	-16.148	17.198	1.00	53.16	L	C
ATOM	3180	C	VAL	15	124.858	-14.575	14.606	1.00	47.29	L	C
ATOM	3181	O	VAL	15	125.164	-15.712	14.250	1.00	47.29	L	O
ATOM	3182	N	GLY	16	125.537	-13.495	14.247	1.00	32.44	L	N
ATOM	3183	CA	GLY	16	126.728	-13.615	13.431	1.00	32.44	L	C
ATOM	3184	C	GLY	16	126.506	-13.463	11.945	1.00	32.44	L	C
ATOM	3185	O	GLY	16	127.467	-13.306	11.191	1.00	32.44	L	O
ATOM	3186	N	ASP	17	125.255	-13.524	11.510	1.00	32.03	L	N
ATOM	3187	CA	ASP	17	124.959	-13.367	10.092	1.00	32.03	L	C
ATOM	3188	CB	ASP	17	123.533	-13.814	9.788	1.00	55.01	L	C
ATOM	3189	CG	ASP	17	123.344	-15.291	9.961	1.00	55.01	L	C
ATOM	3190	OD1	ASP	17	122.211	-15.771	9.739	1.00	55.01	L	O
ATOM	3191	OD2	ASP	17	124.331	-15.965	10.320	1.00	55.01	L	O
ATOM	3192	C	ASP	17	125.109	-11.905	9.677	1.00	32.03	L	C
ATOM	3193	O	ASP	17	125.041	-10.997	10.517	1.00	32.03	L	O
ATOM	3194	N	ARG	18	125.324	-11.680	8.385	1.00	40.86	L	N
ATOM	3195	CA	ARG	18	125.447	-10.325	7.875	1.00	40.86	L	C
ATOM	3196	CB	ARG	18	126.587	-10.231	6.865	1.00	78.37	L	C
ATOM	3197	CG	ARG	18	126.790	-8.842	6.293	1.00	78.37	L	C
ATOM	3198	CD	ARG	18	128.223	-8.662	5.812	1.00	78.37	L	C
ATOM	3199	NE	ARG	18	128.413	-7.408	5.087	1.00	78.37	L	N
ATOM	3200	CZ	ARG	18	127.841	-7.131	3.918	1.00	78.37	L	C
ATOM	3201	NH1	ARG	18	127.042	-8.021	3.336	1.00	78.37	L	N
ATOM	3202	NH2	ARG	18	128.064	-5.960	3.334	1.00	78.37	L	N
ATOM	3203	C	ARG	18	124.116	-9.986	7.220	1.00	40.86	L	C
ATOM	3204	O	ARG	18	123.690	-10.656	6.284	1.00	40.86	L	O
ATOM	3205	N	VAL	19	123.455	-8.948	7.721	1.00	26.42	L	N
ATOM	3206	CA	VAL	19	122.157	-8.549	7.193	1.00	26.42	L	C
ATOM	3207	CB	VAL	19	121.154	-8.426	8.335	1.00	32.94	L	C
ATOM	3208	CG1	VAL	19	119.768	-8.214	7.783	1.00	32.94	L	C
ATOM	3209	CG2	VAL	19	121.204	-9.678	9.194	1.00	32.94	L	C
ATOM	3210	C	VAL	19	122.200	-7.235	6.420	1.00	26.42	L	C
ATOM	3211	O	VAL	19	122.902	-6.306	6.798	1.00	26.42	L	O
ATOM	3212	N	THR	20	121.443	-7.160	5.333	1.00	42.24	L	N

Fig. 19: A-45

ATOM	3213	CA	THR	20	121.408	-5.950	4.519	1.00	42.24	L	C
ATOM	3214	CB	THR	20	122.310	-6.097	3.289	1.00	29.90	L	C
ATOM	3215	OG1	THR	20	123.680	-6.127	3.714	1.00	29.90	L	O
ATOM	3216	CG2	THR	20	122.099	-4.944	2.326	1.00	29.90	L	C
ATOM	3217	C	THR	20	120.008	-5.582	4.050	1.00	42.24	L	C
ATOM	3218	O	THR	20	119.477	-6.202	3.127	1.00	42.24	L	O
ATOM	3219	N	ILE	21	119.418	-4.568	4.683	1.00	13.95	L	N
ATOM	3220	CA	ILE	21	118.077	-4.114	4.326	1.00	13.95	L	C
ATOM	3221	CB	ILE	21	117.349	-3.486	5.541	1.00	24.11	L	C
ATOM	3222	CG2	ILE	21	115.892	-3.176	5.186	1.00	24.11	L	C
ATOM	3223	CG1	ILE	21	117.390	-4.457	6.720	1.00	24.11	L	C
ATOM	3224	CD1	ILE	21	116.709	-3.936	7.960	1.00	24.11	L	C
ATOM	3225	C	ILE	21	118.180	-3.081	3.217	1.00	13.95	L	C
ATOM	3226	O	ILE	21	119.036	-2.208	3.251	1.00	13.95	L	O
ATOM	3227	N	THR	22	117.305	-3.190	2.230	1.00	27.07	L	N
ATOM	3228	CA	THR	22	117.304	-2.266	1.107	1.00	27.07	L	C
ATOM	3229	CB	THR	22	117.335	-3.022	-0.239	1.00	29.03	L	C
ATOM	3230	OG1	THR	22	118.613	-3.642	-0.404	1.00	29.03	L	O
ATOM	3231	CG2	THR	22	117.084	-2.084	-1.391	1.00	29.03	L	C
ATOM	3232	C	THR	22	116.067	-1.385	1.123	1.00	27.07	L	C
ATOM	3233	O	THR	22	114.951	-1.871	1.313	1.00	27.07	L	O
ATOM	3234	N	CYS	23	116.281	-0.089	0.916	1.00	32.83	L	N
ATOM	3235	CA	CYS	23	115.203	0.896	0.882	1.00	32.83	L	C
ATOM	3236	C	CYS	23	115.259	1.546	-0.489	1.00	32.83	L	C
ATOM	3237	O	CYS	23	116.250	2.187	-0.837	1.00	32.83	L	O
ATOM	3238	CB	CYS	23	115.424	1.947	1.973	1.00	18.66	L	C
ATOM	3239	SG	CYS	23	114.216	3.310	2.141	1.00	18.66	L	S
ATOM	3240	N	SER	24	114.199	1.355	-1.268	1.00	11.34	L	N
ATOM	3241	CA	SER	24	114.110	1.924	-2.612	1.00	11.34	L	C
ATOM	3242	CB	SER	24	113.696	0.853	-3.614	1.00	28.67	L	C
ATOM	3243	OG	SER	24	114.642	-0.190	-3.632	1.00	28.67	L	O
ATOM	3244	C	SER	24	113.096	3.058	-2.641	1.00	11.34	L	C
ATOM	3245	O	SER	24	111.971	2.910	-2.154	1.00	11.34	L	O
ATOM	3246	N	ALA	25	113.496	4.186	-3.217	1.00	32.05	L	N
ATOM	3247	CA	ALA	25	112.617	5.343	-3.286	1.00	32.05	L	C
ATOM	3248	CB	ALA	25	113.312	6.567	-2.707	1.00	44.86	L	C
ATOM	3249	C	ALA	25	112.139	5.633	-4.699	1.00	32.05	L	C
ATOM	3250	O	ALA	25	112.918	5.619	-5.658	1.00	32.05	L	O
ATOM	3251	N	SER	26	110.839	5.901	-4.803	1.00	26.80	L	N
ATOM	3252	CA	SER	26	110.179	6.204	-6.070	1.00	26.80	L	C
ATOM	3253	CB	SER	26	108.717	6.572	-5.814	1.00	23.33	L	C
ATOM	3254	OG	SER	26	108.617	7.713	-4.984	1.00	23.33	L	O
ATOM	3255	C	SER	26	110.866	7.338	-6.813	1.00	26.80	L	C
ATOM	3256	O	SER	26	110.814	7.404	-8.032	1.00	26.80	L	O
ATOM	3257	N	SER	27	111.496	8.234	-6.066	1.00	22.71	L	N
ATOM	3258	CA	SER	27	112.210	9.363	-6.644	1.00	22.71	L	C
ATOM	3259	CB	SER	27	111.439	10.661	-6.406	1.00	47.74	L	C
ATOM	3260	OG	SER	27	110.105	10.552	-6.862	1.00	47.74	L	O
ATOM	3261	C	SER	27	113.547	9.438	-5.934	1.00	22.71	L	C
ATOM	3262	O	SER	27	113.666	8.982	-4.805	1.00	22.71	L	O
ATOM	3263	N	SER	28	114.555	10.004	-6.586	1.00	37.73	L	N
ATOM	3264	CA	SER	28	115.874	10.121	-5.972	1.00	37.73	L	C
ATOM	3265	CB	SER	28	116.890	10.583	-7.010	1.00	36.75	L	C
ATOM	3266	OG	SER	28	116.486	11.818	-7.573	1.00	36.75	L	O
ATOM	3267	C	SER	28	115.846	11.106	-4.804	1.00	37.73	L	C
ATOM	3268	O	SER	28	115.043	12.038	-4.775	1.00	37.73	L	O
ATOM	3269	N	VAL	29	116.726	10.890	-3.838	1.00	35.34	L	N
ATOM	3270	CA	VAL	29	116.807	11.753	-2.669	1.00	35.34	L	C
ATOM	3271	CB	VAL	29	116.002	11.154	-1.484	1.00	39.96	L	C
ATOM	3272	CG1	VAL	29	114.521	11.097	-1.842	1.00	39.96	L	C
ATOM	3273	CG2	VAL	29	116.506	9.755	-1.147	1.00	39.96	L	C
ATOM	3274	C	VAL	29	118.277	11.895	-2.289	1.00	35.34	L	C
ATOM	3275	O	VAL	29	119.076	11.001	-2.571	1.00	35.34	L	O
ATOM	3276	N	ASN	30	118.641	13.007	-1.658	1.00	55.44	L	N
ATOM	3277	CA	ASN	30	120.033	13.236	-1.278	1.00	55.44	L	C
ATOM	3278	CB	ASN	30	120.252	14.722	-0.974	1.00	66.75	L	C
ATOM	3279	CG	ASN	30	119.176	15.292	-0.071	1.00	66.75	L	C
ATOM	3280	OD1	ASN	30	118.006	15.359	-0.453	1.00	66.75	L	O
ATOM	3281	ND2	ASN	30	119.561	15.694	1.138	1.00	66.75	L	N
ATOM	3282	C	ASN	30	120.510	12.386	-0.095	1.00	55.44	L	C
ATOM	3283	O	ASN	30	121.705	12.099	0.033	1.00	55.44	L	O
ATOM	3284	N	HIS	31	119.586	11.985	0.770	1.00	34.66	L	N
ATOM	3285	CA	HIS	31	119.947	11.172	1.923	1.00	34.66	L	C

Fig. 19: A-46

ATOM	3286	CB	HIS	31	120.290	12.049	3.132	1.00	51.96	L	C
ATOM	3287	CG	HIS	31	121.623	12.725	3.042	1.00	51.96	L	C
ATOM	3288	CD2	HIS	31	122.763	12.534	3.744	1.00	51.96	L	C
ATOM	3289	ND1	HIS	31	121.879	13.763	2.172	1.00	51.96	L	N
ATOM	3290	CE1	HIS	31	123.118	14.186	2.345	1.00	51.96	L	C
ATOM	3291	NE2	HIS	31	123.676	13.457	3.294	1.00	51.96	L	N
ATOM	3292	C	HIS	31	118.811	10.241	2.316	1.00	34.66	L	C
ATOM	3293	O	HIS	31	117.736	10.267	1.707	1.00	34.66	L	O
ATOM	3294	N	MET	32	119.070	9.415	3.332	1.00	24.85	L	N
ATOM	3295	CA	MET	32	118.081	8.489	3.864	1.00	24.85	L	C
ATOM	3296	CB	MET	32	118.189	7.126	3.187	1.00	22.87	L	C
ATOM	3297	CG	MET	32	116.961	6.226	3.394	1.00	22.87	L	C
ATOM	3298	SD	MET	32	115.381	6.922	2.757	1.00	22.87	L	S
ATOM	3299	CE	MET	32	115.727	7.028	1.012	1.00	22.87	L	C
ATOM	3300	C	MET	32	118.316	8.340	5.360	1.00	24.85	L	C
ATOM	3301	O	MET	32	119.454	8.377	5.831	1.00	24.85	L	O
ATOM	3302	N	PHE	33	117.244	8.180	6.118	1.00	7.47	L	N
ATOM	3303	CA	PHE	33	117.391	8.029	7.554	1.00	7.47	L	C
ATOM	3304	CB	PHE	33	116.693	9.171	8.285	1.00	11.22	L	C
ATOM	3305	CG	PHE	33	117.205	10.533	7.901	1.00	11.22	L	C
ATOM	3306	CD1	PHE	33	116.901	11.078	6.652	1.00	11.22	L	C
ATOM	3307	CD2	PHE	33	118.017	11.259	8.776	1.00	11.22	L	C
ATOM	3308	CE1	PHE	33	117.399	12.325	6.275	1.00	11.22	L	C
ATOM	3309	CE2	PHE	33	118.519	12.501	8.407	1.00	11.22	L	C
ATOM	3310	CZ	PHE	33	118.207	13.035	7.149	1.00	11.22	L	C
ATOM	3311	C	PHE	33	116.817	6.702	7.994	1.00	7.47	L	C
ATOM	3312	O	PHE	33	115.959	6.150	7.320	1.00	7.47	L	O
ATOM	3313	N	TRP	34	117.301	6.186	9.118	1.00	15.67	L	N
ATOM	3314	CA	TRP	34	116.815	4.912	9.618	1.00	15.67	L	C
ATOM	3315	CB	TRP	34	117.859	3.818	9.414	1.00	16.49	L	C
ATOM	3316	CG	TRP	34	118.217	3.590	7.992	1.00	16.49	L	C
ATOM	3317	CD2	TRP	34	117.671	2.592	7.123	1.00	16.49	L	C
ATOM	3318	CE2	TRP	34	118.315	2.732	5.872	1.00	16.49	L	C
ATOM	3319	CE3	TRP	34	116.702	1.596	7.279	1.00	16.49	L	C
ATOM	3320	CD1	TRP	34	119.137	4.278	7.259	1.00	16.49	L	C
ATOM	3321	NE1	TRP	34	119.205	3.767	5.984	1.00	16.49	L	N
ATOM	3322	CZ2	TRP	34	118.024	1.914	4.782	1.00	16.49	L	C
ATOM	3323	CZ3	TRP	34	116.409	0.780	6.194	1.00	16.49	L	C
ATOM	3324	CH2	TRP	34	117.069	0.945	4.960	1.00	16.49	L	C
ATOM	3325	C	TRP	34	116.459	4.960	11.086	1.00	15.67	L	C
ATOM	3326	O	TRP	34	117.149	5.593	11.882	1.00	15.67	L	O
ATOM	3327	N	TYR	35	115.370	4.288	11.437	1.00	19.71	L	N
ATOM	3328	CA	TYR	35	114.939	4.229	12.820	1.00	19.71	L	C
ATOM	3329	CB	TYR	35	113.591	4.922	13.007	1.00	25.75	L	C
ATOM	3330	CG	TYR	35	113.623	6.381	12.621	1.00	25.75	L	C
ATOM	3331	CD1	TYR	35	113.255	6.790	11.344	1.00	25.75	L	C
ATOM	3332	CE1	TYR	35	113.310	8.124	10.980	1.00	25.75	L	C
ATOM	3333	CD2	TYR	35	114.052	7.353	13.527	1.00	25.75	L	C
ATOM	3334	CE2	TYR	35	114.110	8.685	13.173	1.00	25.75	L	C
ATOM	3335	CZ	TYR	35	113.737	9.064	11.899	1.00	25.75	L	C
ATOM	3336	OH	TYR	35	113.776	10.384	11.540	1.00	25.75	L	O
ATOM	3337	C	TYR	35	114.821	2.781	13.207	1.00	19.71	L	C
ATOM	3338	O	TYR	35	114.508	1.937	12.373	1.00	19.71	L	O
ATOM	3339	N	GLN	36	115.100	2.491	14.468	1.00	30.18	L	N
ATOM	3340	CA	GLN	36	114.987	1.136	14.964	1.00	30.18	L	C
ATOM	3341	CB	GLN	36	116.292	0.659	15.597	1.00	33.56	L	C
ATOM	3342	CG	GLN	36	116.109	-0.625	16.387	1.00	33.56	L	C
ATOM	3343	CD	GLN	36	117.154	-0.806	17.464	1.00	33.56	L	C
ATOM	3344	OE1	GLN	36	118.296	-1.161	17.179	1.00	33.56	L	O
ATOM	3345	NE2	GLN	36	116.770	-0.550	18.716	1.00	33.56	L	N
ATOM	3346	C	GLN	36	113.902	1.124	16.017	1.00	30.18	L	C
ATOM	3347	O	GLN	36	113.986	1.852	17.008	1.00	30.18	L	O
ATOM	3348	N	GLN	37	112.877	0.311	15.803	1.00	31.84	L	N
ATOM	3349	CA	GLN	37	111.811	0.209	16.778	1.00	31.84	L	C
ATOM	3350	CB	GLN	37	110.467	0.599	16.162	1.00	26.28	L	C
ATOM	3351	CG	GLN	37	109.335	0.494	17.165	1.00	26.28	L	C
ATOM	3352	CD	GLN	37	108.003	0.979	16.632	1.00	26.28	L	C
ATOM	3353	OE1	GLN	37	107.573	0.597	15.537	1.00	26.28	L	O
ATOM	3354	NE2	GLN	37	107.328	1.819	17.417	1.00	26.28	L	N
ATOM	3355	C	GLN	37	111.729	-1.201	17.360	1.00	31.84	L	C
ATOM	3356	O	GLN	37	111.571	-2.189	16.637	1.00	31.84	L	O
ATOM	3357	N	LYS	38	111.861	-1.285	18.676	1.00	33.78	L	N
ATOM	3358	CA	LYS	38	111.776	-2.561	19.366	1.00	33.78	L	C

Fig. 19: A-47

ATOM	3359	CB	LYS	38	112.784	-2.618	20.519	1.00	38.31	L	C
ATOM	3360	CG	LYS	38	114.209	-2.306	20.094	1.00	38.31	L	C
ATOM	3361	CD	LYS	38	115.224	-2.552	21.207	1.00	38.31	L	C
ATOM	3362	CE	LYS	38	115.494	-4.034	21.402	1.00	38.31	L	C
ATOM	3363	NZ	LYS	38	115.954	-4.720	20.154	1.00	38.31	L	N
ATOM	3364	C	LYS	38	110.346	-2.671	19.889	1.00	33.78	L	C
ATOM	3365	O	LYS	38	109.770	-1.690	20.354	1.00	33.78	L	O
ATOM	3366	N	PRO	39	109.757	-3.873	19.818	1.00	36.51	L	N
ATOM	3367	CD	PRO	39	110.419	-5.128	19.422	1.00	56.09	L	C
ATOM	3368	CA	PRO	39	108.389	-4.139	20.271	1.00	36.51	L	C
ATOM	3369	CB	PRO	39	108.376	-5.652	20.409	1.00	56.09	L	C
ATOM	3370	CG	PRO	39	109.254	-6.072	19.283	1.00	56.09	L	C
ATOM	3371	C	PRO	39	107.976	-3.434	21.559	1.00	36.51	L	C
ATOM	3372	O	PRO	39	108.664	-3.523	22.573	1.00	36.51	L	O
ATOM	3373	N	GLY	40	106.846	-2.735	21.503	1.00	29.94	L	N
ATOM	3374	CA	GLY	40	106.330	-2.036	22.667	1.00	29.94	L	C
ATOM	3375	C	GLY	40	107.025	-0.738	23.034	1.00	29.94	L	C
ATOM	3376	O	GLY	40	106.669	-0.119	24.037	1.00	29.94	L	O
ATOM	3377	N	LYS	41	108.019	-0.332	22.243	1.00	32.57	L	N
ATOM	3378	CA	LYS	41	108.754	0.903	22.503	1.00	32.57	L	C
ATOM	3379	CB	LYS	41	110.231	0.611	22.804	1.00	82.45	L	C
ATOM	3380	CG	LYS	41	110.466	-0.251	24.040	1.00	82.45	L	C
ATOM	3381	CD	LYS	41	111.905	-0.157	24.579	1.00	82.45	L	C
ATOM	3382	CE	LYS	41	112.977	-0.603	23.575	1.00	82.45	L	C
ATOM	3383	NZ	LYS	41	113.257	0.396	22.496	1.00	82.45	L	N
ATOM	3384	C	LYS	41	108.656	1.860	21.319	1.00	32.57	L	C
ATOM	3385	O	LYS	41	108.243	1.480	20.227	1.00	32.57	L	O
ATOM	3386	N	ALA	42	109.029	3.112	21.547	1.00	30.66	L	N
ATOM	3387	CA	ALA	42	108.990	4.126	20.502	1.00	30.66	L	C
ATOM	3388	CB	ALA	42	108.980	5.513	21.129	1.00	32.87	L	C
ATOM	3389	C	ALA	42	110.209	3.973	19.606	1.00	30.66	L	C
ATOM	3390	O	ALA	42	111.235	3.436	20.028	1.00	30.66	L	O
ATOM	3391	N	PRO	43	110.112	4.435	18.351	1.00	23.79	L	N
ATOM	3392	CD	PRO	43	108.939	4.976	17.647	1.00	7.10	L	C
ATOM	3393	CA	PRO	43	111.248	4.323	17.440	1.00	23.79	L	C
ATOM	3394	CB	PRO	43	110.727	4.980	16.170	1.00	7.10	L	C
ATOM	3395	CG	PRO	43	109.275	4.677	16.212	1.00	7.10	L	C
ATOM	3396	C	PRO	43	112.476	5.042	18.007	1.00	23.79	L	C
ATOM	3397	O	PRO	43	112.359	5.903	18.877	1.00	23.79	L	O
ATOM	3398	N	LYS	44	113.652	4.678	17.514	1.00	26.42	L	N
ATOM	3399	CA	LYS	44	114.888	5.283	17.972	1.00	26.42	L	C
ATOM	3400	CB	LYS	44	115.656	4.289	18.843	1.00	45.11	L	C
ATOM	3401	CG	LYS	44	115.840	4.724	20.288	1.00	45.11	L	C
ATOM	3402	CD	LYS	44	116.535	3.651	21.131	1.00	45.11	L	C
ATOM	3403	CE	LYS	44	115.656	2.400	21.338	1.00	45.11	L	C
ATOM	3404	NZ	LYS	44	115.359	1.613	20.087	1.00	45.11	L	N
ATOM	3405	C	LYS	44	115.741	5.673	16.767	1.00	26.42	L	C
ATOM	3406	O	LYS	44	115.898	4.888	15.829	1.00	26.42	L	O
ATOM	3407	N	PRO	45	116.287	6.902	16.764	1.00	19.50	L	N
ATOM	3408	CD	PRO	45	116.146	7.943	17.794	1.00	7.61	L	C
ATOM	3409	CA	PRO	45	117.132	7.362	15.649	1.00	19.50	L	C
ATOM	3410	CB	PRO	45	117.638	8.720	16.120	1.00	7.61	L	C
ATOM	3411	CG	PRO	45	116.547	9.180	17.041	1.00	7.61	L	C
ATOM	3412	C	PRO	45	118.273	6.367	15.542	1.00	19.50	L	C
ATOM	3413	O	PRO	45	118.925	6.082	16.549	1.00	19.50	L	O
ATOM	3414	N	TRP	46	118.521	5.848	14.342	1.00	23.41	L	N
ATOM	3415	CA	TRP	46	119.581	4.861	14.158	1.00	23.41	L	C
ATOM	3416	CB	TRP	46	118.980	3.559	13.643	1.00	20.77	L	C
ATOM	3417	CG	TRP	46	119.662	2.382	14.178	1.00	20.77	L	C
ATOM	3418	CD2	TRP	46	119.738	2.007	15.554	1.00	20.77	L	C
ATOM	3419	CE2	TRP	46	120.509	0.829	15.624	1.00	20.77	L	C
ATOM	3420	CE3	TRP	46	119.229	2.554	16.737	1.00	20.77	L	C
ATOM	3421	CD1	TRP	46	120.365	1.446	13.481	1.00	20.77	L	C
ATOM	3422	NE1	TRP	46	120.879	0.504	14.345	1.00	20.77	L	N
ATOM	3423	CZ2	TRP	46	120.786	0.191	16.834	1.00	20.77	L	C
ATOM	3424	CZ3	TRP	46	119.505	1.918	17.938	1.00	20.77	L	C
ATOM	3425	CH2	TRP	46	120.276	0.750	17.977	1.00	20.77	L	C
ATOM	3426	C	TRP	46	120.691	5.302	13.209	1.00	23.41	L	C
ATOM	3427	O	TRP	46	121.871	5.174	13.507	1.00	23.41	L	O
ATOM	3428	N	ILE	47	120.306	5.806	12.048	1.00	21.62	L	N
ATOM	3429	CA	ILE	47	121.275	6.248	11.073	1.00	21.62	L	C
ATOM	3430	CB	ILE	47	121.515	5.160	10.008	1.00	12.16	L	C
ATOM	3431	CG2	ILE	47	122.473	5.668	8.929	1.00	12.16	L	C

Fig. 19: A-48

ATOM	3432	CG1	ILE	47	122.067	3.902	10.670	1.00	12.16	L	C
ATOM	3433	CD1	ILE	47	122.301	2.746	9.686	1.00	12.16	L	C
ATOM	3434	C	ILE	47	120.694	7.482	10.408	1.00	21.62	L	C
ATOM	3435	O	ILE	47	119.600	7.424	9.840	1.00	21.62	L	O
ATOM	3436	N	TYR	48	121.408	8.603	10.510	1.00	27.63	L	N
ATOM	3437	CA	TYR	48	120.961	9.842	9.887	1.00	27.63	L	C
ATOM	3438	CB	TYR	48	120.899	10.992	10.892	1.00	47.89	L	C
ATOM	3439	CG	TYR	48	122.206	11.318	11.564	1.00	47.89	L	C
ATOM	3440	CD1	TYR	48	122.762	10.454	12.502	1.00	47.89	L	C
ATOM	3441	CE1	TYR	48	123.961	10.766	13.143	1.00	47.89	L	C
ATOM	3442	CD2	TYR	48	122.881	12.503	11.277	1.00	47.89	L	C
ATOM	3443	CE2	TYR	48	124.078	12.827	11.907	1.00	47.89	L	C
ATOM	3444	CZ	TYR	48	124.617	11.957	12.843	1.00	47.89	L	C
ATOM	3445	OH	TYR	48	125.803	12.269	13.483	1.00	47.89	L	O
ATOM	3446	C	TYR	48	121.922	10.181	8.766	1.00	27.63	L	C
ATOM	3447	O	TYR	48	122.992	9.575	8.646	1.00	27.63	L	O
ATOM	3448	N	LEU	49	121.535	11.150	7.948	1.00	28.95	L	N
ATOM	3449	CA	LEU	49	122.344	11.550	6.811	1.00	28.95	L	C
ATOM	3450	CB	LEU	49	123.421	12.568	7.232	1.00	11.18	L	C
ATOM	3451	CG	LEU	49	123.051	14.040	7.473	1.00	11.18	L	C
ATOM	3452	CD1	LEU	49	122.174	14.552	6.344	1.00	11.18	L	C
ATOM	3453	CD2	LEU	49	122.333	14.178	8.780	1.00	11.18	L	C
ATOM	3454	C	LEU	49	122.997	10.350	6.117	1.00	28.95	L	C
ATOM	3455	O	LEU	49	124.204	10.323	5.920	1.00	28.95	L	O
ATOM	3456	N	THR	50	122.192	9.351	5.777	1.00	29.56	L	N
ATOM	3457	CA	THR	50	122.666	8.165	5.072	1.00	29.56	L	C
ATOM	3458	CB	THR	50	123.352	8.566	3.770	1.00	23.05	L	C
ATOM	3459	OG1	THR	50	122.490	9.434	3.040	1.00	23.05	L	O
ATOM	3460	CG2	THR	50	123.647	7.335	2.923	1.00	23.05	L	C
ATOM	3461	C	THR	50	123.582	7.152	5.767	1.00	29.56	L	C
ATOM	3462	O	THR	50	123.229	5.976	5.888	1.00	29.56	L	O
ATOM	3463	N	SER	51	124.757	7.586	6.203	1.00	25.90	L	N
ATOM	3464	CA	SER	51	125.697	6.670	6.839	1.00	25.90	L	C
ATOM	3465	CB	SER	51	126.976	6.594	6.003	1.00	41.07	L	C
ATOM	3466	OG	SER	51	127.467	7.893	5.715	1.00	41.07	L	O
ATOM	3467	C	SER	51	126.049	6.998	8.287	1.00	25.90	L	C
ATOM	3468	O	SER	51	126.578	6.160	9.015	1.00	25.90	L	O
ATOM	3469	N	ASN	52	125.749	8.211	8.712	1.00	36.32	L	N
ATOM	3470	CA	ASN	52	126.050	8.615	10.075	1.00	36.32	L	C
ATOM	3471	CB	ASN	52	125.741	10.092	10.247	1.00	35.00	L	C
ATOM	3472	CG	ASN	52	126.708	10.954	9.499	1.00	35.00	L	C
ATOM	3473	OD1	ASN	52	127.881	11.022	9.857	1.00	35.00	L	O
ATOM	3474	ND2	ASN	52	126.236	11.608	8.439	1.00	35.00	L	N
ATOM	3475	C	ASN	52	125.288	7.815	11.109	1.00	36.32	L	C
ATOM	3476	O	ASN	52	124.059	7.766	11.078	1.00	36.32	L	O
ATOM	3477	N	LEU	53	126.018	7.190	12.027	1.00	27.25	L	N
ATOM	3478	CA	LEU	53	125.387	6.408	13.080	1.00	27.25	L	C
ATOM	3479	CB	LEU	53	126.355	5.366	13.631	1.00	36.82	L	C
ATOM	3480	CG	LEU	53	126.949	4.324	12.682	1.00	36.82	L	C
ATOM	3481	CD1	LEU	53	127.640	3.266	13.531	1.00	36.82	L	C
ATOM	3482	CD2	LEU	53	125.876	3.674	11.822	1.00	36.82	L	C
ATOM	3483	C	LEU	53	124.938	7.312	14.219	1.00	27.25	L	C
ATOM	3484	O	LEU	53	125.643	8.241	14.581	1.00	27.25	L	O
ATOM	3485	N	ALA	54	123.763	7.043	14.779	1.00	46.43	L	N
ATOM	3486	CA	ALA	54	123.251	7.827	15.897	1.00	46.43	L	C
ATOM	3487	CB	ALA	54	121.938	7.272	16.373	1.00	9.56	L	C
ATOM	3488	C	ALA	54	124.267	7.728	17.008	1.00	46.43	L	C
ATOM	3489	O	ALA	54	125.380	7.254	16.794	1.00	46.43	L	O
ATOM	3490	N	SER	55	123.891	8.140	18.208	1.00	82.41	L	N
ATOM	3491	CA	SER	55	124.847	8.081	19.290	1.00	82.41	L	C
ATOM	3492	CB	SER	55	124.439	9.036	20.406	1.00	85.12	L	C
ATOM	3493	OG	SER	55	125.561	9.342	21.215	1.00	85.12	L	O
ATOM	3494	C	SER	55	125.049	6.675	19.850	1.00	82.41	L	C
ATOM	3495	O	SER	55	126.187	6.226	20.004	1.00	82.41	L	O
ATOM	3496	N	GLY	56	123.957	5.970	20.137	1.00	57.94	L	N
ATOM	3497	CA	GLY	56	124.074	4.632	20.701	1.00	57.94	L	C
ATOM	3498	C	GLY	56	124.408	3.486	19.758	1.00	57.94	L	C
ATOM	3499	O	GLY	56	125.101	2.545	20.136	1.00	57.94	L	O
ATOM	3500	N	VAL	57	123.914	3.562	18.530	1.00	69.56	L	N
ATOM	3501	CA	VAL	57	124.131	2.519	17.530	1.00	69.56	L	C
ATOM	3502	CB	VAL	57	123.809	3.053	16.108	1.00	49.85	L	C
ATOM	3503	CG1	VAL	57	123.682	1.898	15.128	1.00	49.85	L	C
ATOM	3504	CG2	VAL	57	122.529	3.875	16.139	1.00	49.85	L	C

Fig. 19: A-49

ATOM	3505	C	VAL	57	125.544	1.929	17.513	1.00	69.56	L	C
ATOM	3506	O	VAL	57	126.515	2.637	17.244	1.00	69.56	L	O
ATOM	3507	N	PRO	58	125.674	0.618	17.799	1.00	24.22	L	N
ATOM	3508	CD	PRO	58	124.609	-0.342	18.141	1.00	44.23	L	C
ATOM	3509	CA	PRO	58	126.978	-0.046	17.802	1.00	24.22	L	C
ATOM	3510	CB	PRO	58	126.638	-1.472	18.237	1.00	44.23	L	C
ATOM	3511	CG	PRO	58	125.244	-1.653	17.772	1.00	44.23	L	C
ATOM	3512	C	PRO	58	127.609	0.017	16.415	1.00	24.22	L	C
ATOM	3513	O	PRO	58	126.903	-0.083	15.400	1.00	24.22	L	O
ATOM	3514	N	SER	59	128.935	0.174	16.381	1.00	54.17	L	N
ATOM	3515	CA	SER	59	129.691	0.295	15.134	1.00	54.17	L	C
ATOM	3516	CB	SER	59	131.184	0.489	15.438	1.00	118.98	L	C
ATOM	3517	OG	SER	59	131.729	-0.615	16.139	1.00	118.98	L	O
ATOM	3518	C	SER	59	129.528	-0.815	14.096	1.00	54.17	L	C
ATOM	3519	O	SER	59	130.015	-0.672	12.970	1.00	54.17	L	O
ATOM	3520	N	ARG	60	128.861	-1.914	14.449	1.00	62.94	L	N
ATOM	3521	CA	ARG	60	128.659	-2.983	13.473	1.00	62.94	L	C
ATOM	3522	CB	ARG	60	128.247	-4.291	14.159	1.00	67.90	L	C
ATOM	3523	CG	ARG	60	127.110	-4.165	15.136	1.00	67.90	L	C
ATOM	3524	CD	ARG	60	126.572	-5.533	15.506	1.00	67.90	L	C
ATOM	3525	NE	ARG	60	125.638	-5.453	16.621	1.00	67.90	L	N
ATOM	3526	CZ	ARG	60	125.978	-5.050	17.840	1.00	67.90	L	C
ATOM	3527	NH1	ARG	60	127.230	-4.696	18.093	1.00	67.90	L	N
ATOM	3528	NH2	ARG	60	125.070	-5.002	18.807	1.00	67.90	L	N
ATOM	3529	C	ARG	60	127.596	-2.555	12.459	1.00	62.94	L	C
ATOM	3530	O	ARG	60	127.471	-3.146	11.382	1.00	62.94	L	O
ATOM	3531	N	PHE	61	126.839	-1.517	12.814	1.00	65.80	L	N
ATOM	3532	CA	PHE	61	125.799	-0.979	11.943	1.00	65.80	L	C
ATOM	3533	CB	PHE	61	124.718	-0.270	12.752	1.00	20.54	L	C
ATOM	3534	CG	PHE	61	123.650	-1.177	13.278	1.00	20.54	L	C
ATOM	3535	CD1	PHE	61	123.613	-1.519	14.628	1.00	20.54	L	C
ATOM	3536	CD2	PHE	61	122.656	-1.662	12.428	1.00	20.54	L	C
ATOM	3537	CE1	PHE	61	122.593	-2.330	15.133	1.00	20.54	L	C
ATOM	3538	CE2	PHE	61	121.627	-2.476	12.914	1.00	20.54	L	C
ATOM	3539	CZ	PHE	61	121.594	-2.809	14.270	1.00	20.54	L	C
ATOM	3540	C	PHE	61	126.389	0.019	10.964	1.00	65.80	L	C
ATOM	3541	O	PHE	61	127.300	0.773	11.300	1.00	65.80	L	O
ATOM	3542	N	SER	62	125.851	0.030	9.754	1.00	31.43	L	N
ATOM	3543	CA	SER	62	126.317	0.941	8.722	1.00	31.43	L	C
ATOM	3544	CB	SER	62	127.530	0.355	8.001	1.00	48.53	L	C
ATOM	3545	OG	SER	62	127.212	-0.890	7.412	1.00	48.53	L	O
ATOM	3546	C	SER	62	125.211	1.216	7.714	1.00	31.43	L	C
ATOM	3547	O	SER	62	124.402	0.340	7.395	1.00	31.43	L	O
ATOM	3548	N	GLY	63	125.177	2.443	7.216	1.00	26.27	L	N
ATOM	3549	CA	GLY	63	124.168	2.802	6.244	1.00	26.27	L	C
ATOM	3550	C	GLY	63	124.870	3.245	4.988	1.00	26.27	L	C
ATOM	3551	O	GLY	63	126.032	3.634	5.044	1.00	26.27	L	O
ATOM	3552	N	SER	64	124.177	3.201	3.860	1.00	35.51	L	N
ATOM	3553	CA	SER	64	124.789	3.605	2.610	1.00	35.51	L	C
ATOM	3554	CB	SER	64	125.824	2.565	2.193	1.00	33.46	L	C
ATOM	3555	OG	SER	64	126.422	2.920	0.964	1.00	33.46	L	O
ATOM	3556	C	SER	64	123.772	3.783	1.495	1.00	35.51	L	C
ATOM	3557	O	SER	64	122.614	3.371	1.622	1.00	35.51	L	O
ATOM	3558	N	GLY	65	124.209	4.401	0.401	1.00	29.14	L	N
ATOM	3559	CA	GLY	65	123.318	4.594	-0.727	1.00	29.14	L	C
ATOM	3560	C	GLY	65	123.334	5.963	-1.370	1.00	29.14	L	C
ATOM	3561	O	GLY	65	124.127	6.837	-1.024	1.00	29.14	L	O
ATOM	3562	N	SER	66	122.439	6.137	-2.329	1.00	15.93	L	N
ATOM	3563	CA	SER	66	122.305	7.389	-3.052	1.00	15.93	L	C
ATOM	3564	CB	SER	66	123.623	7.750	-3.741	1.00	32.28	L	C
ATOM	3565	OG	SER	66	124.127	6.657	-4.482	1.00	32.28	L	O
ATOM	3566	C	SER	66	121.171	7.264	-4.076	1.00	15.93	L	C
ATOM	3567	O	SER	66	120.609	6.184	-4.284	1.00	15.93	L	O
ATOM	3568	N	GLY	67	120.812	8.378	-4.690	1.00	33.97	L	N
ATOM	3569	CA	GLY	67	119.751	8.349	-5.673	1.00	33.97	L	C
ATOM	3570	C	GLY	67	118.469	7.706	-5.194	1.00	33.97	L	C
ATOM	3571	O	GLY	67	117.757	8.262	-4.361	1.00	33.97	L	O
ATOM	3572	N	THR	68	118.182	6.521	-5.715	1.00	25.46	L	N
ATOM	3573	CA	THR	68	116.954	5.828	-5.366	1.00	25.46	L	C
ATOM	3574	CB	THR	68	116.176	5.455	-6.633	1.00	47.05	L	C
ATOM	3575	OG1	THR	68	117.003	4.636	-7.471	1.00	47.05	L	O
ATOM	3576	CG2	THR	68	115.772	6.704	-7.395	1.00	47.05	L	C
ATOM	3577	C	THR	68	117.132	4.559	-4.539	1.00	25.46	L	C

Fig. 19: A-50

ATOM	3578	O	THR	68	116.144	3.963	-4.103	1.00	25.46	L	O
ATOM	3579	N	ASP	69	118.374	4.134	-4.327	1.00	17.04	L	N
ATOM	3580	CA	ASP	69	118.614	2.921	-3.554	1.00	17.04	L	C
ATOM	3581	CB	ASP	69	119.156	1.812	-4.463	1.00	63.22	L	C
ATOM	3582	CG	ASP	69	118.129	1.354	-5.490	1.00	63.22	L	C
ATOM	3583	OD1	ASP	69	117.087	0.791	-5.083	1.00	63.22	L	O
ATOM	3584	OD2	ASP	69	118.356	1.565	-6.703	1.00	63.22	L	O
ATOM	3585	C	ASP	69	119.544	3.146	-2.372	1.00	17.04	L	C
ATOM	3586	O	ASP	69	120.684	3.567	-2.535	1.00	17.04	L	O
ATOM	3587	N	TYR	70	119.030	2.866	-1.177	1.00	19.76	L	N
ATOM	3588	CA	TYR	70	119.778	3.037	0.061	1.00	19.76	L	C
ATOM	3589	CB	TYR	70	119.130	4.151	0.895	1.00	24.73	L	C
ATOM	3590	CG	TYR	70	119.424	5.544	0.369	1.00	24.73	L	C
ATOM	3591	CD1	TYR	70	120.547	6.255	0.809	1.00	24.73	L	C
ATOM	3592	CE1	TYR	70	120.865	7.511	0.281	1.00	24.73	L	C
ATOM	3593	CD2	TYR	70	118.620	6.129	-0.616	1.00	24.73	L	C
ATOM	3594	CE2	TYR	70	118.931	7.384	-1.153	1.00	24.73	L	C
ATOM	3595	CZ	TYR	70	120.053	8.062	-0.700	1.00	24.73	L	C
ATOM	3596	OH	TYR	70	120.371	9.275	-1.247	1.00	24.73	L	O
ATOM	3597	C	TYR	70	119.812	1.727	0.840	1.00	19.76	L	C
ATOM	3598	O	TYR	70	118.997	0.828	0.599	1.00	19.76	L	O
ATOM	3599	N	THR	71	120.751	1.603	1.772	1.00	26.87	L	N
ATOM	3600	CA	THR	71	120.837	0.366	2.535	1.00	26.87	L	C
ATOM	3601	CB	THR	71	121.754	-0.661	1.828	1.00	34.85	L	C
ATOM	3602	OG1	THR	71	123.107	-0.192	1.860	1.00	34.85	L	O
ATOM	3603	CG2	THR	71	121.329	-0.863	0.376	1.00	34.85	L	C
ATOM	3604	C	THR	71	121.333	0.483	3.977	1.00	26.87	L	C
ATOM	3605	O	THR	71	122.160	1.335	4.306	1.00	26.87	L	O
ATOM	3606	N	LEU	72	120.800	-0.385	4.829	1.00	24.40	L	N
ATOM	3607	CA	LEU	72	121.204	-0.467	6.222	1.00	24.40	L	C
ATOM	3608	CB	LEU	72	119.987	-0.412	7.150	1.00	25.91	L	C
ATOM	3609	CG	LEU	72	120.183	-0.827	8.614	1.00	25.91	L	C
ATOM	3610	CD1	LEU	72	121.539	-0.387	9.105	1.00	25.91	L	C
ATOM	3611	CD2	LEU	72	119.097	-0.207	9.470	1.00	25.91	L	C
ATOM	3612	C	LEU	72	121.875	-1.837	6.296	1.00	24.40	L	C
ATOM	3613	O	LEU	72	121.386	-2.803	5.707	1.00	24.40	L	O
ATOM	3614	N	THR	73	123.000	-1.930	6.990	1.00	38.15	L	N
ATOM	3615	CA	THR	73	123.695	-3.204	7.066	1.00	38.15	L	C
ATOM	3616	CB	THR	73	124.907	-3.217	6.110	1.00	35.63	L	C
ATOM	3617	OG1	THR	73	124.556	-2.566	4.885	1.00	35.63	L	O
ATOM	3618	CG2	THR	73	125.328	-4.649	5.797	1.00	35.63	L	C
ATOM	3619	C	THR	73	124.189	-3.542	8.467	1.00	38.15	L	C
ATOM	3620	O	THR	73	124.719	-2.690	9.177	1.00	38.15	L	O
ATOM	3621	N	ILE	74	123.997	-4.791	8.866	1.00	31.55	L	N
ATOM	3622	CA	ILE	74	124.467	-5.246	10.158	1.00	31.55	L	C
ATOM	3623	CB	ILE	74	123.342	-5.884	10.988	1.00	39.02	L	C
ATOM	3624	CG2	ILE	74	123.734	-5.878	12.461	1.00	39.02	L	C
ATOM	3625	CG1	ILE	74	122.041	-5.099	10.821	1.00	39.02	L	C
ATOM	3626	CD1	ILE	74	120.870	-5.663	11.635	1.00	39.02	L	C
ATOM	3627	C	ILE	74	125.504	-6.313	9.814	1.00	31.55	L	C
ATOM	3628	O	ILE	74	125.146	-7.434	9.440	1.00	31.55	L	O
ATOM	3629	N	SER	75	126.782	-5.951	9.921	1.00	48.74	L	N
ATOM	3630	CA	SER	75	127.888	-6.857	9.605	1.00	48.74	L	C
ATOM	3631	CB	SER	75	129.209	-6.106	9.727	1.00	44.70	L	C
ATOM	3632	OG	SER	75	129.306	-5.485	10.994	1.00	44.70	L	O
ATOM	3633	C	SER	75	127.940	-8.129	10.456	1.00	48.74	L	C
ATOM	3634	O	SER	75	128.346	-9.184	9.970	1.00	48.74	L	O
ATOM	3635	N	SER	76	127.544	-8.021	11.722	1.00	53.77	L	N
ATOM	3636	CA	SER	76	127.530	-9.165	12.635	1.00	53.77	L	C
ATOM	3637	CB	SER	76	128.773	-9.166	13.521	1.00	79.21	L	C
ATOM	3638	OG	SER	76	128.707	-10.224	14.463	1.00	79.21	L	O
ATOM	3639	C	SER	76	126.288	-9.102	13.515	1.00	53.77	L	C
ATOM	3640	O	SER	76	126.306	-8.533	14.604	1.00	53.77	L	O
ATOM	3641	N	LEU	77	125.211	-9.704	13.036	1.00	35.38	L	N
ATOM	3642	CA	LEU	77	123.946	-9.691	13.756	1.00	35.38	L	C
ATOM	3643	CB	LEU	77	122.955	-10.639	13.085	1.00	37.68	L	C
ATOM	3644	CG	LEU	77	121.514	-10.154	12.995	1.00	37.68	L	C
ATOM	3645	CD1	LEU	77	120.623	-11.329	12.638	1.00	37.68	L	C
ATOM	3646	CD2	LEU	77	121.080	-9.548	14.317	1.00	37.68	L	C
ATOM	3647	C	LEU	77	124.096	-10.080	15.215	1.00	35.38	L	C
ATOM	3648	O	LEU	77	124.714	-11.086	15.531	1.00	35.38	L	O
ATOM	3649	N	GLN	78	123.527	-9.279	16.105	1.00	50.91	L	N
ATOM	3650	CA	GLN	78	123.589	-9.577	17.527	1.00	50.91	L	C

Fig. 19: A-51

ATOM	3651	CB	GLN	78	124.201	-8.408	18.290	1.00	82.93	L	C
ATOM	3652	CG	GLN	78	125.653	-8.159	17.938	1.00	82.93	L	C
ATOM	3653	CD	GLN	78	126.525	-9.385	18.135	1.00	82.93	L	C
ATOM	3654	OE1	GLN	78	126.509	-10.007	19.200	1.00	82.93	L	O
ATOM	3655	NE2	GLN	78	127.299	-9.736	17.109	1.00	82.93	L	N
ATOM	3656	C	GLN	78	122.192	-9.880	18.062	1.00	50.91	L	C
ATOM	3657	O	GLN	78	121.197	-9.411	17.519	1.00	50.91	L	O
ATOM	3658	N	PRO	79	122.104	-10.680	19.135	1.00	74.65	L	N
ATOM	3659	CD	PRO	79	123.228	-11.171	19.952	1.00	43.98	L	C
ATOM	3660	CA	PRO	79	120.821	-11.049	19.743	1.00	74.65	L	C
ATOM	3661	CB	PRO	79	121.243	-11.963	20.887	1.00	43.98	L	C
ATOM	3662	CG	PRO	79	122.577	-11.373	21.284	1.00	43.98	L	C
ATOM	3663	C	PRO	79	120.033	-9.830	20.224	1.00	74.65	L	C
ATOM	3664	O	PRO	79	118.855	-9.922	20.577	1.00	74.65	L	O
ATOM	3665	N	GLU	80	120.697	-8.685	20.221	1.00	42.25	L	N
ATOM	3666	CA	GLU	80	120.080	-7.451	20.659	1.00	42.25	L	C
ATOM	3667	CB	GLU	80	121.085	-6.697	21.527	1.00	40.93	L	C
ATOM	3668	CG	GLU	80	122.485	-6.700	20.958	1.00	40.93	L	C
ATOM	3669	CD	GLU	80	123.424	-5.786	21.726	1.00	40.93	L	C
ATOM	3670	OE1	GLU	80	123.013	-4.648	22.033	1.00	40.93	L	O
ATOM	3671	OE2	GLU	80	124.572	-6.197	22.009	1.00	40.93	L	O
ATOM	3672	C	GLU	80	119.602	-6.575	19.489	1.00	42.25	L	C
ATOM	3673	O	GLU	80	118.723	-5.726	19.656	1.00	42.25	L	O
ATOM	3674	N	ASP	81	120.189	-6.787	18.312	1.00	42.48	L	N
ATOM	3675	CA	ASP	81	119.835	-6.037	17.108	1.00	42.48	L	C
ATOM	3676	CB	ASP	81	120.867	-6.254	16.005	1.00	43.12	L	C
ATOM	3677	CG	ASP	81	122.262	-5.914	16.441	1.00	43.12	L	C
ATOM	3678	OD1	ASP	81	122.422	-5.003	17.281	1.00	43.12	L	O
ATOM	3679	OD2	ASP	81	123.205	-6.549	15.924	1.00	43.12	L	O
ATOM	3680	C	ASP	81	118.495	-6.488	16.564	1.00	42.48	L	C
ATOM	3681	O	ASP	81	118.086	-6.063	15.488	1.00	42.48	L	O
ATOM	3682	N	PHE	82	117.810	-7.351	17.299	1.00	48.53	L	N
ATOM	3683	CA	PHE	82	116.544	-7.856	16.822	1.00	48.53	L	C
ATOM	3684	CB	PHE	82	116.337	-9.265	17.368	1.00	189.91	L	C
ATOM	3685	CG	PHE	82	117.320	-10.260	16.810	1.00	189.91	L	C
ATOM	3686	CD1	PHE	82	117.227	-10.676	15.485	1.00	189.91	L	C
ATOM	3687	CD2	PHE	82	118.369	-10.741	17.587	1.00	189.91	L	C
ATOM	3688	CE1	PHE	82	118.164	-11.554	14.940	1.00	189.91	L	C
ATOM	3689	CE2	PHE	82	119.311	-11.622	17.048	1.00	189.91	L	C
ATOM	3690	CZ	PHE	82	119.207	-12.027	15.725	1.00	189.91	L	C
ATOM	3691	C	PHE	82	115.359	-6.953	17.094	1.00	48.53	L	C
ATOM	3692	O	PHE	82	114.857	-6.863	18.216	1.00	48.53	L	O
ATOM	3693	N	ALA	83	114.939	-6.271	16.032	1.00	31.52	L	N
ATOM	3694	CA	ALA	83	113.813	-5.350	16.052	1.00	31.52	L	C
ATOM	3695	CB	ALA	83	114.217	-4.051	16.723	1.00	63.37	L	C
ATOM	3696	C	ALA	83	113.398	-5.090	14.605	1.00	31.52	L	C
ATOM	3697	O	ALA	83	113.816	-5.808	13.693	1.00	31.52	L	O
ATOM	3698	N	THR	84	112.565	-4.075	14.395	1.00	28.09	L	N
ATOM	3699	CA	THR	84	112.124	-3.733	13.045	1.00	28.09	L	C
ATOM	3700	CB	THR	84	110.572	-3.799	12.928	1.00	15.50	L	C
ATOM	3701	OG1	THR	84	110.127	-3.002	11.822	1.00	15.50	L	O
ATOM	3702	CG2	THR	84	109.922	-3.332	14.207	1.00	15.50	L	C
ATOM	3703	C	THR	84	112.664	-2.346	12.659	1.00	28.09	L	C
ATOM	3704	O	THR	84	112.505	-1.373	13.400	1.00	28.09	L	O
ATOM	3705	N	TYR	85	113.316	-2.282	11.496	1.00	21.31	L	N
ATOM	3706	CA	TYR	85	113.935	-1.055	11.000	1.00	21.31	L	C
ATOM	3707	CB	TYR	85	115.367	-1.338	10.517	1.00	19.63	L	C
ATOM	3708	CG	TYR	85	116.240	-1.976	11.566	1.00	19.63	L	C
ATOM	3709	CD1	TYR	85	115.988	-3.279	12.021	1.00	19.63	L	C
ATOM	3710	CE1	TYR	85	116.718	-3.834	13.061	1.00	19.63	L	C
ATOM	3711	CD2	TYR	85	117.255	-1.259	12.174	1.00	19.63	L	C
ATOM	3712	CE2	TYR	85	117.990	-1.807	13.217	1.00	19.63	L	C
ATOM	3713	CZ	TYR	85	117.711	-3.087	13.655	1.00	19.63	L	C
ATOM	3714	OH	TYR	85	118.405	-3.592	14.722	1.00	19.63	L	O
ATOM	3715	C	TYR	85	113.173	-0.365	9.882	1.00	21.31	L	C
ATOM	3716	O	TYR	85	112.768	-0.996	8.900	1.00	21.31	L	O
ATOM	3717	N	TYR	86	113.015	0.948	10.046	1.00	18.01	L	N
ATOM	3718	CA	TYR	86	112.321	1.806	9.090	1.00	18.01	L	C
ATOM	3719	CB	TYR	86	111.242	2.632	9.790	1.00	24.73	L	C
ATOM	3720	CG	TYR	86	110.130	1.846	10.421	1.00	24.73	L	C
ATOM	3721	CD1	TYR	86	109.020	1.459	9.679	1.00	24.73	L	C
ATOM	3722	CE1	TYR	86	107.971	0.756	10.278	1.00	24.73	L	C
ATOM	3723	CD2	TYR	86	110.177	1.508	11.773	1.00	24.73	L	C

Fig. 19: A-52

ATOM	3724	CE2	TYR	86	109.140	0.804	12.378	1.00	24.73	L	C
ATOM	3725	CZ	TYR	86	108.042	0.438	11.628	1.00	24.73	L	C
ATOM	3726	OH	TYR	86	107.002	-0.204	12.238	1.00	24.73	L	O
ATOM	3727	C	TYR	86	113.280	2.798	8.465	1.00	18.01	L	C
ATOM	3728	O	TYR	86	114.110	3.378	9.158	1.00	18.01	L	O
ATOM	3729	N	CYS	87	113.170	2.996	7.158	1.00	20.53	L	N
ATOM	3730	CA	CYS	87	113.989	3.999	6.494	1.00	20.53	L	C
ATOM	3731	C	CYS	87	113.021	5.156	6.335	1.00	20.53	L	C
ATOM	3732	O	CYS	87	111.806	4.954	6.351	1.00	20.53	L	O
ATOM	3733	CB	CYS	87	114.509	3.527	5.133	1.00	17.33	L	C
ATOM	3734	SG	CYS	87	113.306	2.900	3.921	1.00	17.33	L	S
ATOM	3735	N	GLN	88	113.545	6.363	6.212	1.00	10.63	L	N
ATOM	3736	CA	GLN	88	112.696	7.534	6.083	1.00	10.63	L	C
ATOM	3737	CB	GLN	88	112.393	8.083	7.482	1.00	18.09	L	C
ATOM	3738	CG	GLN	88	111.509	9.303	7.525	1.00	18.09	L	C
ATOM	3739	CD	GLN	88	112.256	10.547	7.971	1.00	18.09	L	C
ATOM	3740	OE1	GLN	88	112.946	10.539	8.987	1.00	18.09	L	O
ATOM	3741	NE2	GLN	88	112.106	11.627	7.219	1.00	18.09	L	N
ATOM	3742	C	GLN	88	113.390	8.583	5.219	1.00	10.63	L	C
ATOM	3743	O	GLN	88	114.626	8.680	5.198	1.00	10.63	L	O
ATOM	3744	N	GLN	89	112.600	9.357	4.483	1.00	11.94	L	N
ATOM	3745	CA	GLN	89	113.171	10.386	3.625	1.00	11.94	L	C
ATOM	3746	CB	GLN	89	112.877	10.073	2.152	1.00	25.01	L	C
ATOM	3747	CG	GLN	89	111.407	10.008	1.776	1.00	25.01	L	C
ATOM	3748	CD	GLN	89	110.786	11.377	1.579	1.00	25.01	L	C
ATOM	3749	OE1	GLN	89	111.373	12.247	0.935	1.00	25.01	L	O
ATOM	3750	NE2	GLN	89	109.591	11.571	2.119	1.00	25.01	L	N
ATOM	3751	C	GLN	89	112.606	11.732	4.023	1.00	11.94	L	C
ATOM	3752	O	GLN	89	111.498	11.802	4.552	1.00	11.94	L	O
ATOM	3753	N	TRP	90	113.375	12.794	3.792	1.00	19.62	L	N
ATOM	3754	CA	TRP	90	112.948	14.144	4.145	1.00	19.62	L	C
ATOM	3755	CB	TRP	90	113.773	14.667	5.336	1.00	17.27	L	C
ATOM	3756	CG	TRP	90	115.220	15.018	5.023	1.00	17.27	L	C
ATOM	3757	CD2	TRP	90	116.174	15.611	5.918	1.00	17.27	L	C
ATOM	3758	CE2	TRP	90	117.373	15.797	5.189	1.00	17.27	L	C
ATOM	3759	CE3	TRP	90	116.132	16.005	7.267	1.00	17.27	L	C
ATOM	3760	CD1	TRP	90	115.869	14.867	3.823	1.00	17.27	L	C
ATOM	3761	NE1	TRP	90	117.156	15.334	3.918	1.00	17.27	L	N
ATOM	3762	CZ2	TRP	90	118.522	16.363	5.759	1.00	17.27	L	C
ATOM	3763	CZ3	TRP	90	117.284	16.570	7.839	1.00	17.27	L	C
ATOM	3764	CH2	TRP	90	118.462	16.741	7.080	1.00	17.27	L	C
ATOM	3765	C	TRP	90	113.074	15.093	2.947	1.00	19.62	L	C
ATOM	3766	O	TRP	90	112.783	16.289	3.048	1.00	19.62	L	O
ATOM	3767	N	SER	91	113.494	14.552	1.807	1.00	12.71	L	N
ATOM	3768	CA	SER	91	113.662	15.359	0.600	1.00	12.71	L	C
ATOM	3769	CB	SER	91	114.504	14.587	-0.414	1.00	23.55	L	C
ATOM	3770	OG	SER	91	115.762	14.248	0.137	1.00	23.55	L	O
ATOM	3771	C	SER	91	112.344	15.800	-0.054	1.00	12.71	L	C
ATOM	3772	O	SER	91	112.284	16.860	-0.680	1.00	12.71	L	O
ATOM	3773	N	GLY	92	111.297	14.986	0.096	1.00	23.24	L	N
ATOM	3774	CA	GLY	92	110.008	15.310	-0.493	1.00	23.24	L	C
ATOM	3775	C	GLY	92	108.867	15.347	0.509	1.00	23.24	L	C
ATOM	3776	O	GLY	92	108.931	14.718	1.567	1.00	23.24	L	O
ATOM	3777	N	ASN	93	107.811	16.078	0.169	1.00	31.94	L	N
ATOM	3778	CA	ASN	93	106.663	16.206	1.048	1.00	31.94	L	C
ATOM	3779	CB	ASN	93	106.307	17.670	1.203	1.00	23.71	L	C
ATOM	3780	CG	ASN	93	107.400	18.448	1.896	1.00	23.71	L	C
ATOM	3781	OD1	ASN	93	107.790	19.525	1.445	1.00	23.71	L	O
ATOM	3782	ND2	ASN	93	107.905	17.905	3.006	1.00	23.71	L	N
ATOM	3783	C	ASN	93	105.478	15.454	0.507	1.00	31.94	L	C
ATOM	3784	O	ASN	93	105.227	15.478	-0.692	1.00	31.94	L	O
ATOM	3785	N	PRO	94	104.724	14.779	1.386	1.00	29.10	L	N
ATOM	3786	CD	PRO	94	103.575	13.939	1.009	1.00	1.87	L	C
ATOM	3787	CA	PRO	94	104.950	14.713	2.830	1.00	29.10	L	C
ATOM	3788	CB	PRO	94	103.651	14.113	3.340	1.00	1.87	L	C
ATOM	3789	CG	PRO	94	103.336	13.137	2.269	1.00	1.87	L	C
ATOM	3790	C	PRO	94	106.131	13.823	3.167	1.00	29.10	L	C
ATOM	3791	O	PRO	94	106.516	12.987	2.361	1.00	29.10	L	O
ATOM	3792	N	TRP	95	106.711	14.011	4.349	1.00	16.41	L	N
ATOM	3793	CA	TRP	95	107.810	13.155	4.772	1.00	16.41	L	C
ATOM	3794	CB	TRP	95	108.425	13.629	6.094	1.00	13.37	L	C
ATOM	3795	CG	TRP	95	109.201	14.906	5.979	1.00	13.37	L	C
ATOM	3796	CD2	TRP	95	109.284	15.950	6.954	1.00	13.37	L	C

Fig. 19: A-53

ATOM	3797	CE2	TRP	95	110.104	16.960	6.412	1.00	13.37	L	C
ATOM	3798	CE3	TRP	95	108.743	16.132	8.229	1.00	13.37	L	C
ATOM	3799	CD1	TRP	95	109.963	15.312	4.917	1.00	13.37	L	C
ATOM	3800	NE1	TRP	95	110.504	16.543	5.168	1.00	13.37	L	N
ATOM	3801	CZ2	TRP	95	110.394	18.144	7.107	1.00	13.37	L	C
ATOM	3802	CZ3	TRP	95	109.030	17.305	8.919	1.00	13.37	L	C
ATOM	3803	CH2	TRP	95	109.845	18.297	8.358	1.00	13.37	L	C
ATOM	3804	C	TRP	95	107.226	11.751	4.942	1.00	16.41	L	C
ATOM	3805	O	TRP	95	106.136	11.575	5.484	1.00	16.41	L	O
ATOM	3806	N	THR	96	107.956	10.748	4.481	1.00	6.71	L	N
ATOM	3807	CA	THR	96	107.465	9.388	4.563	1.00	6.71	L	C
ATOM	3808	CB	THR	96	106.963	8.932	3.172	1.00	11.59	L	C
ATOM	3809	OG1	THR	96	108.045	8.991	2.235	1.00	11.59	L	O
ATOM	3810	CG2	THR	96	105.859	9.852	2.674	1.00	11.59	L	C
ATOM	3811	C	THR	96	108.489	8.369	5.087	1.00	6.71	L	C
ATOM	3812	O	THR	96	109.703	8.621	5.121	1.00	6.71	L	O
ATOM	3813	N	PHE	97	107.966	7.222	5.513	1.00	24.36	L	N
ATOM	3814	CA	PHE	97	108.777	6.119	6.013	1.00	24.36	L	C
ATOM	3815	CB	PHE	97	108.327	5.689	7.418	1.00	11.10	L	C
ATOM	3816	CG	PHE	97	108.422	6.762	8.461	1.00	11.10	L	C
ATOM	3817	CD1	PHE	97	107.541	7.831	8.460	1.00	11.10	L	C
ATOM	3818	CD2	PHE	97	109.391	6.685	9.470	1.00	11.10	L	C
ATOM	3819	CE1	PHE	97	107.612	8.821	9.453	1.00	11.10	L	C
ATOM	3820	CE2	PHE	97	109.475	7.665	10.468	1.00	11.10	L	C
ATOM	3821	CZ	PHE	97	108.577	8.738	10.456	1.00	11.10	L	C
ATOM	3822	C	PHE	97	108.532	4.950	5.062	1.00	24.36	L	C
ATOM	3823	O	PHE	97	107.613	4.990	4.241	1.00	24.36	L	O
ATOM	3824	N	GLY	98	109.362	3.919	5.168	1.00	21.54	L	N
ATOM	3825	CA	GLY	98	109.183	2.727	4.350	1.00	21.54	L	C
ATOM	3826	C	GLY	98	108.266	1.849	5.184	1.00	21.54	L	C
ATOM	3827	O	GLY	98	107.977	2.196	6.339	1.00	21.54	L	O
ATOM	3828	N	GLN	99	107.796	0.728	4.645	1.00	11.59	L	N
ATOM	3829	CA	GLN	99	106.894	-0.114	5.442	1.00	11.59	L	C
ATOM	3830	CB	GLN	99	106.211	-1.197	4.593	1.00	37.88	L	C
ATOM	3831	CG	GLN	99	106.810	-1.403	3.238	1.00	37.88	L	C
ATOM	3832	CD	GLN	99	108.266	-1.748	3.319	1.00	37.88	L	C
ATOM	3833	OE1	GLN	99	108.638	-2.821	3.796	1.00	37.88	L	O
ATOM	3834	NE2	GLN	99	109.110	-0.832	2.866	1.00	37.88	L	N
ATOM	3835	C	GLN	99	107.586	-0.758	6.634	1.00	11.59	L	C
ATOM	3836	O	GLN	99	106.943	-1.317	7.508	1.00	11.59	L	O
ATOM	3837	N	GLY	100	108.902	-0.640	6.684	1.00	24.72	L	N
ATOM	3838	CA	GLY	100	109.633	-1.225	7.785	1.00	24.72	L	C
ATOM	3839	C	GLY	100	110.055	-2.630	7.425	1.00	24.72	L	C
ATOM	3840	O	GLY	100	109.402	-3.279	6.606	1.00	24.72	L	O
ATOM	3841	N	THR	101	111.157	-3.084	8.017	1.00	23.77	L	N
ATOM	3842	CA	THR	101	111.685	-4.424	7.780	1.00	23.77	L	C
ATOM	3843	CB	THR	101	113.019	-4.382	7.040	1.00	10.18	L	C
ATOM	3844	OG1	THR	101	112.790	-4.076	5.659	1.00	10.18	L	O
ATOM	3845	CG2	THR	101	113.735	-5.716	7.173	1.00	10.18	L	C
ATOM	3846	C	THR	101	111.908	-5.076	9.129	1.00	23.77	L	C
ATOM	3847	O	THR	101	112.689	-4.582	9.942	1.00	23.77	L	O
ATOM	3848	N	LYS	102	111.223	-6.188	9.365	1.00	19.34	L	N
ATOM	3849	CA	LYS	102	111.347	-6.858	10.641	1.00	19.34	L	C
ATOM	3850	CB	LYS	102	110.009	-7.496	11.027	1.00	36.70	L	C
ATOM	3851	CG	LYS	102	109.872	-7.774	12.521	1.00	36.70	L	C
ATOM	3852	CD	LYS	102	108.464	-8.244	12.876	1.00	36.70	L	C
ATOM	3853	CE	LYS	102	108.313	-8.467	14.372	1.00	36.70	L	C
ATOM	3854	NZ	LYS	102	108.632	-7.218	15.120	1.00	36.70	L	N
ATOM	3855	C	LYS	102	112.449	-7.907	10.608	1.00	19.34	L	C
ATOM	3856	O	LYS	102	112.530	-8.703	9.661	1.00	19.34	L	O
ATOM	3857	N	VAL	103	113.304	-7.894	11.634	1.00	20.01	L	N
ATOM	3858	CA	VAL	103	114.378	-8.868	11.714	1.00	20.01	L	C
ATOM	3859	CB	VAL	103	115.793	-8.188	11.567	1.00	24.69	L	C
ATOM	3860	CG1	VAL	103	115.696	-6.991	10.636	1.00	24.69	L	C
ATOM	3861	CG2	VAL	103	116.361	-7.780	12.908	1.00	24.69	L	C
ATOM	3862	C	VAL	103	114.280	-9.654	13.031	1.00	20.01	L	C
ATOM	3863	O	VAL	103	114.380	-9.075	14.117	1.00	20.01	L	O
ATOM	3864	N	GLU	104	114.047	-10.969	12.927	1.00	25.78	L	N
ATOM	3865	CA	GLU	104	113.948	-11.831	14.106	1.00	25.78	L	C
ATOM	3866	CB	GLU	104	112.662	-12.666	14.098	1.00	117.28	L	C
ATOM	3867	CG	GLU	104	112.589	-13.728	13.022	1.00	117.28	L	C
ATOM	3868	CD	GLU	104	112.095	-13.176	11.705	1.00	117.28	L	C
ATOM	3869	OE1	GLU	104	112.047	-13.942	10.717	1.00	117.28	L	O

Fig. 19: A-54

ATOM	3870	OE2	GLU	104	111.747	-11.975	11.660	1.00	117.28	L	O
ATOM	3871	C	GLU	104	115.148	-12.759	14.179	1.00	25.78	L	C
ATOM	3872	O	GLU	104	115.852	-12.955	13.185	1.00	25.78	L	O
ATOM	3873	N	ILE	105	115.368	-13.324	15.365	1.00	16.82	L	N
ATOM	3874	CA	ILE	105	116.489	-14.228	15.621	1.00	16.82	L	C
ATOM	3875	CB	ILE	105	116.771	-14.386	17.124	1.00	41.57	L	C
ATOM	3876	CG2	ILE	105	118.226	-14.701	17.335	1.00	41.57	L	C
ATOM	3877	CG1	ILE	105	116.372	-13.111	17.873	1.00	41.57	L	C
ATOM	3878	CD1	ILE	105	116.594	-13.151	19.385	1.00	41.57	L	C
ATOM	3879	C	ILE	105	116.204	-15.611	15.102	1.00	16.82	L	C
ATOM	3880	O	ILE	105	115.251	-16.250	15.543	1.00	16.82	L	O
ATOM	3881	N	LYS	106	117.008	-16.076	14.153	1.00	39.65	L	N
ATOM	3882	CA	LYS	106	116.807	-17.422	13.653	1.00	39.65	L	C
ATOM	3883	CB	LYS	106	117.310	-17.587	12.217	1.00	48.57	L	C
ATOM	3884	CG	LYS	106	116.947	-18.952	11.631	1.00	48.57	L	C
ATOM	3885	CD	LYS	106	117.401	-19.148	10.179	1.00	48.57	L	C
ATOM	3886	CE	LYS	106	117.087	-20.579	9.702	1.00	48.57	L	C
ATOM	3887	NZ	LYS	106	117.672	-20.948	8.369	1.00	48.57	L	N
ATOM	3888	C	LYS	106	117.598	-18.310	14.600	1.00	39.65	L	C
ATOM	3889	O	LYS	106	118.804	-18.122	14.782	1.00	38.70	L	O
ATOM	3890	N	ARG	107	116.894	-19.242	15.235	1.00	14.86	L	N
ATOM	3891	CA	ARG	107	117.492	-20.178	16.174	1.00	14.86	L	C
ATOM	3892	CB	ARG	107	117.158	-19.771	17.605	1.00	20.96	L	C
ATOM	3893	CG	ARG	107	115.687	-19.532	17.832	1.00	20.96	L	C
ATOM	3894	CD	ARG	107	115.296	-19.930	19.239	1.00	20.96	L	C
ATOM	3895	NE	ARG	107	115.615	-21.335	19.502	1.00	20.96	L	N
ATOM	3896	CZ	ARG	107	115.513	-21.910	20.692	1.00	20.96	L	C
ATOM	3897	NH1	ARG	107	115.096	-21.206	21.732	1.00	20.96	L	N
ATOM	3898	NH2	ARG	107	115.843	-23.182	20.840	1.00	20.96	L	N
ATOM	3899	C	ARG	107	116.986	-21.595	15.899	1.00	14.86	L	C
ATOM	3900	O	ARG	107	116.062	-21.796	15.107	1.00	14.86	L	O
ATOM	3901	N	THR	108	117.606	-22.575	16.545	1.00	15.74	L	N
ATOM	3902	CA	THR	108	117.220	-23.963	16.354	1.00	15.74	L	C
ATOM	3903	CB	THR	108	118.025	-24.921	17.260	1.00	26.88	L	C
ATOM	3904	OG1	THR	108	118.232	-24.320	18.548	1.00	26.88	L	O
ATOM	3905	CG2	THR	108	119.347	-25.257	16.618	1.00	26.88	L	C
ATOM	3906	C	THR	108	115.756	-24.161	16.653	1.00	15.74	L	C
ATOM	3907	O	THR	108	115.179	-23.450	17.481	1.00	15.74	L	O
ATOM	3908	N	VAL	109	115.170	-25.134	15.963	1.00	14.98	L	N
ATOM	3909	CA	VAL	109	113.775	-25.469	16.136	1.00	12.60	L	C
ATOM	3910	CB	VAL	109	113.368	-26.593	15.189	1.00	15.46	L	C
ATOM	3911	CG1	VAL	109	111.987	-27.105	15.527	1.00	14.41	L	C
ATOM	3912	CG2	VAL	109	113.383	-26.074	13.789	1.00	13.59	L	C
ATOM	3913	C	VAL	109	113.517	-25.909	17.565	1.00	13.54	L	C
ATOM	3914	O	VAL	109	114.393	-26.477	18.236	1.00	21.28	L	O
ATOM	3915	N	ALA	110	112.313	-25.637	18.036	1.00	11.81	L	N
ATOM	3916	CA	ALA	110	111.953	-26.001	19.383	1.00	12.99	L	C
ATOM	3917	CB	ALA	110	112.312	-24.878	20.330	1.00	8.30	L	C
ATOM	3918	C	ALA	110	110.463	-26.281	19.426	1.00	13.63	L	C
ATOM	3919	O	ALA	110	109.654	-25.390	19.158	1.00	15.92	L	O
ATOM	3920	N	ALA	111	110.112	-27.525	19.758	1.00	25.70	L	N
ATOM	3921	CA	ALA	111	108.715	-27.951	19.838	1.00	26.75	L	C
ATOM	3922	CB	ALA	111	108.641	-29.446	20.087	1.00	23.32	L	C
ATOM	3923	C	ALA	111	107.981	-27.198	20.936	1.00	25.59	L	C
ATOM	3924	O	ALA	111	108.525	-26.926	22.008	1.00	29.44	L	O
ATOM	3925	N	PRO	112	106.720	-26.857	20.686	1.00	20.76	L	N
ATOM	3926	CD	PRO	112	105.901	-27.063	19.477	1.00	26.01	L	C
ATOM	3927	CA	PRO	112	105.975	-26.125	21.707	1.00	26.81	L	C
ATOM	3928	CB	PRO	112	104.938	-25.381	20.882	1.00	26.37	L	C
ATOM	3929	CG	PRO	112	104.550	-26.457	19.876	1.00	24.71	L	C
ATOM	3930	C	PRO	112	105.322	-27.058	22.703	1.00	30.67	L	C
ATOM	3931	O	PRO	112	104.936	-28.166	22.353	1.00	31.28	L	O
ATOM	3932	N	SER	113	105.220	-26.618	23.947	1.00	12.97	L	N
ATOM	3933	CA	SER	113	104.530	-27.410	24.944	1.00	16.57	L	C
ATOM	3934	CB	SER	113	105.027	-27.079	26.334	1.00	14.96	L	C
ATOM	3935	OG	SER	113	106.427	-27.168	26.370	1.00	27.37	L	O
ATOM	3936	C	SER	113	103.099	-26.913	24.815	1.00	15.10	L	C
ATOM	3937	O	SER	113	102.884	-25.708	24.770	1.00	12.98	L	O
ATOM	3938	N	VAL	114	102.111	-27.792	24.731	1.00	10.23	L	N
ATOM	3939	CA	VAL	114	100.766	-27.258	24.630	1.00	9.98	L	C
ATOM	3940	CB	VAL	114	99.989	-27.808	23.413	1.00	7.82	L	C
ATOM	3941	CG1	VAL	114	100.921	-27.972	22.212	1.00	4.17	L	C
ATOM	3942	CG2	VAL	114	99.331	-29.100	23.777	1.00	9.35	L	C

Fig. 19: A-55

ATOM	3943	C	VAL	114	99.992	-27.558	25.899	1.00	9.84	L	C
ATOM	3944	O	VAL	114	100.318	-28.494	26.628	1.00	12.49	L	O
ATOM	3945	N	PHE	115	98.981	-26.728	26.153	1.00	26.11	L	N
ATOM	3946	CA	PHE	115	98.109	-26.840	27.318	1.00	30.12	L	C
ATOM	3947	CB	PHE	115	98.581	-25.896	28.416	1.00	36.06	L	C
ATOM	3948	CG	PHE	115	100.030	-26.015	28.706	1.00	35.84	L	C
ATOM	3949	CD1	PHE	115	100.505	-27.040	29.513	1.00	38.16	L	C
ATOM	3950	CD2	PHE	115	100.935	-25.146	28.115	1.00	34.45	L	C
ATOM	3951	CE1	PHE	115	101.854	-27.203	29.723	1.00	41.30	L	C
ATOM	3952	CE2	PHE	115	102.287	-25.302	28.319	1.00	38.56	L	C
ATOM	3953	CZ	PHE	115	102.749	-26.335	29.126	1.00	39.82	L	C
ATOM	3954	C	PHE	115	96.727	-26.410	26.873	1.00	32.06	L	C
ATOM	3955	O	PHE	115	96.590	-25.543	26.017	1.00	32.56	L	O
ATOM	3956	N	ILE	116	95.694	-27.018	27.432	1.00	24.34	L	N
ATOM	3957	CA	ILE	116	94.354	-26.608	27.069	1.00	18.54	L	C
ATOM	3958	CB	ILE	116	93.606	-27.735	26.309	1.00	15.62	L	C
ATOM	3959	CG2	ILE	116	93.239	-28.855	27.249	1.00	4.34	L	C
ATOM	3960	CG1	ILE	116	92.377	-27.145	25.615	1.00	12.45	L	C
ATOM	3961	CD1	ILE	116	91.695	-28.089	24.646	1.00	4.28	L	C
ATOM	3962	C	ILE	116	93.661	-26.233	28.371	1.00	19.64	L	C
ATOM	3963	O	ILE	116	93.931	-26.834	29.412	1.00	19.05	L	O
ATOM	3964	N	PHE	117	92.802	-25.217	28.308	1.00	17.52	L	N
ATOM	3965	CA	PHE	117	92.066	-24.715	29.475	1.00	21.17	L	C
ATOM	3966	CB	PHE	117	92.501	-23.295	29.828	1.00	22.98	L	C
ATOM	3967	CG	PHE	117	93.922	-23.177	30.280	1.00	26.62	L	C
ATOM	3968	CD1	PHE	117	94.293	-23.562	31.559	1.00	29.31	L	C
ATOM	3969	CD2	PHE	117	94.882	-22.653	29.433	1.00	28.01	L	C
ATOM	3970	CE1	PHE	117	95.599	-23.421	31.988	1.00	28.27	L	C
ATOM	3971	CE2	PHE	117	96.186	-22.511	29.854	1.00	26.58	L	C
ATOM	3972	CZ	PHE	117	96.550	-22.895	31.134	1.00	28.58	L	C
ATOM	3973	C	PHE	117	90.585	-24.642	29.194	1.00	24.71	L	C
ATOM	3974	O	PHE	117	90.167	-23.964	28.261	1.00	29.18	L	O
ATOM	3975	N	PRO	118	89.768	-25.323	30.007	1.00	23.78	L	N
ATOM	3976	CD	PRO	118	90.235	-26.376	30.926	1.00	9.40	L	C
ATOM	3977	CA	PRO	118	88.300	-25.354	29.883	1.00	26.26	L	C
ATOM	3978	CB	PRO	118	87.907	-26.568	30.718	1.00	9.92	L	C
ATOM	3979	CG	PRO	118	89.159	-27.404	30.763	1.00	12.26	L	C
ATOM	3980	C	PRO	118	87.660	-24.081	30.455	1.00	29.72	L	C
ATOM	3981	O	PRO	118	88.231	-23.440	31.338	1.00	31.19	L	O
ATOM	3982	N	PRO	119	86.464	-23.699	29.966	1.00	9.50	L	N
ATOM	3983	CD	PRO	119	85.678	-24.330	28.892	1.00	26.21	L	C
ATOM	3984	CA	PRO	119	85.787	-22.493	30.479	1.00	9.82	L	C
ATOM	3985	CB	PRO	119	84.413	-22.555	29.826	1.00	24.20	L	C
ATOM	3986	CG	PRO	119	84.703	-23.219	28.519	1.00	27.52	L	C
ATOM	3987	C	PRO	119	85.682	-22.566	32.001	1.00	15.21	L	C
ATOM	3988	O	PRO	119	85.463	-23.630	32.561	1.00	17.89	L	O
ATOM	3989	N	SER	120	85.843	-21.435	32.665	1.00	31.09	L	N
ATOM	3990	CA	SER	120	85.765	-21.378	34.118	1.00	35.08	L	C
ATOM	3991	CB	SER	120	86.299	-20.027	34.586	1.00	17.54	L	C
ATOM	3992	OG	SER	120	85.709	-18.983	33.832	1.00	27.86	L	O
ATOM	3993	C	SER	120	84.334	-21.550	34.623	1.00	35.73	L	C
ATOM	3994	O	SER	120	83.370	-21.381	33.869	1.00	35.32	L	O
ATOM	3995	N	ASP	121	84.185	-21.896	35.897	1.00	24.20	L	N
ATOM	3996	CA	ASP	121	82.842	-22.015	36.465	1.00	27.07	L	C
ATOM	3997	CB	ASP	121	82.897	-22.458	37.937	1.00	55.35	L	C
ATOM	3998	CG	ASP	121	83.160	-23.950	38.101	1.00	60.98	L	C
ATOM	3999	OD1	ASP	121	82.573	-24.736	37.331	1.00	62.35	L	O
ATOM	4000	OD2	ASP	121	83.934	-24.337	39.008	1.00	63.66	L	O
ATOM	4001	C	ASP	121	82.194	-20.627	36.384	1.00	26.11	L	C
ATOM	4002	O	ASP	121	81.053	-20.474	35.941	1.00	23.12	L	O
ATOM	4003	N	GLU	122	82.954	-19.617	36.794	1.00	48.87	L	N
ATOM	4004	CA	GLU	122	82.490	-18.234	36.797	1.00	47.43	L	C
ATOM	4005	CB	GLU	122	83.596	-17.328	37.348	1.00	56.26	L	C
ATOM	4006	CG	GLU	122	83.180	-15.870	37.529	1.00	59.80	L	C
ATOM	4007	CD	GLU	122	84.328	-14.966	37.984	1.00	63.49	L	C
ATOM	4008	OE1	GLU	122	84.099	-13.741	38.109	1.00	64.12	L	O
ATOM	4009	OE2	GLU	122	85.453	-15.472	38.213	1.00	63.98	L	O
ATOM	4010	C	GLU	122	82.018	-17.703	35.434	1.00	47.22	L	C
ATOM	4011	O	GLU	122	80.884	-17.232	35.303	1.00	45.96	L	O
ATOM	4012	N	GLN	123	82.881	-17.774	34.424	1.00	34.52	L	N
ATOM	4013	CA	GLN	123	82.523	-17.273	33.102	1.00	32.32	L	C
ATOM	4014	CB	GLN	123	83.643	-17.511	32.097	1.00	23.68	L	C
ATOM	4015	CG	GLN	123	83.286	-17.000	30.723	1.00	24.85	L	C

Fig. 19: A-56

ATOM	4016	CD	GLN	123	84.089	-17.644	29.635	1.00	26.94	L	C
ATOM	4017	OE1	GLN	123	83.877	-17.369	28.463	1.00	23.36	L	O
ATOM	4018	NE2	GLN	123	85.017	-18.511	30.010	1.00	24.66	L	N
ATOM	4019	C	GLN	123	81.256	-17.909	32.565	1.00	32.32	L	C
ATOM	4020	O	GLN	123	80.424	-17.233	31.969	1.00	29.27	L	O
ATOM	4021	N	LEU	124	81.128	-19.218	32.745	1.00	36.22	L	N
ATOM	4022	CA	LEU	124	79.938	-19.926	32.288	1.00	37.57	L	C
ATOM	4023	CB	LEU	124	80.075	-21.425	32.570	1.00	20.16	L	C
ATOM	4024	CG	LEU	124	80.878	-22.173	31.498	1.00	19.96	L	C
ATOM	4025	CD1	LEU	124	81.099	-23.623	31.892	1.00	15.21	L	C
ATOM	4026	CD2	LEU	124	80.123	-22.085	30.176	1.00	18.53	L	C
ATOM	4027	C	LEU	124	78.722	-19.355	33.003	1.00	41.33	L	C
ATOM	4028	O	LEU	124	77.648	-19.204	32.417	1.00	43.14	L	O
ATOM	4029	N	LYS	125	78.912	-19.022	34.274	1.00	101.23	L	N
ATOM	4030	CA	LYS	125	77.856	-18.441	35.090	1.00	102.45	L	C
ATOM	4031	CB	LYS	125	78.355	-18.285	36.534	1.00	60.11	L	C
ATOM	4032	CG	LYS	125	77.286	-18.376	37.612	1.00	62.95	L	C
ATOM	4033	CD	LYS	125	76.737	-19.797	37.713	1.00	68.67	L	C
ATOM	4034	CE	LYS	125	75.726	-19.942	38.847	1.00	73.14	L	C
ATOM	4035	NZ	LYS	125	75.101	-21.299	38.895	1.00	74.11	L	N
ATOM	4036	C	LYS	125	77.545	-17.065	34.494	1.00	104.22	L	C
ATOM	4037	O	LYS	125	77.004	-16.195	35.168	1.00	105.97	L	O
ATOM	4038	N	SER	126	77.892	-16.880	33.222	1.00	44.02	L	N
ATOM	4039	CA	SER	126	77.693	-15.614	32.522	1.00	43.14	L	C
ATOM	4040	CB	SER	126	79.045	-14.925	32.308	1.00	48.89	L	C
ATOM	4041	OG	SER	126	78.953	-13.915	31.324	1.00	52.18	L	O
ATOM	4042	C	SER	126	76.995	-15.769	31.176	1.00	41.22	L	C
ATOM	4043	O	SER	126	76.469	-14.802	30.631	1.00	40.32	L	O
ATOM	4044	N	GLY	127	77.007	-16.978	30.626	1.00	29.57	L	N
ATOM	4045	CA	GLY	127	76.340	-17.190	29.355	1.00	30.30	L	C
ATOM	4046	C	GLY	127	77.266	-17.332	28.168	1.00	29.68	L	C
ATOM	4047	O	GLY	127	76.818	-17.391	27.022	1.00	30.41	L	O
ATOM	4048	N	THR	128	78.564	-17.375	28.432	1.00	60.53	L	N
ATOM	4049	CA	THR	128	79.530	-17.531	27.360	1.00	57.77	L	C
ATOM	4050	CB	THR	128	80.105	-16.180	26.921	1.00	55.78	L	C
ATOM	4051	OG1	THR	128	79.080	-15.424	26.264	1.00	56.94	L	O
ATOM	4052	CG2	THR	128	81.259	-16.381	25.960	1.00	54.81	L	C
ATOM	4053	C	THR	128	80.643	-18.434	27.830	1.00	56.24	L	C
ATOM	4054	O	THR	128	80.979	-18.446	29.015	1.00	51.99	L	O
ATOM	4055	N	ALA	129	81.201	-19.203	26.901	1.00	18.93	L	N
ATOM	4056	CA	ALA	129	82.275	-20.125	27.232	1.00	17.83	L	C
ATOM	4057	CB	ALA	129	81.779	-21.558	27.108	1.00	65.23	L	C
ATOM	4058	C	ALA	129	83.512	-19.937	26.374	1.00	17.59	L	C
ATOM	4059	O	ALA	129	83.443	-19.993	25.148	1.00	23.96	L	O
ATOM	4060	N	SER	130	84.652	-19.729	27.020	1.00	24.31	L	N
ATOM	4061	CA	SER	130	85.905	-19.560	26.298	1.00	19.76	L	C
ATOM	4062	CB	SER	130	86.565	-18.256	26.741	1.00	18.21	L	C
ATOM	4063	OG	SER	130	85.724	-17.142	26.477	1.00	20.32	L	O
ATOM	4064	C	SER	130	86.835	-20.755	26.573	1.00	16.63	L	C
ATOM	4065	O	SER	130	87.037	-21.141	27.732	1.00	19.43	L	O
ATOM	4066	N	VAL	131	87.370	-21.371	25.521	1.00	11.62	L	N
ATOM	4067	CA	VAL	131	88.294	-22.502	25.686	1.00	9.15	L	C
ATOM	4068	CB	VAL	131	87.848	-23.743	24.872	1.00	17.04	L	C
ATOM	4069	CG1	VAL	131	88.738	-24.927	25.196	1.00	21.32	L	C
ATOM	4070	CG2	VAL	131	86.413	-24.081	25.180	1.00	16.62	L	C
ATOM	4071	C	VAL	131	89.647	-22.030	25.156	1.00	9.42	L	C
ATOM	4072	O	VAL	131	89.731	-21.557	24.025	1.00	13.02	L	O
ATOM	4073	N	VAL	132	90.704	-22.146	25.956	1.00	21.24	L	N
ATOM	4074	CA	VAL	132	92.011	-21.677	25.501	1.00	16.30	L	C
ATOM	4075	CB	VAL	132	92.573	-20.538	26.414	1.00	43.77	L	C
ATOM	4076	CG1	VAL	132	93.958	-20.122	25.934	1.00	47.77	L	C
ATOM	4077	CG2	VAL	132	91.645	-19.324	26.393	1.00	44.24	L	C
ATOM	4078	C	VAL	132	93.081	-22.743	25.374	1.00	17.14	L	C
ATOM	4079	O	VAL	132	93.372	-23.482	26.320	1.00	14.49	L	O
ATOM	4080	N	CYS	133	93.662	-22.793	24.178	1.00	23.86	L	N
ATOM	4081	CA	CYS	133	94.737	-23.713	23.822	1.00	24.13	L	C
ATOM	4082	C	CYS	133	96.034	-22.880	23.891	1.00	24.10	L	C
ATOM	4083	O	CYS	133	96.072	-21.744	23.425	1.00	27.83	L	O
ATOM	4084	CB	CYS	133	94.486	-24.219	22.399	1.00	19.56	L	C
ATOM	4085	SG	CYS	133	95.558	-25.537	21.738	1.00	32.96	L	S
ATOM	4086	N	LEU	134	97.085	-23.432	24.482	1.00	36.02	L	N
ATOM	4087	CA	LEU	134	98.343	-22.709	24.591	1.00	34.35	L	C
ATOM	4088	CB	LEU	134	98.658	-22.383	26.058	1.00	16.71	L	C

Fig. 19: A-57

ATOM	4089	CG	LEU	134	100.079	-21.843	26.376	1.00	12.52	L	C
ATOM	4090	CD1	LEU	134	100.297	-20.468	25.729	1.00	9.26	L	C
ATOM	4091	CD2	LEU	134	100.275	-21.746	27.892	1.00	9.75	L	C
ATOM	4092	C	LEU	134	99.532	-23.457	24.001	1.00	33.88	L	C
ATOM	4093	O	LEU	134	99.820	-24.595	24.378	1.00	33.96	L	O
ATOM	4094	N	LEU	135	100.206	-22.802	23.060	1.00	23.69	L	N
ATOM	4095	CA	LEU	135	101.406	-23.336	22.441	1.00	29.22	L	C
ATOM	4096	CB	LEU	135	101.353	-23.150	20.926	1.00	1.87	L	C
ATOM	4097	CG	LEU	135	100.337	-24.016	20.168	1.00	4.32	L	C
ATOM	4098	CD1	LEU	135	98.962	-23.751	20.672	1.00	5.12	L	C
ATOM	4099	CD2	LEU	135	100.392	-23.713	18.681	1.00	3.70	L	C
ATOM	4100	C	LEU	135	102.454	-22.437	23.097	1.00	29.43	L	C
ATOM	4101	O	LEU	135	102.401	-21.216	22.977	1.00	30.81	L	O
ATOM	4102	N	ASN	136	103.394	-23.047	23.810	1.00	17.75	L	N
ATOM	4103	CA	ASN	136	104.393	-22.299	24.550	1.00	20.05	L	C
ATOM	4104	CB	ASN	136	104.179	-22.576	26.016	1.00	15.03	L	C
ATOM	4105	CG	ASN	136	104.905	-21.615	26.885	1.00	19.57	L	C
ATOM	4106	OD1	ASN	136	105.767	-22.017	27.666	1.00	25.01	L	O
ATOM	4107	ND2	ASN	136	104.569	-20.327	26.769	1.00	19.54	L	N
ATOM	4108	C	ASN	136	105.856	-22.526	24.212	1.00	18.78	L	C
ATOM	4109	O	ASN	136	106.283	-23.651	23.963	1.00	17.25	L	O
ATOM	4110	N	ASN	137	106.619	-21.436	24.240	1.00	28.11	L	N
ATOM	4111	CA	ASN	137	108.053	-21.425	23.950	1.00	27.19	L	C
ATOM	4112	CB	ASN	137	108.869	-21.844	25.173	1.00	13.82	L	C
ATOM	4113	CG	ASN	137	108.594	-20.986	26.387	1.00	24.17	L	C
ATOM	4114	OD1	ASN	137	108.027	-19.901	26.281	1.00	19.30	L	O
ATOM	4115	ND2	ASN	137	109.009	-21.468	27.558	1.00	29.25	L	N
ATOM	4116	C	ASN	137	108.486	-22.292	22.783	1.00	25.42	L	C
ATOM	4117	O	ASN	137	109.125	-23.324	22.977	1.00	28.31	L	O
ATOM	4118	N	PHE	138	108.152	-21.880	21.571	1.00	45.01	L	N
ATOM	4119	CA	PHE	138	108.557	-22.652	20.412	1.00	41.21	L	C
ATOM	4120	CB	PHE	138	107.362	-23.361	19.777	1.00	23.11	L	C
ATOM	4121	CG	PHE	138	106.230	-22.452	19.442	1.00	20.89	L	C
ATOM	4122	CD1	PHE	138	105.342	-22.043	20.433	1.00	18.63	L	C
ATOM	4123	CD2	PHE	138	106.055	-21.993	18.137	1.00	19.93	L	C
ATOM	4124	CE1	PHE	138	104.289	-21.189	20.134	1.00	11.59	L	C
ATOM	4125	CE2	PHE	138	105.010	-21.138	17.818	1.00	16.52	L	C
ATOM	4126	CZ	PHE	138	104.118	-20.730	18.818	1.00	14.07	L	C
ATOM	4127	C	PHE	138	109.248	-21.794	19.369	1.00	36.81	L	C
ATOM	4128	O	PHE	138	109.456	-20.594	19.559	1.00	35.37	L	O
ATOM	4129	N	TYR	139	109.606	-22.437	18.267	1.00	17.70	L	N
ATOM	4130	CA	TYR	139	110.283	-21.797	17.159	1.00	20.93	L	C
ATOM	4131	CB	TYR	139	111.660	-21.300	17.579	1.00	31:56	L	C
ATOM	4132	CG	TYR	139	112.317	-20.472	16.502	1.00	31.46	L	C
ATOM	4133	CD1	TYR	139	112.207	-19.083	16.502	1.00	26.49	L	C
ATOM	4134	CE1	TYR	139	112.725	-18.327	15.462	1.00	25.20	L	C
ATOM	4135	CD2	TYR	139	112.974	-21.083	15.428	1.00	25.20	L	C
ATOM	4136	CE2	TYR	139	113.490	-20.336	14.386	1.00	25.20	L	C
ATOM	4137	CZ	TYR	139	113.358	-18.960	14.407	1.00	25.20	L	C
ATOM	4138	OH	TYR	139	113.820	-18.216	13.353	1.00	28.00	L	O
ATOM	4139	C	TYR	139	110.447	-22.917	16.166	1.00	20.32	L	C
ATOM	4140	O	TYR	139	110.798	-24.022	16.550	1.00	25.25	L	O
ATOM	4141	N	PRO	140	110.223	-22.662	14.876	1.00	34.32	L	N
ATOM	4142	CD	PRO	140	110.342	-23.783	13.937	1.00	6.42	L	C
ATOM	4143	CA	PRO	140	109.824	-21.443	14.171	1.00	30.02	L	C
ATOM	4144	CB	PRO	140	109.691	-21.901	12.723	1.00	2.76	L	C
ATOM	4145	CG	PRO	140	110.570	-23.070	12.643	1.00	4.42	L	C
ATOM	4146	C	PRO	140	108.502	-20.939	14.685	1.00	31.53	L	C
ATOM	4147	O	PRO	140	107.830	-21.612	15.466	1.00	29.36	L	O
ATOM	4148	N	ARG	141	108.119	-19.764	14.203	1.00	22.83	L	N
ATOM	4149	CA	ARG	141	106.871	-19.115	14.588	1.00	27.99	L	C
ATOM	4150	CB	ARG	141	106.931	-17.657	14.148	1.00	21.70	L	C
ATOM	4151	CG	ARG	141	105.753	-16.783	14.473	1.00	25.87	L	C
ATOM	4152	CD	ARG	141	106.157	-15.358	14.129	1.00	37.20	L	C
ATOM	4153	NE	ARG	141	105.187	-14.366	14.564	1.00	43.19	L	N
ATOM	4154	CZ	ARG	141	104.001	-14.188	13.995	1.00	43.90	L	C
ATOM	4155	NH1	ARG	141	103.642	-14.941	12.960	1.00	39.57	L	N
ATOM	4156	NH2	ARG	141	103.173	-13.262	14.464	1.00	42.44	L	N
ATOM	4157	C	ARG	141	105.668	-19.798	13.960	1.00	30.81	L	C
ATOM	4158	O	ARG	141	104.585	-19.815	14.537	1.00	34.71	L	O
ATOM	4159	N	GLU	142	105.860	-20.365	12.776	1.00	28.20	L	N
ATOM	4160	CA	GLU	142	104.756	-21.013	12.091	1.00	24.33	L	C
ATOM	4161	CB	GLU	142	105.171	-21.552	10.725	1.00	7.98	L	C

Fig. 19: A-58

ATOM	4162	CG	GLU	142	105.741	-20.523	9.781	1.00	19.00	L	C
ATOM	4163	CD	GLU	142	107.096	-20.051	10.217	1.00	27.12	L	C
ATOM	4164	OE1	GLU	142	107.152	-18.970	10.837	1.00	31.02	L	O
ATOM	4165	OE2	GLU	142	108.095	-20.772	9.952	1.00	33.88	L	O
ATOM	4166	C	GLU	142	104.154	-22.151	12.878	1.00	22.94	L	C
ATOM	4167	O	GLU	142	104.753	-23.220	13.021	1.00	26.95	L	O
ATOM	4168	N	ALA	143	102.958	-21.909	13.386	1.00	30.55	L	N
ATOM	4169	CA	ALA	143	102.238	-22.914	14.130	1.00	32.81	L	C
ATOM	4170	CB	ALA	143	102.260	-22.593	15.640	1.00	21.32	L	C
ATOM	4171	C	ALA	143	100.819	-22.862	13.579	1.00	34.94	L	C
ATOM	4172	O	ALA	143	100.373	-21.832	13.058	1.00	38.69	L	O
ATOM	4173	N	LYS	144	100.120	-23.981	13.677	1.00	46.96	L	N
ATOM	4174	CA	LYS	144	98.761	-24.047	13.197	1.00	49.64	L	C
ATOM	4175	CB	LYS	144	98.734	-24.807	11.870	1.00	34.36	L	C
ATOM	4176	CG	LYS	144	97.631	-24.370	10.922	1.00	44.31	L	C
ATOM	4177	CD	LYS	144	97.441	-25.358	9.772	1.00	55.06	L	C
ATOM	4178	CE	LYS	144	96.888	-26.699	10.279	1.00	57.35	L	C
ATOM	4179	NZ	LYS	144	96.807	-27.761	9.225	1.00	58.76	L	N
ATOM	4180	C	LYS	144	97.934	-24.771	14.266	1.00	52.97	L	C
ATOM	4181	O	LYS	144	98.340	-25.822	14.775	1.00	51.55	L	O
ATOM	4182	N	VAL	145	96.791	-24.194	14.630	1.00	15.87	L	N
ATOM	4183	CA	VAL	145	95.927	-24.813	15.629	1.00	21.71	L	C
ATOM	4184	CB	VAL	145	95.790	-23.937	16.905	1.00	8.53	L	C
ATOM	4185	CG1	VAL	145	94.817	-24.597	17.889	1.00	7.53	L	C
ATOM	4186	CG2	VAL	145	97.151	-23.769	17.570	1.00	8.28	L	C
ATOM	4187	C	VAL	145	94.536	-25.074	15.073	1.00	25.32	L	C
ATOM	4188	O	VAL	145	93.909	-24.193	14.497	1.00	27.49	L	O
ATOM	4189	N	GLN	146	94.055	-26.296	15.231	1.00	39.17	L	N
ATOM	4190	CA	GLN	146	92.729	-26.611	14.743	1.00	38.70	L	C
ATOM	4191	CB	GLN	146	92.798	-27.679	13.653	1.00	72.09	L	C
ATOM	4192	CG	GLN	146	93.678	-27.281	12.482	1.00	76.00	L	C
ATOM	4193	CD	GLN	146	93.630	-28.276	11.339	1.00	75.94	L	C
ATOM	4194	OE1	GLN	146	92.616	-28.399	10.654	1.00	76.92	L	O
ATOM	4195	NE2	GLN	146	94.730	-28.997	11.130	1.00	77.33	L	N
ATOM	4196	C	GLN	146	91.880	-27.094	15.904	1.00	37.70	L	C
ATOM	4197	O	GLN	146	92.302	-27.965	16.667	1.00	34.46	L	O
ATOM	4198	N	TRP	147	90.699	-26.498	16.048	1.00	30.86	L	N
ATOM	4199	CA	TRP	147	89.777	-26.878	17.102	1.00	30.91	L	C
ATOM	4200	CB	TRP	147	88.947	-25.687	17.556	1.00	36.68	L	C
ATOM	4201	CG	TRP	147	89.689	-24.788	18.432	1.00	34.29	L	C
ATOM	4202	CD2	TRP	147	89.927	-24.969	19.825	1.00	32.37	L	C
ATOM	4203	CE2	TRP	147	90.723	-23.885	20.258	1.00	33.31	L	C
ATOM	4204	CE3	TRP	147	89.552	-25.943	20.752	1.00	31.13	L	C
ATOM	4205	CD1	TRP	147	90.326	-23.641	18.077	1.00	36.68	L	C
ATOM	4206	NE1	TRP	147	90.951	-23.086	19.168	1.00	33.41	L	N
ATOM	4207	CZ2	TRP	147	91.150	-23.747	21.587	1.00	31.66	L	C
ATOM	4208	CZ3	TRP	147	89.977	-25.808	22.073	1.00	33.39	L	C
ATOM	4209	CH2	TRP	147	90.767	-24.716	22.476	1.00	33.58	L	C
ATOM	4210	C	TRP	147	88.844	-27.963	16.611	1.00	33.36	L	C
ATOM	4211	O	TRP	147	88.440	-27.968	15.453	1.00	34.42	L	O
ATOM	4212	N	LYS	148	88.495	-28.877	17.501	1.00	28.86	L	N
ATOM	4213	CA	LYS	148	87.609	-29.958	17.147	1.00	29.96	L	C
ATOM	4214	CB	LYS	148	88.431	-31.196	16.787	1.00	35.94	L	C
ATOM	4215	CG	LYS	148	88.353	-31.585	15.320	1.00	39.31	L	C
ATOM	4216	CD	LYS	148	89.726	-31.865	14.715	1.00	45.24	L	C
ATOM	4217	CE	LYS	148	90.421	-33.078	15.337	1.00	45.54	L	C
ATOM	4218	NZ	LYS	148	91.826	-33.267	14.818	1.00	44.96	L	N
ATOM	4219	C	LYS	148	86.712	-30.227	18.340	1.00	32.40	L	C
ATOM	4220	O	LYS	148	87.197	-30.505	19.438	1.00	31.51	L	O
ATOM	4221	N	VAL	149	85.404	-30.124	18.118	1.00	22.85	L	N
ATOM	4222	CA	VAL	149	84.406	-30.352	19.161	1.00	20.04	L	C
ATOM	4223	CB	VAL	149	83.453	-29.167	19.269	1.00	1.90	L	C
ATOM	4224	CG1	VAL	149	82.408	-29.440	20.364	1.00	1.90	L	C
ATOM	4225	CG2	VAL	149	84.242	-27.899	19.563	1.00	1.90	L	C
ATOM	4226	C	VAL	149	83.580	-31.605	18.862	1.00	23.24	L	C
ATOM	4227	O	VAL	149	82.835	-31.642	17.883	1.00	24.43	L	O
ATOM	4228	N	ASP	150	83.679	-32.611	19.731	1.00	18.00	L	N
ATOM	4229	CA	ASP	150	82.974	-33.863	19.502	1.00	21.30	L	C
ATOM	4230	CB	ASP	150	81.464	-33.661	19.459	1.00	45.33	L	C
ATOM	4231	CG	ASP	150	80.862	-33.543	20.840	1.00	50.39	L	C
ATOM	4232	OD1	ASP	150	81.334	-34.248	21.760	1.00	51.76	L	O
ATOM	4233	OD2	ASP	150	79.910	-32.756	21.007	1.00	53.67	L	O
ATOM	4234	C	ASP	150	83.487	-34.293	18.152	1.00	22.51	L	C

Fig. 19: A-59

ATOM	4235	O	ASP	150	82.737	-34.683	17.268	1.00	23.76	L	O
ATOM	4236	N	ASN	151	84.800	-34.161	18.007	1.00	36.79	L	N
ATOM	4237	CA	ASN	151	85.493	-34.524	16.789	1.00	39.62	L	C
ATOM	4238	CB	ASN	151	85.425	-36.041	16.614	1.00	29.22	L	C
ATOM	4239	CG	ASN	151	86.220	-36.776	17.683	1.00	38.58	L	C
ATOM	4240	OD1	ASN	151	87.450	-36.736	17.686	1.00	42.16	L	O
ATOM	4241	ND2	ASN	151	85.522	-37.430	18.608	1.00	39.63	L	N
ATOM	4242	C	ASN	151	84.985	-33.778	15.557	1.00	37.90	L	C
ATOM	4243	O	ASN	151	85.224	-34.183	14.425	1.00	41.98	L	O
ATOM	4244	N	ALA	152	84.293	-32.672	15.793	1.00	26.76	L	N
ATOM	4245	CA	ALA	152	83.802	-31.838	14.703	1.00	29.16	L	C
ATOM	4246	CB	ALA	152	82.421	-31.261	15.034	1.00	1.87	L	C
ATOM	4247	C	ALA	152	84.801	-30.698	14.501	1.00	30.47	L	C
ATOM	4248	O	ALA	152	84.940	-29.813	15.355	1.00	32.16	L	O
ATOM	4249	N	LEU	153	85.502	-30.724	13.375	1.00	37.66	L	N
ATOM	4250	CA	LEU	153	86.470	-29.684	13.073	1.00	38.47	L	C
ATOM	4251	CB	LEU	153	87.021	-29.896	11.656	1.00	33.69	L	C
ATOM	4252	CG	LEU	153	87.944	-28.864	11.005	1.00	36.76	L	C
ATOM	4253	CD1	LEU	153	87.112	-27.705	10.466	1.00	35.54	L	C
ATOM	4254	CD2	LEU	153	88.999	-28.394	12.004	1.00	35.80	L	C
ATOM	4255	C	LEU	153	85.796	-28.315	13.206	1.00	37.05	L	C
ATOM	4256	O	LEU	153	84.632	-28.150	12.870	1.00	37.53	L	O
ATOM	4257	N	GLN	154	86.524	-27.342	13.732	1.00	42.87	L	N
ATOM	4258	CA	GLN	154	85.984	-26.006	13.885	1.00	41.76	L	C
ATOM	4259	CB	GLN	154	86.346	-25.438	15.255	1.00	24.84	L	C
ATOM	4260	CG	GLN	154	85.653	-26.133	16.403	1.00	25.94	L	C
ATOM	4261	CD	GLN	154	84.146	-26.162	16.225	1.00	28.42	L	C
ATOM	4262	OE1	GLN	154	83.495	-25.115	16.127	1.00	30.98	L	O
ATOM	4263	NE2	GLN	154	83.584	-27.365	16.176	1.00	27.76	L	N
ATOM	4264	C	GLN	154	86.574	-25.139	12.793	1.00	40.20	L	C
ATOM	4265	O	GLN	154	87.702	-25.363	12.350	1.00	39.24	L	O
ATOM	4266	N	SER	155	85.813	-24.146	12.359	1.00	42.27	L	N
ATOM	4267	CA	SER	155	86.269	-23.257	11.306	1.00	44.34	L	C
ATOM	4268	CB	SER	155	85.770	-23.768	9.952	1.00	47.84	L	C
ATOM	4269	OG	SER	155	86.319	-23.035	8.872	1.00	49.98	L	O
ATOM	4270	C	SER	155	85.693	-21.888	11.600	1.00	40.94	L	C
ATOM	4271	O	SER	155	86.208	-20.864	11.160	1.00	39.18	L	O
ATOM	4272	N	GLY	156	84.621	-21.877	12.374	1.00	21.85	L	N
ATOM	4273	CA	GLY	156	83.986	-20.619	12.702	1.00	22.33	L	C
ATOM	4274	C	GLY	156	84.732	-19.585	13.544	1.00	22.19	L	C
ATOM	4275	O	GLY	156	85.518	-18.793	13.032	1.00	19.16	L	O
ATOM	4276	N	ASN	157	84.484	-19.595	14.850	1.00	39.06	L	N
ATOM	4277	CA	ASN	157	85.088	-18.595	15.697	1.00	40.50	L	C
ATOM	4278	CB	ASN	157	83.992	-17.700	16.281	1.00	106.22	L	C
ATOM	4279	CG	ASN	157	83.201	-16.977	15.200	1.00	109.22	L	C
ATOM	4280	OD1	ASN	157	83.779	-16.402	14.277	1.00	109.54	L	O
ATOM	4281	ND2	ASN	157	81.874	-16.999	15.313	1.00	114.95	L	N
ATOM	4282	C	ASN	157	86.059	-18.997	16.790	1.00	41.01	L	C
ATOM	4283	O	ASN	157	85.713	-19.566	17.827	1.00	40.41	L	O
ATOM	4284	N	SER	158	87.299	-18.635	16.520	1.00	42.44	L	N
ATOM	4285	CA	SER	158	88.409	-18.862	17.405	1.00	35.84	L	C
ATOM	4286	CB	SER	158	89.078	-20.173	17.047	1.00	10.55	L	C
ATOM	4287	OG	SER	158	89.643	-20.069	15.757	1.00	10.12	L	O
ATOM	4288	C	SER	158	89.326	-17.691	17.059	1.00	34.29	L	C
ATOM	4289	O	SER	158	89.197	-17.092	15.992	1.00	32.27	L	O
ATOM	4290	N	GLN	159	90.238	-17.345	17.952	1.00	34.35	L	N
ATOM	4291	CA	GLN	159	91.133	-16.250	17.652	1.00	31.73	L	C
ATOM	4292	CB	GLN	159	90.538	-14.932	18.130	1.00	20.18	L	C
ATOM	4293	CG	GLN	159	89.399	-14.413	17.266	1.00	21.46	L	C
ATOM	4294	CD	GLN	159	89.053	-12.981	17.608	1.00	25.67	L	C
ATOM	4295	OE1	GLN	159	88.796	-12.658	18.762	1.00	28.88	L	O
ATOM	4296	NE2	GLN	159	89.051	-12.114	16.606	1.00	25.13	L	N
ATOM	4297	C	GLN	159	92.502	-16.452	18.255	1.00	29.74	L	C
ATOM	4298	O	GLN	159	92.647	-16.711	19.449	1.00	28.24	L	O
ATOM	4299	N	GLU	160	93.514	-16.327	17.414	1.00	31.36	L	N
ATOM	4300	CA	GLU	160	94.872	-16.510	17.865	1.00	24.49	L	C
ATOM	4301	CB	GLU	160	95.646	-17.316	16.834	1.00	58.94	L	C
ATOM	4302	CG	GLU	160	94.977	-18.617	16.476	1.00	59.06	L	C
ATOM	4303	CD	GLU	160	95.890	-19.506	15.678	1.00	67.10	L	C
ATOM	4304	OE1	GLU	160	95.463	-20.619	15.285	1.00	71.37	L	O
ATOM	4305	OE2	GLU	160	97.043	-19.078	15.452	1.00	65.02	L	O
ATOM	4306	C	GLU	160	95.591	-15.199	18.140	1.00	20.89	L	C
ATOM	4307	O	GLU	160	95.211	-14.141	17.654	1.00	14.39	L	O

Fig. 19: A-60

ATOM	4308	N	SER	161	96.639	-15.293	18.941	1.00	19.35	L	N
ATOM	4309	CA	SER	161	97.456	-14.151	19.310	1.00	16.36	L	C
ATOM	4310	CB	SER	161	96.953	-13.486	20.597	1.00	26.12	L	C
ATOM	4311	OG	SER	161	97.935	-12.623	21.157	1.00	26.54	L	O
ATOM	4312	C	SER	161	98.811	-14.751	19.556	1.00	11.36	L	C
ATOM	4313	O	SER	161	98.934	-15.799	20.191	1.00	11.86	L	O
ATOM	4314	N	VAL	162	99.833	-14.086	19.053	1.00	21.19	L	N
ATOM	4315	CA	VAL	162	101.170	-14.592	19.215	1.00	22.81	L	C
ATOM	4316	CB	VAL	162	101.764	-14.965	17.832	1.00	29.37	L	C
ATOM	4317	CG1	VAL	162	101.449	-13.865	16.834	1.00	33.68	L	C
ATOM	4318	CG2	VAL	162	103.270	-15.178	17.933	1.00	33.85	L	C
ATOM	4319	C	VAL	162	101.997	-13.524	19.877	1.00	25.31	L	C
ATOM	4320	O	VAL	162	101.835	-12.349	19.566	1.00	32.55	L	O
ATOM	4321	N	THR	163	102.861	-13.928	20.805	1.00	22.97	L	N
ATOM	4322	CA	THR	163	103.735	-12.975	21.475	1.00	21.36	L	C
ATOM	4323	CB	THR	163	104.424	-13.567	22.719	1.00	4.31	L	C
ATOM	4324	OG1	THR	163	105.214	-14.705	22.342	1.00	10.67	L	O
ATOM	4325	CG2	THR	163	103.411	-13.966	23.748	1.00	4.70	L	C
ATOM	4326	C	THR	163	104.842	-12.550	20.520	1.00	20.43	L	C
ATOM	4327	O	THR	163	104.880	-12.951	19.350	1.00	20.01	L	O
ATOM	4328	N	GLU	164	105.741	-11.722	21.022	1.00	16.64	L	N
ATOM	4329	CA	GLU	164	106.844	-11.283	20.211	1.00	24.33	L	C
ATOM	4330	CB	GLU	164	107.182	-9.828	20.515	1.00	53.60	L	C
ATOM	4331	CG	GLU	164	107.982	-9.187	19.415	1.00	64.34	L	C
ATOM	4332	CD	GLU	164	107.202	-9.144	18.126	1.00	70.19	L	C
ATOM	4333	OE1	GLU	164	106.337	-8.252	17.994	1.00	69.97	L	O
ATOM	4334	OE2	GLU	164	107.442	-10.011	17.257	1.00	73.61	L	O
ATOM	4335	C	GLU	164	107.989	-12.190	20.635	1.00	22.81	L	C
ATOM	4336	O	GLU	164	107.990	-12.697	21.765	1.00	25.48	L	O
ATOM	4337	N	GLN	165	108.948	-12.407	19.734	1.00	26.35	L	N
ATOM	4338	CA	GLN	165	110.100	-13.261	20.018	1.00	31.24	L	C
ATOM	4339	CB	GLN	165	111.181	-13.024	18.967	1.00	24.53	L	C
ATOM	4340	CG	GLN	165	111.927	-14.274	18.584	1.00	20.02	L	C
ATOM	4341	CD	GLN	165	112.911	-14.054	17.454	1.00	22.62	L	C
ATOM	4342	OE1	GLN	165	113.487	-15.005	16.930	1.00	23.83	L	O
ATOM	4343	NE2	GLN	165	113.118	-12.794	17.080	1.00	19.11	L	N
ATOM	4344	C	GLN	165	110.633	-12.941	21.412	1.00	35.11	L	C
ATOM	4345	O	GLN	165	110.857	-11.783	21.739	1.00	31.98	L	O
ATOM	4346	N	ASP	166	110.826	-13.963	22.236	1.00	20.85	L	N
ATOM	4347	CA	ASP	166	111.311	-13.741	23.592	1.00	27.22	L	C
ATOM	4348	CB	ASP	166	111.206	-15.030	24.402	1.00	40.40	L	C
ATOM	4349	CG	ASP	166	111.513	-14.813	25.872	1.00	48.39	L	C
ATOM	4350	OD1	ASP	166	112.706	-14.808	26.246	1.00	51.89	L	O
ATOM	4351	OD2	ASP	166	110.555	-14.631	26.655	1.00	52.06	L	O
ATOM	4352	C	ASP	166	112.741	-13.205	23.656	1.00	29.80	L	C
ATOM	4353	O	ASP	166	113.659	-13.787	23.079	1.00	33.62	L	O
ATOM	4354	N	SER	167	112.923	-12.098	24.371	1.00	40.62	L	N
ATOM	4355	CA	SER	167	114.238	-11.463	24.521	1.00	38.35	L	C
ATOM	4356	CB	SER	167	114.089	-10.092	25.191	1.00	42.38	L	C
ATOM	4357	OG	SER	167	113.564	-10.221	26.499	1.00	53.10	L	O
ATOM	4358	C	SER	167	115.229	-12.312	25.325	1.00	40.21	L	C
ATOM	4359	O	SER	167	116.373	-11.913	25.544	1.00	45.86	L	O
ATOM	4360	N	LYS	168	114.777	-13.475	25.782	1.00	39.00	L	N
ATOM	4361	CA	LYS	168	115.637	-14.383	26.527	1.00	40.59	L	C
ATOM	4362	CB	LYS	168	114.968	-14.809	27.837	1.00	73.78	L	C
ATOM	4363	CG	LYS	168	115.002	-13.726	28.916	1.00	80.02	L	C
ATOM	4364	CD	LYS	168	114.141	-12.523	28.554	1.00	89.23	L	C
ATOM	4365	CE	LYS	168	112.663	-12.805	28.778	1.00	96.32	L	C
ATOM	4366	NZ	LYS	168	112.355	-13.017	30.222	1.00	95.77	L	N
ATOM	4367	C	LYS	168	115.959	-15.597	25.650	1.00	39.39	L	C
ATOM	4368	O	LYS	168	117.046	-15.671	25.077	1.00	43.53	L	O
ATOM	4369	N	ASP	169	115.011	-16.522	25.506	1.00	18.93	L	N
ATOM	4370	CA	ASP	169	115.240	-17.716	24.686	1.00	15.08	L	C
ATOM	4371	CB	ASP	169	114.476	-18.913	25.262	1.00	29.81	L	C
ATOM	4372	CG	ASP	169	112.992	-18.648	25.407	1.00	32.60	L	C
ATOM	4373	OD1	ASP	169	112.397	-18.049	24.488	1.00	27.93	L	O
ATOM	4374	OD2	ASP	169	112.415	-19.054	26.441	1.00	29.85	L	O
ATOM	4375	C	ASP	169	114.914	-17.596	23.193	1.00	15.61	L	C
ATOM	4376	O	ASP	169	115.038	-18.571	22.459	1.00	9.73	L	O
ATOM	4377	N	SER	170	114.490	-16.418	22.747	1.00	28.98	L	N
ATOM	4378	CA	SER	170	114.170	-16.202	21.331	1.00	26.94	L	C
ATOM	4379	CB	SER	170	115.401	-16.487	20.433	1.00	15.64	L	C
ATOM	4380	OG	SER	170	116.466	-15.560	20.636	1.00	17.90	L	O

Fig. 19: A-61

ATOM	4381	C	SER	170	112.995	-17.042	20.825	1.00	25.42	L	C
ATOM	4382	O	SER	170	112.916	-17.345	19.636	1.00	25.18	L	O
ATOM	4383	N	THR	171	112.071	-17.411	21.702	1.00	22.07	L	N
ATOM	4384	CA	THR	171	110.946	-18.222	21.247	1.00	22.16	L	C
ATOM	4385	CB	THR	171	110.658	-19.406	22.212	1.00	16.53	L	C
ATOM	4386	OG1	THR	171	110.127	-18.911	23.452	1.00	18.93	L	O
ATOM	4387	CG2	THR	171	111.939	-20.191	22.471	1.00	18.13	L	C
ATOM	4388	C	THR	171	109.657	-17.437	21.064	1.00	26.03	L	C
ATOM	4389	O	THR	171	109.601	-16.235	21.327	1.00	31.48	L	O
ATOM	4390	N	TYR	172	108.633	-18.147	20.596	1.00	7.82	L	N
ATOM	4391	CA	TYR	172	107.297	-17.600	20.373	1.00	6.45	L	C
ATOM	4392	CB	TYR	172	106.934	-17.706	18.894	1.00	43.65	L	C
ATOM	4393	CG	TYR	172	107.809	-16.890	17.974	1.00	37.38	L	C
ATOM	4394	CD1	TYR	172	107.652	-15.507	17.865	1.00	32.97	L	C
ATOM	4395	CE1	TYR	172	108.438	-14.759	16.977	1.00	32.97	L	C
ATOM	4396	CD2	TYR	172	108.776	-17.508	17.181	1.00	37.97	L	C
ATOM	4397	CE2	TYR	172	109.565	-16.774	16.296	1.00	34.76	L	C
ATOM	4398	CZ	TYR	172	109.391	-15.405	16.194	1.00	32.97	L	C
ATOM	4399	OH	TYR	172	110.163	-14.703	15.294	1.00	32.97	L	O
ATOM	4400	C	TYR	172	106.255	-18.364	21.212	1.00	6.45	L	C
ATOM	4401	O	TYR	172	106.431	-19.539	21.528	1.00	9.78	L	O
ATOM	4402	N	SER	173	105.183	-17.687	21.600	1.00	23.67	L	N
ATOM	4403	CA	SER	173	104.123	-18.323	22.370	1.00	25.48	L	C
ATOM	4404	CB	SER	173	104.165	-17.902	23.834	1.00	31.18	L	C
ATOM	4405	OG	SER	173	105.281	-18.492	24.468	1.00	25.15	L	O
ATOM	4406	C	SER	173	102.836	-17.886	21.728	1.00	26.94	L	C
ATOM	4407	O	SER	173	102.611	-16.699	21.473	1.00	27.36	L	O
ATOM	4408	N	LEU	174	101.980	-18.857	21.474	1.00	22.39	L	N
ATOM	4409	CA	LEU	174	100.734	-18.593	20.791	1.00	25.49	L	C
ATOM	4410	CB	LEU	174	100.836	-19.238	19.399	1.00	22.33	L	C
ATOM	4411	CG	LEU	174	99.682	-19.165	18.422	1.00	13.39	L	C
ATOM	4412	CD1	LEU	174	100.207	-19.296	17.013	1.00	17.21	L	C
ATOM	4413	CD2	LEU	174	98.663	-20.257	18.769	1.00	10.23	L	C
ATOM	4414	C	LEU	174	99.510	-19.075	21.562	1.00	27.64	L	C
ATOM	4415	O	LEU	174	99.542	-20.111	22.229	1.00	30.82	L	O
ATOM	4416	N	SER	175	98.433	-18.306	21.470	1.00	22.56	L	N
ATOM	4417	CA	SER	175	97.200	-18.651	22.162	1.00	25.61	L	C
ATOM	4418	CB	SER	175	96.913	-17.644	23.292	1.00	28.99	L	C
ATOM	4419	OG	SER	175	96.487	-16.378	22.794	1.00	32.45	L	O
ATOM	4420	C	SER	175	96.009	-18.693	21.214	1.00	29.48	L	C
ATOM	4421	O	SER	175	95.733	-17.718	20.511	1.00	30.81	L	O
ATOM	4422	N	SER	176	95.316	-19.829	21.181	1.00	31.99	L	N
ATOM	4423	CA	SER	176	94.125	-19.957	20.346	1.00	32.77	L	C
ATOM	4424	CB	SER	176	94.154	-21.247	19.514	1.00	10.71	L	C
ATOM	4425	OG	SER	176	93.247	-21.176	18.421	1.00	10.34	L	O
ATOM	4426	C	SER	176	92.985	-19.991	21.352	1.00	29.41	L	C
ATOM	4427	O	SER	176	93.042	-20.712	22.350	1.00	29.56	L	O
ATOM	4428	N	THR	177	91.963	-19.183	21.118	1.00	38.41	L	N
ATOM	4429	CA	THR	177	90.846	-19.136	22.042	1.00	37.60	L	C
ATOM	4430	CB	THR	177	90.742	-17.741	22.706	1.00	7.23	L	C
ATOM	4431	OG1	THR	177	92.000	-17.399	23.318	1.00	10.12	L	O
ATOM	4432	CG2	THR	177	89.631	-17.728	23.773	1.00	2.94	L	C
ATOM	4433	C	THR	177	89.551	-19.455	21.311	1.00	35.94	L	C
ATOM	4434	O	THR	177	89.133	-18.709	20.425	1.00	37.02	L	O
ATOM	4435	N	LEU	178	88.941	-20.584	21.669	1.00	33.89	L	N
ATOM	4436	CA	LEU	178	87.682	-21.015	21.072	1.00	32.44	L	C
ATOM	4437	CB	LEU	178	87.587	-22.542	21.069	1.00	26.21	L	C
ATOM	4438	CG	LEU	178	86.291	-23.170	20.539	1.00	27.24	L	C
ATOM	4439	CD1	LEU	178	86.077	-22.824	19.070	1.00	27.77	L	C
ATOM	4440	CD2	LEU	178	86.367	-24.683	20.730	1.00	15.35	L	C
ATOM	4441	C	LEU	178	86.552	-20.412	21.901	1.00	32.70	L	C
ATOM	4442	O	LEU	178	86.476	-20.589	23.120	1.00	29.14	L	O
ATOM	4443	N	THR	179	85.669	-19.683	21.244	1.00	21.74	L	N
ATOM	4444	CA	THR	179	84.598	-19.059	21.983	1.00	27.65	L	C
ATOM	4445	CB	THR	179	84.804	-17.547	22.031	1.00	33.66	L	C
ATOM	4446	OG1	THR	179	83.651	-16.929	22.608	1.00	34.46	L	O
ATOM	4447	CG2	THR	179	85.056	-17.005	20.633	1.00	33.07	L	C
ATOM	4448	C	THR	179	83.223	-19.377	21.430	1.00	32.00	L	C
ATOM	4449	O	THR	179	82.928	-19.104	20.271	1.00	32.92	L	O
ATOM	4450	N	LEU	180	82.398	-19.981	22.278	1.00	32.07	L	N
ATOM	4451	CA	LEU	180	81.035	-20.349	21.922	1.00	33.73	L	C
ATOM	4452	CB	LEU	180	80.936	-21.831	21.528	1.00	30.85	L	C
ATOM	4453	CG	LEU	180	82.059	-22.804	21.881	1.00	33.56	L	C

Fig. 19: A-62

ATOM	4454	CD1	LEU	180	82.518	-22.589	23.309	1.00	36.03	L	C
ATOM	4455	CD2	LEU	180	81.552	-24.220	21.697	1.00	34.15	L	C
ATOM	4456	C	LEU	180	80.093	-20.062	23.084	1.00	37.58	L	C
ATOM	4457	O	LEU	180	80.526	-19.899	24.229	1.00	37.41	L	O
ATOM	4458	N	SER	181	78.801	-20.000	22.772	1.00	28.10	L	N
ATOM	4459	CA	SER	181	77.778	-19.711	23.770	1.00	31.26	L	C
ATOM	4460	CB	SER	181	76.433	-19.537	23.087	1.00	22.13	L	C
ATOM	4461	OG	SER	181	76.019	-20.764	22.513	1.00	25.39	L	O
ATOM	4462	C	SER	181	77.655	-20.802	24.815	1.00	33.74	L	C
ATOM	4463	O	SER	181	77.917	-21.978	24.533	1.00	33.98	L	O
ATOM	4464	N	LYS	182	77.247	-20.402	26.019	1.00	29.35	L	N
ATOM	4465	CA	LYS	182	77.060	-21.339	27.120	1.00	30.58	L	C
ATOM	4466	CB	LYS	182	76.375	-20.647	28.307	1.00	27.86	L	C
ATOM	4467	CG	LYS	182	76.341	-21.446	29.627	1.00	29.57	L	C
ATOM	4468	CD	LYS	182	74.912	-21.752	30.107	1.00	31.50	L	C
ATOM	4469	CE	LYS	182	74.863	-22.027	31.619	1.00	34.15	L	C
ATOM	4470	NZ	LYS	182	73.622	-22.756	32.099	1.00	38.40	L	N
ATOM	4471	C	LYS	182	76.167	-22.438	26.573	1.00	28.49	L	C
ATOM	4472	O	LYS	182	76.358	-23.618	26.878	1.00	20.36	L	O
ATOM	4473	N	ALA	183	75.206	-22.030	25.743	1.00	42.67	L	N
ATOM	4474	CA	ALA	183	74.252	-22.937	25.108	1.00	43.14	L	C
ATOM	4475	CB	ALA	183	73.319	-22.150	24.203	1.00	20.20	L	C
ATOM	4476	C	ALA	183	74.929	-24.053	24.313	1.00	42.26	L	C
ATOM	4477	O	ALA	183	74.645	-25.229	24.531	1.00	43.50	L	O
ATOM	4478	N	ASP	184	75.820	-23.691	23.395	1.00	37.65	L	N
ATOM	4479	CA	ASP	184	76.523	-24.692	22.587	1.00	39.98	L	C
ATOM	4480	CB	ASP	184	77.271	-24.023	21.434	1.00	60.24	L	C
ATOM	4481	CG	ASP	184	76.362	-23.219	20.545	1.00	66.97	L	C
ATOM	4482	OD1	ASP	184	75.360	-23.784	20.055	1.00	70.29	L	O
ATOM	4483	OD2	ASP	184	76.653	-22.023	20.335	1.00	70.50	L	O
ATOM	4484	C	ASP	184	77.519	-25.525	23.395	1.00	38.91	L	C
ATOM	4485	O	ASP	184	77.531	-26.753	23.308	1.00	36.50	L	O
ATOM	4486	N	TYR	185	78.362	-24.849	24.167	1.00	50.74	L	N
ATOM	4487	CA	TYR	185	79.352	-25.544	24.972	1.00	51.74	L	C
ATOM	4488	CB	TYR	185	80.011	-24.589	25.965	1.00	23.76	L	C
ATOM	4489	CG	TYR	185	81.104	-25.256	26.771	1.00	21.08	L	C
ATOM	4490	CD1	TYR	185	82.328	-25.552	26.192	1.00	16.43	L	C
ATOM	4491	CE1	TYR	185	83.332	-26.186	26.915	1.00	15.99	L	C
ATOM	4492	CD2	TYR	185	80.905	-25.613	28.104	1.00	17.64	L	C
ATOM	4493	CE2	TYR	185	81.902	-26.244	28.839	1.00	14.97	L	C
ATOM	4494	CZ	TYR	185	83.118	-26.526	28.235	1.00	14.93	L	C
ATOM	4495	OH	TYR	185	84.141	-27.119	28.944	1.00	16.56	L	O
ATOM	4496	C	TYR	185	78.729	-26.695	25.756	1.00	52.88	L	C
ATOM	4497	O	TYR	185	79.364	-27.728	25.978	1.00	52.42	L	O
ATOM	4498	N	GLU	186	77.484	-26.505	26.177	1.00	52.93	L	N
ATOM	4499	CA	GLU	186	76.787	-27.509	26.965	1.00	54.71	L	C
ATOM	4500	CB	GLU	186	75.643	-26.870	27.748	1.00	28.62	L	C
ATOM	4501	CG	GLU	186	76.067	-26.060	28.955	1.00	35.11	L	C
ATOM	4502	CD	GLU	186	74.876	-25.493	29.702	1.00	38.66	L	C
ATOM	4503	OE1	GLU	186	75.089	-24.850	30.746	1.00	41.21	L	O
ATOM	4504	OE2	GLU	186	73.725	-25.689	29.245	1.00	36.89	L	O
ATOM	4505	C	GLU	186	76.242	-28.694	26.190	1.00	52.40	L	C
ATOM	4506	O	GLU	186	76.029	-29.755	26.769	1.00	48.88	L	O
ATOM	4507	N	LYS	187	76.004	-28.538	24.895	1.00	35.74	L	N
ATOM	4508	CA	LYS	187	75.472	-29.662	24.147	1.00	37.64	L	C
ATOM	4509	CB	LYS	187	74.507	-29.173	23.057	1.00	53.22	L	C
ATOM	4510	CG	LYS	187	75.138	-28.512	21.849	1.00	54.27	L	C
ATOM	4511	CD	LYS	187	74.055	-27.941	20.930	1.00	53.80	L	C
ATOM	4512	CE	LYS	187	74.665	-27.203	19.740	1.00	49.76	L	C
ATOM	4513	NZ	LYS	187	73.707	-26.272	19.069	1.00	48.24	L	N
ATOM	4514	C	LYS	187	76.568	-30.553	23.549	1.00	36.73	L	C
ATOM	4515	O	LYS	187	76.287	-31.436	22.732	1.00	37.96	L	O
ATOM	4516	N	HIS	188	77.813	-30.339	23.972	1.00	23.77	L	N
ATOM	4517	CA	HIS	188	78.934	-31.124	23.468	1.00	21.36	L	C
ATOM	4518	CB	HIS	188	79.811	-30.257	22.562	1.00	41.13	L	C
ATOM	4519	CG	HIS	188	79.099	-29.774	21.338	1.00	42.53	L	C
ATOM	4520	CD2	HIS	188	78.800	-28.524	20.913	1.00	44.25	L	C
ATOM	4521	ND1	HIS	188	78.562	-30.633	20.405	1.00	41.45	L	N
ATOM	4522	CE1	HIS	188	77.961	-29.935	19.458	1.00	45.45	L	C
ATOM	4523	NE2	HIS	188	78.090	-28.652	19.743	1.00	43.75	L	N
ATOM	4524	C	HIS	188	79.743	-31.715	24.610	1.00	19.53	L	C
ATOM	4525	O	HIS	188	79.648	-31.253	25.751	1.00	19.70	L	O
ATOM	4526	N	LYS	189	80.521	-32.747	24.294	1.00	33.83	L	N

Fig. 19: A-63

ATOM	4527	CA	LYS	189	81.334	-33.445	25.281	1.00	33.86	L	C
ATOM	4528	CB	LYS	189	81.136	-34.957	25.152	1.00	43.10	L	C
ATOM	4529	CG	LYS	189	79.898	-35.516	25.815	1.00	47.03	L	C
ATOM	4530	CD	LYS	189	79.974	-37.041	25.887	1.00	53.76	L	C
ATOM	4531	CE	LYS	189	79.997	-37.680	24.505	1.00	59.30	L	C
ATOM	4532	NZ	LYS	189	78.694	-37.545	23.794	1.00	59.64	L	N
ATOM	4533	C	LYS	189	82.831	-33.155	25.201	1.00	33.18	L	C
ATOM	4534	O	LYS	189	83.435	-32.657	26.155	1.00	36.85	L	O
ATOM	4535	N	VAL	190	83.435	-33.482	24.069	1.00	39.67	L	N
ATOM	4536	CA	VAL	190	84.860	-33.260	23.916	1.00	35.33	L	C
ATOM	4537	CB	VAL	190	85.516	-34.439	23.214	1.00	33.71	L	C
ATOM	4538	CG1	VAL	190	85.356	-35.648	24.059	1.00	26.86	L	C
ATOM	4539	CG2	VAL	190	84.880	-34.657	21.855	1.00	36.79	L	C
ATOM	4540	C	VAL	190	85.249	-31.992	23.170	1.00	35.17	L	C
ATOM	4541	O	VAL	190	84.656	-31.641	22.141	1.00	36.62	L	O
ATOM	4542	N	TYR	191	86.256	-31.319	23.718	1.00	27.65	L	N
ATOM	4543	CA	TYR	191	86.811	-30.105	23.152	1.00	26.85	L	C
ATOM	4544	CB	TYR	191	86.554	-28.934	24.095	1.00	16.61	L	C
ATOM	4545	CG	TYR	191	85.109	-28.475	24.056	1.00	23.44	L	C
ATOM	4546	CD1	TYR	191	84.654	-27.650	23.030	1.00	27.57	L	C
ATOM	4547	CE1	TYR	191	83.322	-27.300	22.929	1.00	29.06	L	C
ATOM	4548	CD2	TYR	191	84.178	-28.937	24.991	1.00	24.37	L	C
ATOM	4549	CE2	TYR	191	82.838	-28.592	24.894	1.00	25.88	L	C
ATOM	4550	CZ	TYR	191	82.419	-27.773	23.859	1.00	28.22	L	C
ATOM	4551	OH	TYR	191	81.097	-27.419	23.745	1.00	30.91	L	O
ATOM	4552	C	TYR	191	88.295	-30.381	23.010	1.00	28.07	L	C
ATOM	4553	O	TYR	191	88.946	-30.821	23.960	1.00	29.13	L	O
ATOM	4554	N	ALA	192	88.837	-30.159	21.822	1.00	17.93	L	N
ATOM	4555	CA	ALA	192	90.246	-30.425	21.621	1.00	13.94	L	C
ATOM	4556	CB	ALA	192	90.424	-31.850	21.160	1.00	12.32	L	C
ATOM	4557	C	ALA	192	90.921	-29.489	20.640	1.00	14.27	L	C
ATOM	4558	O	ALA	192	90.271	-28.885	19.784	1.00	14.89	L	O
ATOM	4559	N	CYS	193	92.234	-29.362	20.787	1.00	20.91	L	N
ATOM	4560	CA	CYS	193	93.015	-28.544	19.883	1.00	19.50	L	C
ATOM	4561	C	CYS	193	94.268	-29.301	19.502	1.00	17.29	L	C
ATOM	4562	O	CYS	193	95.057	-29.729	20.352	1.00	15.43	L	O
ATOM	4563	CB	CYS	193	93.361	-27.183	20.490	1.00	44.80	L	C
ATOM	4564	SG	CYS	193	94.412	-27.194	21.962	1.00	52.58	L	S
ATOM	4565	N	GLU	194	94.411	-29.480	18.195	1.00	24.90	L	N
ATOM	4566	CA	GLU	194	95.522	-30.193	17.600	1.00	25.90	L	C
ATOM	4567	CB	GLU	194	95.004	-30.956	16.384	1.00	66.26	L	C
ATOM	4568	CG	GLU	194	95.979	-31.887	15.718	1.00	77.97	L	C
ATOM	4569	CD	GLU	194	95.392	-32.479	14.461	1.00	83.25	L	C
ATOM	4570	OE1	GLU	194	95.276	-31.738	13.462	1.00	80.00	L	O
ATOM	4571	OE2	GLU	194	95.028	-33.674	14.477	1.00	89.05	L	O
ATOM	4572	C	GLU	194	96.546	-29.158	17.175	1.00	25.27	L	C
ATOM	4573	O	GLU	194	96.204	-28.171	16.538	1.00	23.30	L	O
ATOM	4574	N	VAL	195	97.798	-29.373	17.537	1.00	38.95	L	N
ATOM	4575	CA	VAL	195	98.850	-28.443	17.168	1.00	34.83	L	C
ATOM	4576	CB	VAL	195	99.715	-28.048	18.403	1.00	15.18	L	C
ATOM	4577	CG1	VAL	195	100.911	-27.210	17.971	1.00	11.26	L	C
ATOM	4578	CG2	VAL	195	98.869	-27.268	19.395	1.00	16.15	L	C
ATOM	4579	C	VAL	195	99.730	-29.115	16.126	1.00	34.14	L	C
ATOM	4580	O	VAL	195	99.964	-30.319	16.180	1.00	32.63	L	O
ATOM	4581	N	THR	196	100.190	-28.340	15.157	1.00	43.12	L	N
ATOM	4582	CA	THR	196	101.063	-28.876	14.135	1.00	42.44	L	C
ATOM	4583	CB	THR	196	100.411	-28.867	12.764	1.00	26.65	L	C
ATOM	4584	OG1	THR	196	99.001	-28.673	12.909	1.00	36.35	L	O
ATOM	4585	CG2	THR	196	100.671	-30.180	12.067	1.00	28.65	L	C
ATOM	4586	C	THR	196	102.233	-27.927	14.121	1.00	42.04	L	C
ATOM	4587	O	THR	196	102.049	-26.710	14.053	1.00	37.83	L	O
ATOM	4588	N	HIS	197	103.437	-28.479	14.186	1.00	32.41	L	N
ATOM	4589	CA	HIS	197	104.623	-27.653	14.217	1.00	27.77	L	C
ATOM	4590	CB	HIS	197	104.867	-27.172	15.651	1.00	21.71	L	C
ATOM	4591	CG	HIS	197	105.914	-26.113	15.762	1.00	23.27	L	C
ATOM	4592	CD2	HIS	197	105.817	-24.761	15.753	1.00	17.64	L	C
ATOM	4593	ND1	HIS	197	107.257	-26.402	15.868	1.00	25.39	L	N
ATOM	4594	CE1	HIS	197	107.944	-25.274	15.923	1.00	22.67	L	C
ATOM	4595	NE2	HIS	197	107.093	-24.264	15.854	1.00	24.76	L	N
ATOM	4596	C	HIS	197	105.825	-28.417	13.708	1.00	24.98	L	C
ATOM	4597	O	HIS	197	105.932	-29.629	13.885	1.00	29.24	L	O
ATOM	4598	N	GLN	198	106.728	-27.687	13.070	1.00	28.46	L	N
ATOM	4599	CA	GLN	198	107.944	-28.252	12.515	1.00	26.49	L	C

Fig. 19: A-64

ATOM	4600	CB	GLN	198	108.840	-27.114	12.048	1.00	34.42	L	C
ATOM	4601	CG	GLN	198	110.091	-27.549	11.333	1.00	36.17	L	C
ATOM	4602	CD	GLN	198	110.868	-26.365	10.821	1.00	48.65	L	C
ATOM	4603	OE1	GLN	198	110.286	-25.414	10.299	1.00	57.22	L	O
ATOM	4604	NE2	GLN	198	112.185	-26.414	10.956	1.00	51.65	L	N
ATOM	4605	C	GLN	198	108.681	-29.107	13.541	1.00	29.43	L	C
ATOM	4606	O	GLN	198	109.331	-30.088	13.182	1.00	31.15	L	O
ATOM	4607	N	GLY	199	108.568	-28.728	14.815	1.00	31.39	L	N
ATOM	4608	CA	GLY	199	109.234	-29.452	15.887	1.00	36.65	L	C
ATOM	4609	C	GLY	199	108.465	-30.636	16.444	1.00	39.08	L	C
ATOM	4610	O	GLY	199	108.880	-31.244	17.425	1.00	43.81	L	O
ATOM	4611	N	LEU	200	107.339	-30.961	15.823	1.00	25.48	L	N
ATOM	4612	CA	LEU	200	106.510	-32.087	16.247	1.00	22.67	L	C
ATOM	4613	CB	LEU	200	105.094	-31.597	16.570	1.00	31.49	L	C
ATOM	4614	CG	LEU	200	104.868	-31.002	17.964	1.00	34.60	L	C
ATOM	4615	CD1	LEU	200	106.036	-30.149	18.361	1.00	37.97	L	C
ATOM	4616	CD2	LEU	200	103.592	-30.188	17.967	1.00	34.28	L	C
ATOM	4617	C	LEU	200	106.463	-33.152	15.144	1.00	23.29	L	C
ATOM	4618	O	LEU	200	106.089	-32.869	14.003	1.00	24.15	L	O
ATOM	4619	N	SER	201	106.860	-34.372	15.499	1.00	21.11	L	N
ATOM	4620	CA	SER	201	106.886	-35.503	14.570	1.00	24.08	L	C
ATOM	4621	CB	SER	201	107.367	-36.747	15.311	1.00	27.13	L	C
ATOM	4622	OG	SER	201	106.702	-36.875	16.561	1.00	28.99	L	O
ATOM	4623	C	SER	201	105.510	-35.761	13.957	1.00	24.14	L	C
ATOM	4624	O	SER	201	105.392	-36.267	12.835	1.00	25.49	L	O
ATOM	4625	N	SER	202	104.476	-35.405	14.717	1.00	17.09	L	N
ATOM	4626	CA	SER	202	103.086	-35.562	14.302	1.00	21.15	L	C
ATOM	4627	CB	SER	202	102.636	-37.010	14.522	1.00	43.22	L	C
ATOM	4628	OG	SER	202	103.011	-37.462	15.810	1.00	46.12	L	O
ATOM	4629	C	SER	202	102.265	-34.603	15.155	1.00	21.60	L	C
ATOM	4630	O	SER	202	102.656	-34.296	16.282	1.00	27.36	L	O
ATOM	4631	N	PRO	203	101.119	-34.121	14.636	1.00	22.94	L	N
ATOM	4632	CD	PRO	203	100.457	-34.478	13.368	1.00	32.35	L	C
ATOM	4633	CA	PRO	203	100.290	-33.187	15.407	1.00	18.89	L	C
ATOM	4634	CB	PRO	203	98.971	-33.177	14.643	1.00	26.47	L	C
ATOM	4635	CG	PRO	203	99.416	-33.370	13.223	1.00	29.48	L	C
ATOM	4636	C	PRO	203	100.128	-33.646	16.836	1.00	18.90	L	C
ATOM	4637	O	PRO	203	100.178	-34.842	17.100	1.00	21.86	L	O
ATOM	4638	N	VAL	204	99.980	-32.693	17.753	1.00	28.11	L	N
ATOM	4639	CA	VAL	204	99.794	-32.996	19.172	1.00	29.99	L	C
ATOM	4640	CB	VAL	204	100.759	-32.201	20.081	1.00	20.42	L	C
ATOM	4641	CG1	VAL	204	100.254	-32.204	21.512	1.00	20.30	L	C
ATOM	4642	CG2	VAL	204	102.141	-32.819	20.036	1.00	15.23	L	C
ATOM	4643	C	VAL	204	98.393	-32.574	19.514	1.00	33.93	L	C
ATOM	4644	O	VAL	204	97.887	-31.601	18.963	1.00	35.36	L	O
ATOM	4645	N	THR	205	97.755	-33.293	20.422	1.00	45.34	L	N
ATOM	4646	CA	THR	205	96.402	-32.933	20.787	1.00	46.97	L	C
ATOM	4647	CB	THR	205	95.386	-33.896	20.137	1.00	14.48	L	C
ATOM	4648	OG1	THR	205	95.275	-33.587	18.747	1.00	10.44	L	O
ATOM	4649	CG2	THR	205	94.013	-33.761	20.769	1.00	11.16	L	C
ATOM	4650	C	THR	205	96.169	-32.886	22.280	1.00	47.18	L	C
ATOM	4651	O	THR	205	96.596	-33.763	23.032	1.00	49.19	L	O
ATOM	4652	N	LYS	206	95.513	-31.822	22.709	1.00	22.09	L	N
ATOM	4653	CA	LYS	206	95.167	-31.681	24.108	1.00	26.52	L	C
ATOM	4654	CB	LYS	206	95.791	-30.422	24.710	1.00	41.08	L	C
ATOM	4655	CG	LYS	206	97.208	-30.641	25.215	1.00	44.88	L	C
ATOM	4656	CD	LYS	206	97.269	-31.688	26.312	1.00	47.36	L	C
ATOM	4657	CE	LYS	206	98.654	-31.760	26.957	1.00	49.27	L	C
ATOM	4658	NZ	LYS	206	99.723	-32.144	25.997	1.00	50.40	L	N
ATOM	4659	C	LYS	206	93.653	-31.602	24.100	1.00	29.29	L	C
ATOM	4660	O	LYS	206	93.063	-30.939	23.246	1.00	34.45	L	O
ATOM	4661	N	SER	207	93.026	-32.304	25.033	1.00	32.39	L	N
ATOM	4662	CA	SER	207	91.578	-32.324	25.083	1.00	29.18	L	C
ATOM	4663	CB	SER	207	91.046	-33.364	24.080	1.00	31.23	L	C
ATOM	4664	OG	SER	207	91.613	-34.655	24.294	1.00	31.62	L	O
ATOM	4665	C	SER	207	91.039	-32.624	26.476	1.00	28.78	L	C
ATOM	4666	O	SER	207	91.798	-32.938	27.397	1.00	29.47	L	O
ATOM	4667	N	PHE	208	89.719	-32.517	26.606	1.00	33.89	L	N
ATOM	4668	CA	PHE	208	89.013	-32.777	27.852	1.00	39.79	L	C
ATOM	4669	CB	PHE	208	89.217	-31.615	28.842	1.00	17.06	L	C
ATOM	4670	CG	PHE	208	88.662	-30.300	28.353	1.00	14.11	L	C
ATOM	4671	CD1	PHE	208	89.409	-29.482	27.499	1.00	18.84	L	C
ATOM	4672	CD2	PHE	208	87.376	-29.906	28.690	1.00	11.57	L	C

Fig. 19: A-65

ATOM	4673	CE1	PHE	208	88.879	-28.298	26.990	1.00	19.93	L	C
ATOM	4674	CE2	PHE	208	86.846	-28.729	28.182	1.00	14.34	L	C
ATOM	4675	CZ	PHE	208	87.602	-27.925	27.330	1.00	20.99	L	C
ATOM	4676	C	PHE	208	87.536	-32.873	27.472	1.00	45.59	L	C
ATOM	4677	O	PHE	208	87.168	-32.576	26.335	1.00	47.78	L	O
ATOM	4678	N	ASN	209	86.703	-33.293	28.420	1.00	24.67	L	N
ATOM	4679	CA	ASN	209	85.257	-33.398	28.213	1.00	28.33	L	C
ATOM	4680	CB	ASN	209	84.751	-34.785	28.623	1.00	27.05	L	C
ATOM	4681	CG	ASN	209	85.664	-35.913	28.172	1.00	33.97	L	C
ATOM	4682	OD1	ASN	209	85.777	-36.941	28.841	1.00	34.19	L	O
ATOM	4683	ND2	ASN	209	86.304	-35.732	27.031	1.00	37.01	L	N
ATOM	4684	C	ASN	209	84.630	-32.370	29.160	1.00	29.95	L	C
ATOM	4685	O	ASN	209	85.203	-32.108	30.218	1.00	31.18	L	O
ATOM	4686	N	ARG	210	83.473	-31.800	28.805	1.00	15.88	L	N
ATOM	4687	CA	ARG	210	82.810	-30.829	29.687	1.00	19.72	L	C
ATOM	4688	CB	ARG	210	81.337	-30.721	29.371	1.00	31.19	L	C
ATOM	4689	CG	ARG	210	81.027	-29.666	28.361	1.00	32.77	L	C
ATOM	4690	CD	ARG	210	79.655	-29.104	28.627	1.00	36.35	L	C
ATOM	4691	NE	ARG	210	78.656	-30.166	28.633	1.00	41.72	L	N
ATOM	4692	CZ	ARG	210	77.502	-30.095	29.282	1.00	45.49	L	C
ATOM	4693	NH1	ARG	210	77.204	-29.008	29.981	1.00	46.04	L	N
ATOM	4694	NH2	ARG	210	76.655	-31.112	29.232	1.00	47.73	L	N
ATOM	4695	C	ARG	210	82.964	-31.252	31.137	1.00	22.05	L	C
ATOM	4696	O	ARG	210	82.962	-32.440	31.428	1.00	23.93	L	O
ATOM	4697	N	GLY	211	83.096	-30.291	32.048	1.00	53.99	L	N
ATOM	4698	CA	GLY	211	83.297	-30.638	33.447	1.00	53.99	L	C
ATOM	4699	C	GLY	211	84.740	-31.088	33.630	1.00	53.99	L	C
ATOM	4700	O	GLY	211	85.665	-30.312	33.387	1.00	53.99	L	O
ATOM	4701	N	GLU	212	84.942	-32.336	34.046	1.00	80.95	L	N
ATOM	4702	CA	GLU	212	86.287	-32.890	34.236	1.00	80.95	L	C
ATOM	4703	CB	GLU	212	86.995	-33.004	32.871	1.00	34.07	L	C
ATOM	4704	CG	GLU	212	88.259	-33.888	32.849	1.00	34.07	L	C
ATOM	4705	CD	GLU	212	88.691	-34.311	31.435	1.00	34.07	L	C
ATOM	4706	OE1	GLU	212	89.803	-34.863	31.296	1.00	34.07	L	O
ATOM	4707	OE2	GLU	212	87.923	-34.113	30.468	1.00	34.07	L	O
ATOM	4708	C	GLU	212	87.134	-32.080	35.227	1.00	80.95	L	C
ATOM	4709	O	GLU	212	86.690	-31.043	35.732	1.00	80.95	L	O
ATOM	4710	N	CYS	213	88.341	-32.566	35.516	1.00	81.74	L	N
ATOM	4711	CA	CYS	213	89.243	-31.893	36.450	1.00	81.74	L	C
ATOM	4712	CB	CYS	213	88.990	-32.374	37.883	1.00	54.42	L	C
ATOM	4713	SG	CYS	213	87.479	-31.701	38.656	1.00	54.42	L	S
ATOM	4714	C	CYS	213	90.715	-32.123	36.095	1.00	81.74	L	C
ATOM	4715	O	CYS	213	90.996	-32.758	35.051	1.00	81.74	L	O
ATOM	4716	OXT	CYS	213	91.581	-31.647	36.863	1.00	72.88	L	O
ATOM	4717	MN	MN	400	117.831	24.682	6.345	1.00	34.24	M	
ATOM	4718	CB	THR	145	114.226	73.843	15.327	1.00	72.71	B	C
ATOM	4719	OG1	THR	145	113.673	74.174	16.611	1.00	72.71	B	O
ATOM	4720	CG2	THR	145	114.208	75.069	14.426	1.00	72.71	B	C
ATOM	4721	C	THR	145	113.665	71.399	15.485	1.00	109.74	B	C
ATOM	4722	O	THR	145	113.590	70.290	14.948	1.00	110.14	B	O
ATOM	4723	N	THR	145	111.957	72.996	14.632	1.00	108.12	B	N
ATOM	4724	CA	THR	145	113.414	72.677	14.686	1.00	107.72	B	C
ATOM	4725	N	GLN	146	113.963	71.561	16.769	1.00	79.22	B	N
ATOM	4726	CA	GLN	146	114.224	70.425	17.633	1.00	77.37	B	C
ATOM	4727	CB	GLN	146	115.554	70.620	18.378	1.00	80.28	B	C
ATOM	4728	CG	GLN	146	115.640	71.886	19.208	1.00	80.28	B	C
ATOM	4729	CD	GLN	146	116.952	72.001	19.955	1.00	80.28	B	C
ATOM	4730	OE1	GLN	146	117.150	72.929	20.742	1.00	80.28	B	O
ATOM	4731	NE2	GLN	146	117.858	71.059	19.712	1.00	80.28	B	N
ATOM	4732	C	GLN	146	113.077	70.200	18.620	1.00	77.79	B	C
ATOM	4733	O	GLN	146	112.818	71.018	19.511	1.00	79.65	B	O
ATOM	4734	N	LEU	147	112.383	69.081	18.432	1.00	43.47	B	N
ATOM	4735	CA	LEU	147	111.265	68.710	19.288	1.00	42.60	B	C
ATOM	4736	CB	LEU	147	109.936	68.755	18.525	1.00	51.95	B	C
ATOM	4737	CG	LEU	147	109.450	69.952	17.707	1.00	52.14	B	C
ATOM	4738	CD1	LEU	147	110.464	70.296	16.632	1.00	47.35	B	C
ATOM	4739	CD2	LEU	147	108.114	69.607	17.060	1.00	51.99	B	C
ATOM	4740	C	LEU	147	111.461	67.281	19.756	1.00	41.58	B	C
ATOM	4741	O	LEU	147	112.077	66.470	19.058	1.00	42.88	B	O
ATOM	4742	N	ASP	148	110.944	66.988	20.945	1.00	31.29	B	N
ATOM	4743	CA	ASP	148	110.974	65.640	21.493	1.00	28.75	B	C
ATOM	4744	CB	ASP	148	111.394	65.642	22.960	1.00	32.78	B	C
ATOM	4745	CG	ASP	148	112.897	65.718	23.133	1.00	32.40	B	C

Fig. 19: A-66

ATOM	4746	OD1	ASP	148	113.366	65.715	24.290	1.00	31.51	B	O
ATOM	4747	OD2	ASP	148	113.616	65.777	22.116	1.00	30.58	B	O
ATOM	4748	C	ASP	148	109.526	65.181	21.358	1.00	25.13	B	C
ATOM	4749	O	ASP	148	108.664	65.583	22.128	1.00	24.43	B	O
ATOM	4750	N	ILE	149	109.260	64.368	20.345	1.00	21.33	B	N
ATOM	4751	CA	ILE	149	107.918	63.885	20.105	1.00	20.27	B	C
ATOM	4752	CB	ILE	149	107.610	63.880	18.605	1.00	13.57	B	C
ATOM	4753	CG2	ILE	149	106.140	63.573	18.378	1.00	8.58	B	C
ATOM	4754	CG1	ILE	149	107.932	65.234	17.998	1.00	9.29	B	C
ATOM	4755	CD1	ILE	149	107.697	65.263	16.508	1.00	12.04	B	C
ATOM	4756	C	ILE	149	107.723	62.464	20.629	1.00	21.92	B	C
ATOM	4757	O	ILE	149	108.507	61.563	20.315	1.00	22.32	B	O
ATOM	4758	N	VAL	150	106.680	62.271	21.433	1.00	32.56	B	N
ATOM	4759	CA	VAL	150	106.357	60.950	21.956	1.00	34.12	B	C
ATOM	4760	CB	VAL	150	106.256	60.940	23.492	1.00	12.90	B	C
ATOM	4761	CG1	VAL	150	105.775	59.579	23.967	1.00	15.09	B	C
ATOM	4762	CG2	VAL	150	107.620	61.256	24.110	1.00	14.71	B	C
ATOM	4763	C	VAL	150	105.001	60.604	21.381	1.00	31.68	B	C
ATOM	4764	O	VAL	150	104.057	61.380	21.523	1.00	29.83	B	O
ATOM	4765	N	ILE	151	104.904	59.459	20.714	1.00	36.82	B	N
ATOM	4766	CA	ILE	151	103.640	59.037	20.115	1.00	35.62	B	C
ATOM	4767	CB	ILE	151	103.862	58.436	18.709	1.00	31.63	B	C
ATOM	4768	CG2	ILE	151	102.537	58.084	18.081	1.00	27.99	B	C
ATOM	4769	CG1	ILE	151	104.582	59.454	17.817	1.00	30.05	B	C
ATOM	4770	CD1	ILE	151	104.981	58.916	16.457	1.00	32.03	B	C
ATOM	4771	C	ILE	151	102.978	58.008	21.016	1.00	33.74	B	C
ATOM	4772	O	ILE	151	103.593	57.013	21.394	1.00	33.98	B	O
ATOM	4773	N	VAL	152	101.725	58.254	21.368	1.00	29.85	B	N
ATOM	4774	CA	VAL	152	100.996	57.347	22.243	1.00	30.70	B	C
ATOM	4775	CB	VAL	152	100.279	58.127	23.344	1.00	30.57	B	C
ATOM	4776	CG1	VAL	152	99.721	57.170	24.385	1.00	29.70	B	C
ATOM	4777	CG2	VAL	152	101.245	59.134	23.962	1.00	27.01	B	C
ATOM	4778	C	VAL	152	99.966	56.560	21.451	1.00	28.60	B	C
ATOM	4779	O	VAL	152	98.867	57.044	21.194	1.00	22.20	B	O
ATOM	4780	N	LEU	153	100.324	55.336	21.083	1.00	26.94	B	N
ATOM	4781	CA	LEU	153	99.451	54.479	20.289	1.00	27.05	B	C
ATOM	4782	CB	LEU	153	100.312	53.600	19.370	1.00	31.93	B	C
ATOM	4783	CG	LEU	153	100.518	54.010	17.910	1.00	33.71	B	C
ATOM	4784	CD1	LEU	153	100.287	55.490	17.732	1.00	34.22	B	C
ATOM	4785	CD2	LEU	153	101.914	53.616	17.481	1.00	36.25	B	C
ATOM	4786	C	LEU	153	98.475	53.597	21.058	1.00	28.11	B	C
ATOM	4787	O	LEU	153	98.837	52.930	22.035	1.00	27.11	B	O
ATOM	4788	N	ASP	154	97.228	53.602	20.604	1.00	33.48	B	N
ATOM	4789	CA	ASP	154	96.199	52.768	21.204	1.00	32.96	B	C
ATOM	4790	CB	ASP	154	94.809	53.341	20.911	1.00	34.05	B	C
ATOM	4791	CG	ASP	154	93.[illegible]86	52.502	21.505	1.00	33.25	B	C
ATOM	4792	OD1	ASP	154	93.959	51.385	21.985	1.00	36.76	B	O
ATOM	4793	OD2	ASP	154	92.523	52.960	21.489	1.00	29.57	B	O
ATOM	4794	C	ASP	154	96.362	51.412	20.515	1.00	36.30	B	C
ATOM	4795	O	ASP	154	96.349	51.326	19.285	1.00	32.62	B	O
ATOM	4796	N	GLY	155	96.539	50.361	21.303	1.00	16.68	B	N
ATOM	4797	CA	GLY	155	96.700	49.039	20.732	1.00	18.75	B	C
ATOM	4798	C	GLY	155	95.706	48.058	21.321	1.00	20.01	B	C
ATOM	4799	O	GLY	155	95.856	46.845	21.177	1.00	22.50	B	O
ATOM	4800	N	SER	156	94.692	48.595	21.992	1.00	30.46	B	N
ATOM	4801	CA	SER	156	93.653	47.780	22.612	1.00	35.04	B	C
ATOM	4802	CB	SER	156	92.616	48.670	23.302	1.00	22.70	B	C
ATOM	4803	OG	SER	156	91.999	49.542	22.372	1.00	25.62	B	O
ATOM	4804	C	SER	156	92.962	46.891	21.584	1.00	32.03	B	C
ATOM	4805	O	SER	156	93.057	47.122	20.379	1.00	35.21	B	O
ATOM	4806	N	ASN	157	92.257	45.879	22.074	1.00	34.08	B	N
ATOM	4807	CA	ASN	157	91.565	44.927	21.216	1.00	31.16	B	C
ATOM	4808	CB	ASN	157	90.632	44.046	22.047	1.00	34.61	B	C
ATOM	4809	CG	ASN	157	91.378	42.971	22.811	1.00	36.10	B	C
ATOM	4810	OD1	ASN	157	90.795	42.270	23.638	1.00	33.17	B	O
ATOM	4811	ND2	ASN	157	92.672	42.832	22.536	1.00	33.38	B	N
ATOM	4812	C	ASN	157	90.783	45.529	20.069	1.00	29.13	B	C
ATOM	4813	O	ASN	157	90.806	45.003	18.956	1.00	27.11	B	O
ATOM	4814	N	SER	158	90.094	46.631	20.339	1.00	20.01	B	N
ATOM	4815	CA	SER	158	89.275	47.285	19.324	1.00	18.22	B	C
ATOM	4816	CB	SER	158	88.506	48.464	19.936	1.00	15.08	B	C
ATOM	4817	OG	SER	158	89.356	49.363	20.616	1.00	17.79	B	O
ATOM	4818	C	SER	158	90.035	47.739	18.087	1.00	18.99	B	C

Fig. 19: A-67

ATOM	4819	O	SER	158	89.527	47.602	16.984	1.00	16.16	B	O
ATOM	4820	N	ILE	159	91.245	48.269	18.257	1.00	19.55	B	N
ATOM	4821	CA	ILE	159	92.033	48.722	17.110	1.00	24.15	B	C
ATOM	4822	CB	ILE	159	93.423	49.203	17.541	1.00	21.45	B	C
ATOM	4823	CG2	ILE	159	94.256	49.546	16.307	1.00	21.36	B	C
ATOM	4824	CG1	ILE	159	93.293	50.411	18.471	1.00	26.23	B	C
ATOM	4825	CD1	ILE	159	92.779	51.664	17.787	1.00	31.39	B	C
ATOM	4826	C	ILE	159	92.204	47.597	16.089	1.00	28.46	B	C
ATOM	4827	O	ILE	159	92.638	46.502	16.434	1.00	27.87	B	O
ATOM	4828	N	TYR	160	91.863	47.876	14.832	1.00	56.09	B	N
ATOM	4829	CA	TYR	160	91.959	46.886	13.756	1.00	58.22	B	C
ATOM	4830	CB	TYR	160	90.931	45.768	13.980	1.00	40.50	B	C
ATOM	4831	CG	TYR	160	90.932	44.654	12.939	1.00	37.26	B	C
ATOM	4832	CD1	TYR	160	91.606	43.449	13.172	1.00	39.68	B	C
ATOM	4833	CE1	TYR	160	91.602	42.423	12.225	1.00	37.28	B	C
ATOM	4834	CD2	TYR	160	90.254	44.803	11.722	1.00	34.91	B	C
ATOM	4835	CE2	TYR	160	90.251	43.782	10.770	1.00	38.62	B	C
ATOM	4836	CZ	TYR	160	90.926	42.598	11.030	1.00	37.97	B	C
ATOM	4837	OH	TYR	160	90.922	41.597	10.095	1.00	42.97	B	O
ATOM	4838	C	TYR	160	91.696	47.533	12.400	1.00	59.94	B	C
ATOM	4839	O	TYR	160	90.730	48.276	12.232	1.00	65.86	B	O
ATOM	4840	N	PRO	161	92.548	47.241	11.407	1.00	26.83	B	N
ATOM	4841	CD	PRO	161	92.182	47.499	10.002	1.00	24.03	B	C
ATOM	4842	CA	PRO	161	93.721	46.362	11.479	1.00	25.11	B	C
ATOM	4843	CB	PRO	161	93.784	45.785	10.075	1.00	28.41	B	C
ATOM	4844	CG	PRO	161	93.364	46.960	9.239	1.00	31.57	B	C
ATOM	4845	C	PRO	161	95.008	47.109	11.857	1.00	23.77	B	C
ATOM	4846	O	PRO	161	95.234	48.238	11.413	1.00	23.09	B	O
ATOM	4847	N	TRP	162	95.856	46.463	12.654	1.00	23.22	B	N
ATOM	4848	CA	TRP	162	97.108	47.062	13.111	1.00	24.29	B	C
ATOM	4849	CB	TRP	162	97.922	46.022	13.878	1.00	29.42	B	C
ATOM	4850	CG	TRP	162	99.067	46.586	14.670	1.00	29.94	B	C
ATOM	4851	CD2	TRP	162	99.004	47.603	15.676	1.00	24.78	B	C
ATOM	4852	CE2	TRP	162	100.308	47.769	16.185	1.00	28.33	B	C
ATOM	4853	CE3	TRP	162	97.973	48.389	16.201	1.00	24.19	B	C
ATOM	4854	CD1	TRP	162	100.369	46.192	14.611	1.00	29.13	B	C
ATOM	4855	NE1	TRP	162	101.123	46.898	15.516	1.00	31.00	B	N
ATOM	4856	CZ2	TRP	162	100.607	48.687	17.195	1.00	26.87	B	C
ATOM	4857	CZ3	TRP	162	98.274	49.303	17.208	1.00	22.52	B	C
ATOM	4858	CH2	TRP	162	99.580	49.441	17.691	1.00	27.43	B	C
ATOM	4859	C	TRP	162	97.961	47.663	11.988	1.00	26.07	B	C
ATOM	4860	O	TRP	162	98.554	48.734	12.161	1.00	25.22	B	O
ATOM	4861	N	GLU	163	98.010	46.979	10.843	1.00	39.64	B	N
ATOM	4862	CA	GLU	163	98.797	47.432	9.693	1.00	41.42	B	C
ATOM	4863	CB	GLU	163	98.585	46.509	8.485	1.00	121.98	B	C
ATOM	4864	CG	GLU	163	97.219	46.612	7.826	1.00	128.29	B	C
ATOM	4865	CD	GLU	163	97.206	46.043	6.418	1.00	130.43	B	C
ATOM	4866	OE1	GLU	163	97.894	46.611	5.541	1.00	132.14	B	O
ATOM	4867	OE2	GLU	163	96.512	45.029	6.187	1.00	129.39	B	O
ATOM	4868	C	GLU	163	98.491	48.867	9.280	1.00	41.08	B	C
ATOM	4869	O	GLU	163	99.390	49.609	8.881	1.00	37.25	B	O
ATOM	4870	N	SER	164	97.225	49.262	9.368	1.00	24.58	B	N
ATOM	4871	CA	SER	164	96.850	50.620	8.989	1.00	21.77	B	C
ATOM	4872	CB	SER	164	95.320	50.772	8.984	1.00	53.34	B	C
ATOM	4873	OG	SER	164	94.722	49.950	7.992	1.00	59.23	B	O
ATOM	4874	C	SER	164	97.484	51.619	9.956	1.00	22.53	B	C
ATOM	4875	O	SER	164	97.993	52.661	9.536	1.00	25.73	B	O
ATOM	4876	N	VAL	165	97.451	51.286	11.247	1.00	28.47	B	N
ATOM	4877	CA	VAL	165	98.027	52.137	12.280	1.00	27.86	B	C
ATOM	4878	CB	VAL	165	97.841	51.525	13.680	1.00	11.01	B	C
ATOM	4879	CG1	VAL	165	98.722	52.245	14.697	1.00	12.40	B	C
ATOM	4880	CG2	VAL	165	96.376	51.622	14.089	1.00	14.01	B	C
ATOM	4881	C	VAL	165	99.509	52.334	12.028	1.00	29.02	B	C
ATOM	4882	O	VAL	165	100.032	53.444	12.137	1.00	30.84	B	O
ATOM	4883	N	ILE	166	100.184	51.248	11.678	1.00	20.94	B	N
ATOM	4884	CA	ILE	166	101.613	51.305	11.400	1.00	20.26	B	C
ATOM	4885	CB	ILE	166	102.211	49.894	11.330	1.00	40.92	B	C
ATOM	4886	CG2	ILE	166	103.697	49.962	10.986	1.00	40.13	B	C
ATOM	4887	CG1	ILE	166	102.017	49.214	12.687	1.00	40.78	B	C
ATOM	4888	CD1	ILE	166	102.580	47.823	12.762	1.00	37.18	B	C
ATOM	4889	C	ILE	166	101.920	52.073	10.121	1.00	19.71	B	C
ATOM	4890	O	ILE	166	102.909	52.792	10.059	1.00	21.46	B	O
ATOM	4891	N	ALA	167	101.076	51.927	9.106	1.00	22.08	B	N

Fig. 19: A-68

ATOM	4892	CA	ALA	167	101.271	52.670	7.866	1.00	22.68	B	C
ATOM	4893	CB	ALA	167	100.207	52.309	6.859	1.00	1.87	B	C
ATOM	4894	C	ALA	167	101.165	54.150	8.224	1.00	23.89	B	C
ATOM	4895	O	ALA	167	101.881	54.989	7.684	1.00	20.49	B	O
ATOM	4896	N	PHE	168	100.261	54.458	9.147	1.00	25.99	B	N
ATOM	4897	CA	PHE	168	100.083	55.823	9.583	1.00	24.51	B	C
ATOM	4898	CB	PHE	168	98.964	55.902	10.623	1.00	28.51	B	C
ATOM	4899	CG	PHE	168	98.962	57.185	11.406	1.00	27.01	B	C
ATOM	4900	CD1	PHE	168	99.549	57.240	12.671	1.00	28.61	B	C
ATOM	4901	CD2	PHE	168	98.409	58.341	10.872	1.00	25.32	B	C
ATOM	4902	CE1	PHE	168	99.587	58.424	13.392	1.00	27.09	B	C
ATOM	4903	CE2	PHE	168	98.442	59.529	11.587	1.00	27.14	B	C
ATOM	4904	CZ	PHE	168	99.034	59.570	12.853	1.00	29.63	B	C
ATOM	4905	C	PHE	168	101.397	56.325	10.178	1.00	25.37	B	C
ATOM	4906	O	PHE	168	101.832	57.446	9.908	1.00	21.81	B	O
ATOM	4907	N	LEU	169	102.030	55.488	10.990	1.00	25.37	B	N
ATOM	4908	CA	LEU	169	103.286	55.867	11.611	1.00	27.96	B	C
ATOM	4909	CB	LEU	169	103.749	54.790	12.585	1.00	24.35	B	C
ATOM	4910	CG	LEU	169	103.127	54.723	13.977	1.00	23.51	B	C
ATOM	4911	CD1	LEU	169	103.983	53.810	14.831	1.00	19.97	B	C
ATOM	4912	CD2	LEU	169	103.079	56.105	14.609	1.00	20.37	B	C
ATOM	4913	C	LEU	169	104.357	56.081	10.555	1.00	30.26	B	C
ATOM	4914	O	LEU	169	105.055	57.095	10.555	1.00	31.69	B	O
ATOM	4915	N	ASN	170	104.488	55.115	9.655	1.00	28.40	B	N
ATOM	4916	CA	ASN	170	105.470	55.208	8.591	1.00	25.53	B	C
ATOM	4917	CB	ASN	170	105.243	54.077	7.580	1.00	72.75	B	C
ATOM	4918	CG	ASN	170	106.484	53.768	6.747	1.00	76.17	B	C
ATOM	4919	OD1	ASN	170	106.703	54.346	5.680	1.00	71.70	B	O
ATOM	4920	ND2	ASN	170	107.307	52.854	7.242	1.00	74.08	B	N
ATOM	4921	C	ASN	170	105.335	56.578	7.913	1.00	25.54	B	C
ATOM	4922	O	ASN	170	106.242	57.408	7.992	1.00	25.75	B	O
ATOM	4923	N	ASP	171	104.189	56.819	7.275	1.00	35.44	B	N
ATOM	4924	CA	ASP	171	103.940	58.079	6.581	1.00	37.56	B	C
ATOM	4925	CB	ASP	171	102.467	58.179	6.168	1.00	72.00	B	C
ATOM	4926	CG	ASP	171	102.163	57.427	4.880	1.00	79.65	B	C
ATOM	4927	OD1	ASP	171	102.448	56.213	4.805	1.00	81.87	B	O
ATOM	4928	OD2	ASP	171	101.635	58.055	3.937	1.00	81.51	B	O
ATOM	4929	C	ASP	171	104.309	59.289	7.418	1.00	39.05	B	C
ATOM	4930	O	ASP	171	104.975	60.202	6.937	1.00	37.77	B	O
ATOM	4931	N	LEU	172	103.881	59.289	8.674	1.00	36.54	B	N
ATOM	4932	CA	LEU	172	104.152	60.403	9.570	1.00	37.22	B	C
ATOM	4933	CB	LEU	172	103.410	60.204	10.891	1.00	36.27	B	C
ATOM	4934	CG	LEU	172	102.901	61.423	11.674	1.00	35.76	B	C
ATOM	4935	CD1	LEU	172	103.145	61.178	13.158	1.00	33.36	B	C
ATOM	4936	CD2	LEU	172	103.593	62.706	11.237	1.00	33.93	B	C
ATOM	4937	C	LEU	172	105.642	60.561	9.849	1.00	37.56	B	C
ATOM	4938	O	LEU	172	106.212	61.628	9.627	1.00	37.55	B	O
ATOM	4939	N	LEU	173	106.269	59.493	10.337	1.00	40.49	B	N
ATOM	4940	CA	LEU	173	107.692	59.520	10.669	1.00	43.24	B	C
ATOM	4941	CB	LEU	173	108.115	58.215	11.364	1.00	18.13	B	C
ATOM	4942	CG	LEU	173	107.801	57.866	12.826	1.00	19.48	B	C
ATOM	4943	CD1	LEU	173	108.033	59.060	13.729	1.00	23.00	B	C
ATOM	4944	CD2	LEU	173	106.380	57.395	12.943	1.00	20.03	B	C
ATOM	4945	C	LEU	173	108.650	59.772	9.503	1.00	44.67	B	C
ATOM	4946	O	LEU	173	109.601	60.537	9.642	1.00	41.39	B	O
ATOM	4947	N	LYS	174	108.409	59.135	8.360	1.00	37.56	B	N
ATOM	4948	CA	LYS	174	109.304	59.291	7.221	1.00	37.78	B	C
ATOM	4949	CB	LYS	174	108.836	58.421	6.047	1.00	42.14	B	C
ATOM	4950	CG	LYS	174	107.739	58.988	5.169	1.00	42.47	B	C
ATOM	4951	CD	LYS	174	107.472	58.022	4.008	1.00	41.72	B	C
ATOM	4952	CE	LYS	174	106.689	58.660	2.852	1.00	36.97	B	C
ATOM	4953	NZ	LYS	174	105.297	59.097	3.187	1.00	33.44	B	N
ATOM	4954	C	LYS	174	109.511	60.738	6.774	1.00	36.14	B	C
ATOM	4955	O	LYS	174	110.571	61.078	6.245	1.00	37.01	B	O
ATOM	4956	N	ARG	175	108.514	61.589	7.004	1.00	41.42	B	N
ATOM	4957	CA	ARG	175	108.587	63.006	6.635	1.00	43.65	B	C
ATOM	4958	CB	ARG	175	107.182	63.634	6.654	1.00	108.28	B	C
ATOM	4959	CG	ARG	175	106.189	63.149	5.589	1.00	115.21	B	C
ATOM	4960	CD	ARG	175	104.762	63.613	5.939	1.00	119.49	B	C
ATOM	4961	NE	ARG	175	103.895	63.818	4.775	1.00	124.39	B	N
ATOM	4962	CZ	ARG	175	103.454	62.856	3.969	1.00	127.97	B	C
ATOM	4963	NH1	ARG	175	103.793	61.593	4.182	1.00	128.17	B	N
ATOM	4964	NH2	ARG	175	102.666	63.162	2.945	1.00	128.87	B	N

Fig. 19: A-69

ATOM	4965	C	ARG	175	109.471	63.798	7.611	1.00	41.18	B	C
ATOM	4966	O	ARG	175	109.696	64.986	7.411	1.00	41.02	B	O
ATOM	4967	N	MET	176	109.970	63.145	8.660	1.00	47.15	B	N
ATOM	4968	CA	MET	176	110.777	63.821	9.678	1.00	43.63	B	C
ATOM	4969	CB	MET	176	110.320	63.383	11.065	1.00	33.29	B	C
ATOM	4970	CG	MET	176	108.969	63.920	11.456	1.00	30.19	B	C
ATOM	4971	SD	MET	176	108.444	63.366	13.073	1.00	34.33	B	S
ATOM	4972	CE	MET	176	107.041	62.339	12.619	1.00	27.84	B	C
ATOM	4973	C	MET	176	112.284	63.663	9.611	1.00	47.14	B	C
ATOM	4974	O	MET	176	112.795	62.707	9.037	1.00	47.21	B	O
ATOM	4975	N	ASP	177	112.991	64.617	10.213	1.00	51.06	B	N
ATOM	4976	CA	ASP	177	114.451	64.590	10.276	1.00	53.55	B	C
ATOM	4977	CB	ASP	177	115.047	65.944	9.881	1.00	101.95	B	C
ATOM	4978	CG	ASP	177	115.065	66.158	8.381	1.00	104.90	B	C
ATOM	4979	OD1	ASP	177	115.635	67.174	7.934	1.00	104.57	B	O
ATOM	4980	OD2	ASP	177	114.511	65.310	7.647	1.00	106.55	B	O
ATOM	4981	C	ASP	177	114.851	64.249	11.706	1.00	53.47	B	C
ATOM	4982	O	ASP	177	115.107	65.133	12.519	1.00	53.19	B	O
ATOM	4983	N	ILE	178	114.888	62.954	12.003	1.00	55.91	B	N
ATOM	4984	CA	ILE	178	115.236	62.465	13.331	1.00	56.05	B	C
ATOM	4985	CB	ILE	178	114.719	61.004	13.543	1.00	33.37	B	C
ATOM	4986	CG2	ILE	178	115.323	60.410	14.790	1.00	31.65	B	C
ATOM	4987	CG1	ILE	178	113.191	60.985	13.665	1.00	34.43	B	C
ATOM	4988	CD1	ILE	178	112.464	60.671	12.376	1.00	36.27	B	C
ATOM	4989	C	ILE	178	116.743	62.502	13.583	1.00	55.19	B	C
ATOM	4990	O	ILE	178	117.543	62.224	12.686	1.00	57.18	B	O
ATOM	4991	N	GLY	179	117.117	62.846	14.812	1.00	23.09	B	N
ATOM	4992	CA	GLY	179	118.521	62.912	15.178	1.00	22.81	B	C
ATOM	4993	C	GLY	179	118.736	63.508	16.560	1.00	23.57	B	C
ATOM	4994	O	GLY	179	117.931	64.325	17.012	1.00	21.72	B	O
ATOM	4995	N	PRO	180	119.815	63.113	17.265	1.00	39.73	B	N
ATOM	4996	CD	PRO	180	120.782	62.068	16.873	1.00	73.51	B	C
ATOM	4997	CA	PRO	180	120.124	63.620	18.606	1.00	40.79	B	C
ATOM	4998	CB	PRO	180	121.542	63.113	18.840	1.00	72.35	B	C
ATOM	4999	CG	PRO	180	121.502	61.776	18.184	1.00	74.74	B	C
ATOM	5000	C	PRO	180	120.019	65.135	18.697	1.00	42.57	B	C
ATOM	5001	O	PRO	180	119.718	65.680	19.761	1.00	43.21	B	O
ATOM	5002	N	LYS	181	120.268	65.810	17.578	1.00	56.97	B	N
ATOM	5003	CA	LYS	181	120.186	67.265	17.534	1.00	57.39	B	C
ATOM	5004	CB	LYS	181	121.522	67.867	17.092	1.00	83.43	B	C
ATOM	5005	CG	LYS	181	122.677	67.613	18.052	1.00	84.03	B	C
ATOM	5006	CD	LYS	181	122.430	68.205	19.442	1.00	82.89	B	C
ATOM	5007	CE	LYS	181	123.580	67.868	20.394	1.00	85.41	B	C
ATOM	5008	NZ	LYS	181	123.351	68.348	21.790	1.00	84.98	B	N
ATOM	5009	C	LYS	181	119.070	67.736	16.597	1.00	56.74	B	C
ATOM	5010	O	LYS	181	118.973	68.917	16.274	1.00	55.06	B	O
ATOM	5011	N	GLN	182	118.225	66.804	16.167	1.00	33.36	B	N
ATOM	5012	CA	GLN	182	117.112	67.117	15.279	1.00	32.02	B	C
ATOM	5013	CB	GLN	182	117.152	66.219	14.044	1.00	74.94	B	C
ATOM	5014	CG	GLN	182	118.512	66.050	13.424	1.00	76.22	B	C
ATOM	5015	CD	GLN	182	119.037	67.334	12.850	1.00	77.84	B	C
ATOM	5016	OE1	GLN	182	119.266	68.305	13.573	1.00	78.68	B	O
ATOM	5017	NE2	GLN	182	119.230	67.356	11.537	1.00	79.20	B	N
ATOM	5018	C	GLN	182	115.831	66.826	16.046	1.00	30.93	B	C
ATOM	5019	O	GLN	182	115.638	67.278	17.173	1.00	35.26	B	O
ATOM	5020	N	THR	183	114.961	66.046	15.419	1.00	29.87	B	N
ATOM	5021	CA	THR	183	113.706	65.648	16.025	1.00	26.79	B	C
ATOM	5022	CB	THR	183	112.612	65.493	14.962	1.00	31.40	B	C
ATOM	5023	OG1	THR	183	112.484	66.721	14.231	1.00	27.85	B	O
ATOM	5024	CG2	THR	183	111.285	65.127	15.610	1.00	29.08	B	C
ATOM	5025	C	THR	183	113.957	64.288	16.666	1.00	26.45	B	C
ATOM	5026	O	THR	183	114.624	63.428	16.077	1.00	24.98	B	O
ATOM	5027	N	GLN	184	113.464	64.102	17.883	1.00	44.27	B	N
ATOM	5028	CA	GLN	184	113.619	62.822	18.546	1.00	39.92	B	C
ATOM	5029	CB	GLN	184	114.254	62.981	19.920	1.00	33.99	B	C
ATOM	5030	CG	GLN	184	115.752	63.197	19.878	1.00	33.74	B	C
ATOM	5031	CD	GLN	184	116.427	62.766	21.163	1.00	33.21	B	C
ATOM	5032	OE1	GLN	184	116.097	63.258	22.244	1.00	28.91	B	O
ATOM	5033	NE2	GLN	184	117.375	61.835	21.053	1.00	31.51	B	N
ATOM	5034	C	GLN	184	112.227	62.240	18.670	1.00	40.30	B	C
ATOM	5035	O	GLN	184	111.249	62.978	18.834	1.00	37.69	B	O
ATOM	5036	N	VAL	185	112.131	60.918	18.574	1.00	24.17	B	N
ATOM	5037	CA	VAL	185	110.837	60.255	18.649	1.00	22.54	B	C

Fig. 19: A-70

ATOM	5038	CB	VAL	185	110.345	59.858	17.235	1.00	12.44	B	C
ATOM	5039	CG1	VAL	185	109.105	58.990	17.335	1.00	12.43	B	C
ATOM	5040	CG2	VAL	185	110.052	61.103	16.425	1.00	1.87	B	C
ATOM	5041	C	VAL	185	110.840	59.025	19.536	1.00	23.13	B	C
ATOM	5042	O	VAL	185	111.756	58.206	19.510	1.00	20.28	B	O
ATOM	5043	N	GLY	186	109.789	58.914	20.328	1.00	27.91	B	N
ATOM	5044	CA	GLY	186	109.630	57.782	21.213	1.00	29.54	B	C
ATOM	5045	C	GLY	186	108.200	57.319	21.045	1.00	27.52	B	C
ATOM	5046	O	GLY	186	107.308	58.138	20.839	1.00	32.88	B	O
ATOM	5047	N	ILE	187	107.970	56.017	21.105	1.00	20.77	B	N
ATOM	5048	CA	ILE	187	106.617	55.519	20.958	1.00	19.36	B	C
ATOM	5049	CB	ILE	187	106.460	54.729	19.642	1.00	17.70	B	C
ATOM	5050	CG2	ILE	187	105.081	54.079	19.577	1.00	15.03	B	C
ATOM	5051	CG1	ILE	187	106.639	55.676	18.454	1.00	18.22	B	C
ATOM	5052	CD1	ILE	187	106.437	55.033	17.100	1.00	19.27	B	C
ATOM	5053	C	ILE	187	106.160	54.674	22.143	1.00	18.65	B	C
ATOM	5054	O	ILE	187	106.852	53.763	22.590	1.00	17.55	B	O
ATOM	5055	N	VAL	188	104.984	55.015	22.649	1.00	23.72	B	N
ATOM	5056	CA	VAL	188	104.370	54.332	23.774	1.00	23.39	B	C
ATOM	5057	CB	VAL	188	104.053	55.333	24.911	1.00	24.28	B	C
ATOM	5058	CG1	VAL	188	103.055	54.728	25.896	1.00	19.55	B	C
ATOM	5059	CG2	VAL	188	105.320	55.715	25.625	1.00	24.70	B	C
ATOM	5060	C	VAL	188	103.055	53.702	23.303	1.00	21.93	B	C
ATOM	5061	O	VAL	188	102.274	54.341	22.591	1.00	21.34	B	O
ATOM	5062	N	GLN	189	102.815	52.453	23.686	1.00	21.90	B	N
ATOM	5063	CA	GLN	189	101.580	51.785	23.312	1.00	21.58	B	C
ATOM	5064	CB	GLN	189	101.857	50.545	22.463	1.00	19.75	B	C
ATOM	5065	CG	GLN	189	100.577	49.784	22.128	1.00	17.26	B	C
ATOM	5066	CD	GLN	189	100.819	48.495	21.377	1.00	17.97	B	C
ATOM	5067	OE1	GLN	189	99.930	47.647	21.283	1.00	19.19	B	O
ATOM	5068	NE2	GLN	189	102.022	48.340	20.831	1.00	19.01	B	N
ATOM	5069	C	GLN	189	100.820	51.386	24.572	1.00	18.57	B	C
ATOM	5070	O	GLN	189	101.423	50.980	25.567	1.00	16.93	B	O
ATOM	5071	N	TYR	190	99.494	51.500	24.524	1.00	20.56	B	N
ATOM	5072	CA	TYR	190	98.671	51.159	25.680	1.00	24.08	B	C
ATOM	5073	CB	TYR	190	98.255	52.432	26.418	1.00	22.72	B	C
ATOM	5074	CG	TYR	190	97.213	53.255	25.687	1.00	17.37	B	C
ATOM	5075	CD1	TYR	190	95.849	53.072	25.929	1.00	15.48	B	C
ATOM	5076	CE1	TYR	190	94.882	53.820	25.244	1.00	17.37	B	C
ATOM	5077	CD2	TYR	190	97.586	54.207	24.739	1.00	13.48	B	C
ATOM	5078	CE2	TYR	190	96.624	54.957	24.051	1.00	14.90	B	C
ATOM	5079	CZ	TYR	190	95.279	54.760	24.311	1.00	15.79	B	C
ATOM	5080	OH	TYR	190	94.340	55.527	23.663	1.00	14.38	B	O
ATOM	5081	C	TYR	190	97.428	50.342	25.344	1.00	25.93	B	C
ATOM	5082	O	TYR	190	97.000	50.260	24.195	1.00	26.01	B	O
ATOM	5083	N	GLY	191	96.860	49.746	26.385	1.00	24.69	B	N
ATOM	5084	CA	GLY	191	95.675	48.920	26.270	1.00	22.44	B	C
ATOM	5085	C	GLY	191	95.277	48.649	27.701	1.00	23.88	B	C
ATOM	5086	O	GLY	191	94.720	49.532	28.348	1.00	27.26	B	O
ATOM	5087	N	GLU	192	95.572	47.446	28.197	1.00	23.59	B	N
ATOM	5088	CA	GLU	192	95.284	47.084	29.584	1.00	25.60	B	C
ATOM	5089	CB	GLU	192	95.232	45.574	29.758	1.00	40.14	B	C
ATOM	5090	CG	GLU	192	94.135	44.871	29.002	1.00	40.52	B	C
ATOM	5091	CD	GLU	192	94.134	43.382	29.273	1.00	40.71	B	C
ATOM	5092	OE1	GLU	192	93.230	42.690	28.759	1.00	43.60	B	O
ATOM	5093	OE2	GLU	192	95.038	42.906	29.999	1.00	38.58	B	O
ATOM	5094	C	GLU	192	96.465	47.608	30.390	1.00	25.41	B	C
ATOM	5095	O	GLU	192	96.325	48.027	31.536	1.00	26.78	B	O
ATOM	5096	N	ASN	193	97.637	47.569	29.770	1.00	17.36	B	N
ATOM	5097	CA	ASN	193	98.862	48.041	30.395	1.00	18.57	B	C
ATOM	5098	CB	ASN	193	99.814	46.877	30.653	1.00	57.60	B	C
ATOM	5099	CG	ASN	193	99.159	45.755	31.418	1.00	60.77	B	C
ATOM	5100	OD1	ASN	193	98.225	45.115	30.933	1.00	64.88	B	O
ATOM	5101	ND2	ASN	193	99.644	45.509	32.626	1.00	62.88	B	N
ATOM	5102	C	ASN	193	99.510	49.007	29.425	1.00	16.75	B	C
ATOM	5103	O	ASN	193	98.917	49.360	28.413	1.00	17.75	B	O
ATOM	5104	N	VAL	194	100.735	49.418	29.728	1.00	23.63	B	N
ATOM	5105	CA	VAL	194	101.454	50.346	28.866	1.00	25.97	B	C
ATOM	5106	CB	VAL	194	101.516	51.750	29.490	1.00	24.85	B	C
ATOM	5107	CG1	VAL	194	102.014	52.745	28.459	1.00	25.88	B	C
ATOM	5108	CG2	VAL	194	100.153	52.147	30.032	1.00	22.12	B	C
ATOM	5109	C	VAL	194	102.887	49.864	28.661	1.00	23.74	B	C
ATOM	5110	O	VAL	194	103.535	49.384	29.597	1.00	21.86	B	O

Fig. 19: A-71

ATOM	5111	N	THR	195	103.397	49.986	27.444	1.00	25.03	B	N
ATOM	5112	CA	THR	195	104.758	49.552	27.197	1.00	26.21	B	C
ATOM	5113	CB	THR	195	104.797	48.182	26.450	1.00	38.61	B	C
ATOM	5114	OG1	THR	195	104.420	48.360	25.081	1.00	42.62	B	O
ATOM	5115	CG2	THR	195	103.828	47.195	27.087	1.00	40.24	B	C
ATOM	5116	C	THR	195	105.511	50.599	26.391	1.00	27.05	B	C
ATOM	5117	O	THR	195	104.944	51.254	25.514	1.00	29.64	B	O
ATOM	5118	N	HIS	196	106.791	50.765	26.716	1.00	33.64	B	N
ATOM	5119	CA	HIS	196	107.656	51.713	26.029	1.00	33.74	B	C
ATOM	5120	CB	HIS	196	108.815	52.119	26.942	1.00	34.91	B	C
ATOM	5121	CG	HIS	196	108.417	53.011	28.079	1.00	31.41	B	C
ATOM	5122	CD2	HIS	196	108.084	52.725	29.360	1.00	32.04	B	C
ATOM	5123	ND1	HIS	196	108.322	54.382	27.955	1.00	30.06	B	N
ATOM	5124	CE1	HIS	196	107.949	54.901	29.111	1.00	26.78	B	C
ATOM	5125	NE2	HIS	196	107.797	53.918	29.979	1.00	24.99	B	N
ATOM	5126	C	HIS	196	108.219	51.017	24.806	1.00	33.60	B	C
ATOM	5127	O	HIS	196	109.201	50.289	24.932	1.00	32.26	B	O
ATOM	5128	N	GLU	197	107.609	51.216	23.636	1.00	34.73	B	N
ATOM	5129	CA	GLU	197	108.123	50.583	22.417	1.00	32.06	B	C
ATOM	5130	CB	GLU	197	107.313	50.999	21.193	1.00	45.57	B	C
ATOM	5131	CG	GLU	197	105.913	50.386	21.130	1.00	45.91	B	C
ATOM	5132	CD	GLU	197	105.911	48.876	21.303	1.00	44.98	B	C
ATOM	5133	OE1	GLU	197	106.869	48.228	20.834	1.00	43.56	B	O
ATOM	5134	OE2	GLU	197	104.949	48.331	21.892	1.00	46.64	B	O
ATOM	5135	C	GLU	197	109.595	50.958	22.245	1.00	29.53	B	C
ATOM	5136	O	GLU	197	110.447	50.081	22.151	1.00	34.73	B	O
ATOM	5137	N	PHE	198	109.898	52.254	22.203	1.00	32.40	B	N
ATOM	5138	CA	PHE	198	111.293	52.691	22.126	1.00	34.20	B	C
ATOM	5139	CB	PHE	198	111.881	52.501	20.714	1.00	23.77	B	C
ATOM	5140	CG	PHE	198	111.239	53.331	19.636	1.00	22.02	B	C
ATOM	5141	CD1	PHE	198	111.379	54.711	19.614	1.00	28.16	B	C
ATOM	5142	CD2	PHE	198	110.539	52.715	18.597	1.00	16.76	B	C
ATOM	5143	CE1	PHE	198	110.837	55.468	18.571	1.00	24.19	B	C
ATOM	5144	CE2	PHE	198	109.990	53.460	17.548	1.00	22.67	B	C
ATOM	5145	CZ	PHE	198	110.140	54.838	17.536	1.00	26.47	B	C
ATOM	5146	C	PHE	198	111.471	54.120	22.642	1.00	36.88	B	C
ATOM	5147	O	PHE	198	110.631	54.973	22.398	1.00	38.17	B	O
ATOM	5148	N	ASN	199	112.552	54.366	23.386	1.00	21.75	B	N
ATOM	5149	CA	ASN	199	112.810	55.686	23.971	1.00	22.04	B	C
ATOM	5150	CB	ASN	199	113.924	55.613	25.007	1.00	33.57	B	C
ATOM	5151	CG	ASN	199	113.636	54.633	26.105	1.00	34.83	B	C
ATOM	5152	OD1	ASN	199	112.614	54.717	26.785	1.00	36.36	B	O
ATOM	5153	ND2	ASN	199	114.549	53.688	26.295	1.00	33.71	B	N
ATOM	5154	C	ASN	199	113.159	56.792	22.996	1.00	24.50	B	C
ATOM	5155	O	ASN	199	113.569	56.546	21.862	1.00	22.31	B	O
ATOM	5156	N	LEU	200	113.004	58.023	23.473	1.00	27.41	B	N
ATOM	5157	CA	LEU	200	113.286	59.215	22.685	1.00	29.37	B	C
ATOM	5158	CB	LEU	200	113.094	60.467	23.542	1.00	22.93	B	C
ATOM	5159	CG	LEU	200	111.694	61.088	23.545	1.00	20.78	B	C
ATOM	5160	CD1	LEU	200	111.613	62.208	24.578	1.00	25.90	B	C
ATOM	5161	CD2	LEU	200	111.375	61.607	22.140	1.00	21.95	B	C
ATOM	5162	C	LEU	200	114.685	59.223	22.104	1.00	29.77	B	C
ATOM	5163	O	LEU	200	114.899	59.698	20.992	1.00	30.79	B	O
ATOM	5164	N	ASN	201	115.635	58.685	22.856	1.00	32.06	B	N
ATOM	5165	CA	ASN	201	117.027	58.660	22.426	1.00	33.91	B	C
ATOM	5166	CB	ASN	201	117.920	59.105	23.578	1.00	34.75	B	C
ATOM	5167	CG	ASN	201	117.838	58.168	24.769	1.00	37.03	B	C
ATOM	5168	OD1	ASN	201	118.389	58.443	25.832	1.00	37.17	B	O
ATOM	5169	ND2	ASN	201	117.147	57.052	24.592	1.00	34.87	B	N
ATOM	5170	C	ASN	201	117.517	57.309	21.936	1.00	33.96	B	C
ATOM	5171	O	ASN	201	118.723	57.111	21.825	1.00	29.86	B	O
ATOM	5172	N	LYS	202	116.603	56.382	21.653	1.00	35.80	B	N
ATOM	5173	CA	LYS	202	116.990	55.051	21.183	1.00	35.92	B	C
ATOM	5174	CB	LYS	202	115.786	54.107	21.160	1.00	34.30	B	C
ATOM	5175	CG	LYS	202	116.107	52.652	20.788	1.00	35.84	B	C
ATOM	5176	CD	LYS	202	116.841	51.929	21.898	1.00	37.75	B	C
ATOM	5177	CE	LYS	202	116.185	52.179	23.273	1.00	43.50	B	C
ATOM	5178	NZ	LYS	202	114.729	51.801	23.388	1.00	42.52	B	N
ATOM	5179	C	LYS	202	117.617	55.071	19.800	1.00	34.79	B	C
ATOM	5180	O	LYS	202	118.667	54.472	19.589	1.00	32.07	B	O
ATOM	5181	N	TYR	203	116.977	55.747	18.852	1.00	23.81	B	N
ATOM	5182	CA	TYR	203	117.509	55.815	17.491	1.00	23.49	B	C
ATOM	5183	CB	TYR	203	116.466	55.300	16.499	1.00	32.41	B	C

Fig. 19: A-72

ATOM	5184	CG	TYR	203	115.907	53.951	16.886	1.00	31.08	B	C
ATOM	5185	CD1	TYR	203	114.665	53.844	17.509	1.00	31.69	B	C
ATOM	5186	CE1	TYR	203	114.179	52.613	17.930	1.00	28.16	B	C
ATOM	5187	CD2	TYR	203	116.649	52.784	16.689	1.00	33.97	B	C
ATOM	5188	CE2	TYR	203	116.173	51.550	17.109	1.00	36.72	B	C
ATOM	5189	CZ	TYR	203	114.940	51.474	17.730	1.00	36.34	B	C
ATOM	5190	OH	TYR	203	114.466	50.262	18.169	1.00	41.34	B	O
ATOM	5191	C	TYR	203	117.957	57.230	17.114	1.00	24.13	B	C
ATOM	5192	O	TYR	203	117.268	58.211	17.387	1.00	22.30	B	O
ATOM	5193	N	SER	204	119.122	57.323	16.484	1.00	32.64	B	N
ATOM	5194	CA	SER	204	119.693	58.608	16.089	1.00	34.49	B	C
ATOM	5195	CB	SER	204	121.199	58.588	16.320	1.00	50.27	B	C
ATOM	5196	OG	SER	204	121.780	57.499	15.621	1.00	52.10	B	O
ATOM	5197	C	SER	204	119.432	58.924	14.632	1.00	37.07	B	C
ATOM	5198	O	SER	204	119.922	59.919	14.118	1.00	37.58	B	O
ATOM	5199	N	SER	205	118.657	58.082	13.966	1.00	56.25	B	N
ATOM	5200	CA	SER	205	118.379	58.289	12.558	1.00	55.91	B	C
ATOM	5201	CB	SER	205	119.256	57.357	11.734	1.00	30.45	B	C
ATOM	5202	OG	SER	205	118.818	57.302	10.393	1.00	35.94	B	O
ATOM	5203	C	SER	205	116.918	58.067	12.195	1.00	54.04	B	C
ATOM	5204	O	SER	205	116.208	57.320	12.866	1.00	50.30	B	O
ATOM	5205	N	THR	206	116.477	58.718	11.122	1.00	22.26	B	N
ATOM	5206	CA	THR	206	115.105	58.589	10.661	1.00	23.61	B	C
ATOM	5207	CB	THR	206	114.799	59.611	9.560	1.00	36.04	B	C
ATOM	5208	OG1	THR	206	114.968	60.935	10.086	1.00	34.85	B	O
ATOM	5209	CG2	THR	206	113.364	59.438	9.047	1.00	34.41	B	C
ATOM	5210	C	THR	206	114.780	57.188	10.144	1.00	24.20	B	C
ATOM	5211	O	THR	206	113.676	56.683	10.363	1.00	26.99	B	O
ATOM	5212	N	GLU	207	115.719	56.554	9.447	1.00	31.43	B	N
ATOM	5213	CA	GLU	207	115.444	55.210	8.964	1.00	30.59	B	C
ATOM	5214	CB	GLU	207	116.448	54.791	7.893	1.00	74.76	B	C
ATOM	5215	CG	GLU	207	117.897	54.985	8.248	1.00	75.48	B	C
ATOM	5216	CD	GLU	207	118.817	54.402	7.189	1.00	76.89	B	C
ATOM	5217	OE1	GLU	207	118.595	54.668	5.982	1.00	76.12	B	O
ATOM	5218	OE2	GLU	207	119.765	53.679	7.565	1.00	75.79	B	O
ATOM	5219	C	GLU	207	115.462	54.237	10.141	1.00	31.09	B	C
ATOM	5220	O	GLU	207	114.647	53.315	10.194	1.00	31.04	B	O
ATOM	5221	N	GLU	208	116.373	54.449	11.093	1.00	40.73	B	N
ATOM	5222	CA	GLU	208	116.441	53.584	12.267	1.00	42.46	B	C
ATOM	5223	CB	GLU	208	117.542	54.038	13.230	1.00	57.02	B	C
ATOM	5224	CG	GLU	208	118.951	53.899	12.682	1.00	54.49	B	C
ATOM	5225	CD	GLU	208	120.022	54.254	13.703	1.00	54.01	B	C
ATOM	5226	OE1	GLU	208	121.217	54.253	13.333	1.00	59.78	B	O
ATOM	5227	OE2	GLU	208	119.669	54.533	14.873	1.00	52.73	B	O
ATOM	5228	C	GLU	208	115.100	53.611	12.991	1.00	43.16	B	C
ATOM	5229	O	GLU	208	114.637	52.584	13.489	1.00	44.16	B	O
ATOM	5230	N	VAL	209	114.478	54.787	13.046	1.00	30.06	B	N
ATOM	5231	CA	VAL	209	113.190	54.922	13.709	1.00	28.98	B	C
ATOM	5232	CB	VAL	209	112.879	56.399	14.058	1.00	17.77	B	C
ATOM	5233	CG1	VAL	209	111.379	56.612	14.232	1.00	18.10	B	C
ATOM	5234	CG2	VAL	209	113.575	56.762	15.349	1.00	18.79	B	C
ATOM	5235	C	VAL	209	112.098	54.359	12.820	1.00	27.00	B	C
ATOM	5236	O	VAL	209	111.198	53.660	13.296	1.00	25.96	B	O
ATOM	5237	N	LEU	210	112.187	54.655	11.529	1.00	33.19	B	N
ATOM	5238	CA	LEU	210	111.207	54.164	10.570	1.00	33.52	B	C
ATOM	5239	CB	LEU	210	111.557	54.643	9.168	1.00	15.67	B	C
ATOM	5240	CG	LEU	210	110.629	55.672	8.535	1.00	15.91	B	C
ATOM	5241	CD1	LEU	210	111.182	55.981	7.171	1.00	12.46	B	C
ATOM	5242	CD2	LEU	210	109.191	55.157	8.437	1.00	9.36	B	C
ATOM	5243	C	LEU	210	111.152	52.639	10.571	1.00	31.78	B	C
ATOM	5244	O	LEU	210	110.090	52.042	10.382	1.00	32.55	B	O
ATOM	5245	N	VAL	211	112.307	52.017	10.779	1.00	24.37	B	N
ATOM	5246	CA	VAL	211	112.404	50.569	10.809	1.00	24.13	B	C
ATOM	5247	CB	VAL	211	113.852	50.123	10.575	1.00	20.01	B	C
ATOM	5248	CG1	VAL	211	114.002	48.647	10.897	1.00	22.19	B	C
ATOM	5249	CG2	VAL	211	114.239	50.405	9.118	1.00	20.62	B	C
ATOM	5250	C	VAL	211	111.913	49.997	12.129	1.00	23.38	B	C
ATOM	5251	O	VAL	211	111.260	48.958	12.164	1.00	24.06	B	O
ATOM	5252	N	ALA	212	112.230	50.674	13.221	1.00	40.83	B	N
ATOM	5253	CA	ALA	212	111.803	50.203	14.526	1.00	39.81	B	C
ATOM	5254	CB	ALA	212	112.489	51.000	15.612	1.00	28.52	B	C
ATOM	5255	C	ALA	212	110.295	50.339	14.650	1.00	37.62	B	C
ATOM	5256	O	ALA	212	109.626	49.493	15.256	1.00	37.56	B	O

Fig. 19: A-73

ATOM	5257	N	ALA	213	109.759	51.408	14.069	1.00	31.97	B	N
ATOM	5258	CA	ALA	213	108.324	51.658	14.122	1.00	33.14	B	C
ATOM	5259	CB	ALA	213	107.999	52.998	13.459	1.00	19.99	B	C
ATOM	5260	C	ALA	213	107.530	50.535	13.458	1.00	31.94	B	C
ATOM	5261	O	ALA	213	106.556	50.029	14.025	1.00	29.57	B	O
ATOM	5262	N	ASN	214	107.954	50.142	12.258	1.00	35.89	B	N
ATOM	5263	CA	ASN	214	107.264	49.091	11.524	1.00	39.76	B	C
ATOM	5264	CB	ASN	214	107.804	48.970	10.100	1.00	79.46	B	C
ATOM	5265	CG	ASN	214	107.278	50.049	9.190	1.00	81.19	B	C
ATOM	5266	OD1	ASN	214	107.668	51.210	9.296	1.00	83.12	B	O
ATOM	5267	ND2	ASN	214	106.379	49.676	8.289	1.00	81.61	B	N
ATOM	5268	C	ASN	214	107.348	47.738	12.207	1.00	42.15	B	C
ATOM	5269	O	ASN	214	106.583	46.829	11.891	1.00	42.87	B	O
ATOM	5270	N	LYS	215	108.271	47.596	13.148	1.00	30.37	B	N
ATOM	5271	CA	LYS	215	108.418	46.326	13.856	1.00	30.81	B	C
ATOM	5272	CB	LYS	215	109.892	46.059	14.209	1.00	46.54	B	C
ATOM	5273	CG	LYS	215	110.791	45.922	12.978	1.00	54.12	B	C
ATOM	5274	CD	LYS	215	112.062	45.124	13.256	1.00	57.66	B	C
ATOM	5275	CE	LYS	215	112.950	45.778	14.311	1.00	61.12	B	C
ATOM	5276	NZ	LYS	215	114.249	45.057	14.483	1.00	62.11	B	N
ATOM	5277	C	LYS	215	107.560	46.274	15.113	1.00	28.94	B	C
ATOM	5278	O	LYS	215	107.568	45.277	15.832	1.00	30.16	B	O
ATOM	5279	N	ILE	216	106.809	47.341	15.377	1.00	44.32	B	N
ATOM	5280	CA	ILE	216	105.945	47.362	16.553	1.00	41.14	B	C
ATOM	5281	CB	ILE	216	105.443	48.776	16.874	1.00	15.33	B	C
ATOM	5282	CG2	ILE	216	104.492	48.730	18.038	1.00	12.11	B	C
ATOM	5283	CG1	ILE	216	106.616	49.674	17.243	1.00	12.01	B	C
ATOM	5284	CD1	ILE	216	106.191	51.073	17.602	1.00	10.70	B	C
ATOM	5285	C	ILE	216	104.740	46.447	16.369	1.00	39.58	B	C
ATOM	5286	O	ILE	216	104.035	46.498	15.361	1.00	40.28	B	O
ATOM	5287	N	VAL	217	104.524	45.611	17.372	1.00	36.13	B	N
ATOM	5288	CA	VAL	217	103.436	44.647	17.392	1.00	37.90	B	C
ATOM	5289	CB	VAL	217	103.949	43.284	17.887	1.00	59.95	B	C
ATOM	5290	CG1	VAL	217	102.793	42.367	18.217	1.00	59.95	B	C
ATOM	5291	CG2	VAL	217	104.837	42.666	16.829	1.00	59.95	B	C
ATOM	5292	C	VAL	217	102.316	45.111	18.311	1.00	39.06	B	C
ATOM	5293	O	VAL	217	102.565	45.725	19.352	1.00	38.52	B	O
ATOM	5294	N	GLN	218	101.084	44.809	17.914	1.00	32.14	B	N
ATOM	5295	CA	GLN	218	99.907	45.181	18.687	1.00	32.80	B	C
ATOM	5296	CB	GLN	218	98.646	44.976	17.850	1.00	28.44	B	C
ATOM	5297	CG	GLN	218	97.378	45.433	18.528	1.00	28.44	B	C
ATOM	5298	CD	GLN	218	96.153	45.273	17.644	1.00	28.44	B	C
ATOM	5299	OE1	GLN	218	95.096	45.843	17.928	1.00	28.44	B	O
ATOM	5300	NE2	GLN	218	96.283	44.490	16.571	1.00	28.44	B	N
ATOM	5301	C	GLN	218	99.856	44.288	19.913	1.00	32.25	B	C
ATOM	5302	O	GLN	218	99.948	43.079	19.792	1.00	36.00	B	O
ATOM	5303	N	ARG	219	99.709	44.883	21.091	1.00	14.17	B	N
ATOM	5304	CA	ARG	219	99.664	44.114	22.330	1.00	13.82	B	C
ATOM	5305	CB	ARG	219	100.490	44.828	23.394	1.00	43.11	B	C
ATOM	5306	CG	ARG	219	101.627	45.640	22.823	1.00	43.11	B	C
ATOM	5307	CD	ARG	219	102.594	46.039	23.901	1.00	43.11	B	C
ATOM	5308	NE	ARG	219	103.597	45.007	24.124	1.00	43.11	B	N
ATOM	5309	CZ	ARG	219	104.694	44.867	23.384	1.00	43.11	B	C
ATOM	5310	NH1	ARG	219	104.921	45.705	22.369	1.00	43.11	B	N
ATOM	5311	NH2	ARG	219	105.566	43.900	23.661	1.00	43.11	B	N
ATOM	5312	C	ARG	219	98.221	43.910	22.821	1.00	15.03	B	C
ATOM	5313	O	ARG	219	97.976	43.309	23.871	1.00	15.04	B	O
ATOM	5314	N	GLY	220	97.269	44.423	22.048	1.00	30.91	B	N
ATOM	5315	CA	GLY	220	95.868	44.283	22.402	1.00	30.52	B	C
ATOM	5316	C	GLY	220	95.495	44.884	23.742	1.00	30.19	B	C
ATOM	5317	O	GLY	220	96.246	45.674	24.327	1.00	28.53	B	O
ATOM	5318	N	GLY	221	94.316	44.511	24.222	1.00	22.15	B	N
ATOM	5319	CA	GLY	221	93.852	45.009	25.500	1.00	20.72	B	C
ATOM	5320	C	GLY	221	92.348	44.902	25.652	1.00	21.14	B	C
ATOM	5321	O	GLY	221	91.598	45.328	24.776	1.00	17.94	B	O
ATOM	5322	N	ARG	222	91.897	44.327	26.760	1.00	28.36	B	N
ATOM	5323	CA	ARG	222	90.467	44.199	27.011	1.00	29.07	B	C
ATOM	5324	CB	ARG	222	90.204	43.114	28.053	1.00	26.86	B	C
ATOM	5325	CG	ARG	222	90.365	41.713	27.491	1.00	26.86	B	C
ATOM	5326	CD	ARG	222	90.427	40.663	28.578	1.00	26.86	B	C
ATOM	5327	NE	ARG	222	91.679	40.734	29.316	1.00	26.86	B	N
ATOM	5328	CZ	ARG	222	92.021	39.885	30.274	1.00	26.86	B	C
ATOM	5329	NH1	ARG	222	91.201	38.895	30.612	1.00	26.86	B	N

Fig. 19: A-74

ATOM	5330	NH2	ARG	222	93.184	40.027	30.893	1.00	26.86	B	N
ATOM	5331	C	ARG	222	89.899	45.529	27.482	1.00	29.12	B	C
ATOM	5332	O	ARG	222	88.686	45.686	27.599	1.00	29.89	B	O
ATOM	5333	N	GLN	223	90.792	46.477	27.756	1.00	34.74	B	N
ATOM	5334	CA	GLN	223	90.423	47.826	28.182	1.00	33.03	B	C
ATOM	5335	CB	GLN	223	90.700	48.050	29.677	1.00	36.16	B	C
ATOM	5336	CG	GLN	223	89.723	47.394	30.641	1.00	37.60	B	C
ATOM	5337	CD	GLN	223	90.065	45.957	30.915	1.00	38.01	B	C
ATOM	5338	OE1	GLN	223	91.209	45.635	31.230	1.00	38.41	B	O
ATOM	5339	NE2	GLN	223	89.075	45.080	30.811	1.00	38.45	B	N
ATOM	5340	C	GLN	223	91.221	48.849	27.372	1.00	33.77	B	C
ATOM	5341	O	GLN	223	92.122	48.487	26.619	1.00	33.25	B	O
ATOM	5342	N	THR	224	90.893	50.126	27.535	1.00	56.95	B	N
ATOM	5343	CA	THR	224	91.572	51.197	26.820	1.00	54.83	B	C
ATOM	5344	CB	THR	224	90.628	51.834	25.793	1.00	7.14	B	C
ATOM	5345	OG1	THR	224	90.118	50.811	24.930	1.00	7.13	B	O
ATOM	5346	CG2	THR	224	91.357	52.895	24.965	1.00	4.73	B	C
ATOM	5347	C	THR	224	92.002	52.252	27.829	1.00	51.84	B	C
ATOM	5348	O	THR	224	91.290	53.221	28.067	1.00	48.33	B	O
ATOM	5349	N	MET	225	93.175	52.061	28.419	1.00	27.08	B	N
ATOM	5350	CA	MET	225	93.679	52.980	29.426	1.00	27.97	B	C
ATOM	5351	CB	MET	225	94.712	52.269	30.301	1.00	32.79	B	C
ATOM	5352	CG	MET	225	94.280	50.904	30.804	1.00	30.22	B	C
ATOM	5353	SD	MET	225	92.971	50.963	31.995	1.00	37.96	B	S
ATOM	5354	CE	MET	225	93.153	49.343	32.760	1.00	34.54	B	C
ATOM	5355	C	MET	225	94.304	54.237	28.846	1.00	29.00	B	C
ATOM	5356	O	MET	225	95.442	54.561	29.180	1.00	30.46	B	O
ATOM	5357	N	THR	226	93.571	54.953	27.997	1.00	32.08	B	N
ATOM	5358	CA	THR	226	94.102	56.178	27.393	1.00	31.55	B	C
ATOM	5359	CB	THR	226	93.013	56.963	26.655	1.00	28.80	B	C
ATOM	5360	OG1	THR	226	92.395	56.132	25.665	1.00	30.82	B	O
ATOM	5361	CG2	THR	226	93.620	58.170	25.976	1.00	26.52	B	C
ATOM	5362	C	THR	226	94.735	57.104	28.438	1.00	30.15	B	C
ATOM	5363	O	THR	226	95.804	57.672	28.216	1.00	24.84	B	O
ATOM	5364	N	ALA	227	94.075	57.249	29.581	1.00	17.95	B	N
ATOM	5365	CA	ALA	227	94.594	58.094	30.645	1.00	16.89	B	C
ATOM	5366	CB	ALA	227	93.655	58.069	31.829	1.00	18.36	B	C
ATOM	5367	C	ALA	227	95.975	57.633	31.076	1.00	17.55	B	C
ATOM	5368	O	ALA	227	96.898	58.439	31.199	1.00	18.35	B	O
ATOM	5369	N	LEU	228	96.111	56.331	31.307	1.00	19.16	B	N
ATOM	5370	CA	LEU	228	97.384	55.752	31.728	1.00	17.60	B	C
ATOM	5371	CB	LEU	228	97.206	54.252	32.017	1.00	6.84	B	C
ATOM	5372	CG	LEU	228	98.453	53.498	32.483	1.00	14.73	B	C
ATOM	5373	CD1	LEU	228	99.020	54.157	33.734	1.00	12.32	B	C
ATOM	5374	CD2	LEU	228	98.097	52.064	32.732	1.00	11.78	B	C
ATOM	5375	C	LEU	228	98.463	55.955	30.662	1.00	16.78	B	C
ATOM	5376	O	LEU	228	99.605	56.321	30.971	1.00	19.76	B	O
ATOM	5377	N	GLY	229	98.094	55.713	29.408	1.00	21.79	B	N
ATOM	5378	CA	GLY	229	99.033	55.877	28.318	1.00	24.15	B	C
ATOM	5379	C	GLY	229	99.620	57.267	28.293	1.00	26.71	B	C
ATOM	5380	O	GLY	229	100.843	57.422	28.296	1.00	27.30	B	O
ATOM	5381	N	ILE	230	98.756	58.281	28.280	1.00	20.54	B	N
ATOM	5382	CA	ILE	230	99.216	59.666	28.259	1.00	21.87	B	C
ATOM	5383	CB	ILE	230	98.039	60.677	28.160	1.00	18.79	B	C
ATOM	5384	CG2	ILE	230	98.595	62.090	28.034	1.00	18.79	B	C
ATOM	5385	CG1	ILE	230	97.174	60.370	26.933	1.00	18.79	B	C
ATOM	5386	CD1	ILE	230	95.945	61.225	26.807	1.00	18.79	B	C
ATOM	5387	C	ILE	230	100.042	60.007	29.505	1.00	22.13	B	C
ATOM	5388	O	ILE	230	101.101	60.634	29.402	1.00	20.06	B	O
ATOM	5389	N	ASP	231	99.566	59.595	30.677	1.00	30.92	B	N
ATOM	5390	CA	ASP	231	100.286	59.876	31.916	1.00	29.32	B	C
ATOM	5391	CB	ASP	231	99.494	59.354	33.116	1.00	27.91	B	C
ATOM	5392	CG	ASP	231	99.993	59.917	34.442	1.00	34.91	B	C
ATOM	5393	OD1	ASP	231	99.939	61.155	34.644	1.00	33.67	B	O
ATOM	5394	OD2	ASP	231	100.432	59.112	35.288	1.00	38.45	B	O
ATOM	5395	C	ASP	231	101.676	59.231	31.884	1.00	30.30	B	C
ATOM	5396	O	ASP	231	102.669	59.838	32.318	1.00	27.52	B	O
ATOM	5397	N	THR	232	101.741	58.007	31.361	1.00	43.37	B	N
ATOM	5398	CA	THR	232	102.998	57.276	31.260	1.00	42.16	B	C
ATOM	5399	CB	THR	232	102.768	55.830	30.801	1.00	59.43	B	C
ATOM	5400	OG1	THR	232	101.963	55.148	31.771	1.00	57.94	B	O
ATOM	5401	CG2	THR	232	104.097	55.098	30.645	1.00	52.97	B	C
ATOM	5402	C	THR	232	103.939	57.959	30.274	1.00	42.79	B	C

Fig. 19: A-75

ATOM	5403	O	THR	232	105.153	58.050	30.509	1.00	42.96	B	O
ATOM	5404	N	ALA	233	103.383	58.427	29.161	1.00	22.02	B	N
ATOM	5405	CA	ALA	233	104.202	59.116	28.179	1.00	24.67	B	C
ATOM	5406	CB	ALA	233	103.373	59.472	26.961	1.00	49.88	B	C
ATOM	5407	C	ALA	233	104.752	60.385	28.836	1.00	26.98	B	C
ATOM	5408	O	ALA	233	105.862	60.834	28.532	1.00	28.89	B	O
ATOM	5409	N	ARG	234	103.967	60.947	29.751	1.00	50.27	B	N
ATOM	5410	CA	ARG	234	104.361	62.165	30.431	1.00	53.37	B	C
ATOM	5411	CB	ARG	234	103.146	62.842	31.077	1.00	50.29	B	C
ATOM	5412	CG	ARG	234	103.377	64.312	31.390	1.00	50.29	B	C
ATOM	5413	CD	ARG	234	102.536	64.816	32.561	1.00	50.29	B	C
ATOM	5414	NE	ARG	234	103.103	64.432	33.852	1.00	50.29	B	N
ATOM	5415	CZ	ARG	234	102.668	63.418	34.592	1.00	50.29	B	C
ATOM	5416	NH1	ARG	234	101.650	62.682	34.172	1.00	50.29	B	N
ATOM	5417	NH2	ARG	234	103.258	63.135	35.744	1.00	50.29	B	N
ATOM	5418	C	ARG	234	105.406	61.904	31.498	1.00	55.50	B	C
ATOM	5419	O	ARG	234	106.556	62.316	31.368	1.00	55.55	B	O
ATOM	5420	N	LYS	235	105.009	61.196	32.547	1.00	27.28	B	N
ATOM	5421	CA	LYS	235	105.914	60.939	33.660	1.00	27.23	B	C
ATOM	5422	CB	LYS	235	105.129	60.356	34.848	1.00	39.45	B	C
ATOM	5423	CG	LYS	235	104.888	58.857	34.831	1.00	40.60	B	C
ATOM	5424	CD	LYS	235	104.027	58.450	36.030	1.00	40.42	B	C
ATOM	5425	CE	LYS	235	104.119	56.955	36.346	1.00	41.22	B	C
ATOM	5426	NZ	LYS	235	103.715	56.073	35.205	1.00	41.98	B	N
ATOM	5427	C	LYS	235	107.149	60.078	33.375	1.00	27.37	B	C
ATOM	5428	O	LYS	235	108.112	60.118	34.130	1.00	27.71	B	O
ATOM	5429	N	GLU	236	107.133	59.313	32.290	1.00	28.33	B	N
ATOM	5430	CA	GLU	236	108.264	58.454	31.964	1.00	29.95	B	C
ATOM	5431	CB	GLU	236	107.803	56.992	31.884	1.00	47.54	B	C
ATOM	5432	CG	GLU	236	107.861	56.249	33.216	1.00	50.31	B	C
ATOM	5433	CD	GLU	236	107.031	54.965	33.245	1.00	52.79	B	C
ATOM	5434	OE1	GLU	236	107.194	54.118	32.342	1.00	52.88	B	O
ATOM	5435	OE2	GLU	236	106.219	54.797	34.184	1.00	52.63	B	O
ATOM	5436	C	GLU	236	108.966	58.840	30.670	1.00	28.50	B	C
ATOM	5437	O	GLU	236	110.092	59.336	30.684	1.00	29.93	B	O
ATOM	5438	N	ALA	237	108.287	58.617	29.552	1.00	22.73	B	N
ATOM	5439	CA	ALA	237	108.860	58.901	28.248	1.00	20.20	B	C
ATOM	5440	CB	ALA	237	107.783	58.831	27.180	1.00	41.37	B	C
ATOM	5441	C	ALA	237	109.562	60.233	28.187	1.00	19.04	B	C
ATOM	5442	O	ALA	237	110.636	60.344	27.589	1.00	17.46	B	O
ATOM	5443	N	PHE	238	108.962	61.242	28.810	1.00	29.57	B	N
ATOM	5444	CA	PHE	238	109.530	62.580	28.795	1.00	29.00	B	C
ATOM	5445	CB	PHE	238	108.419	63.620	28.752	1.00	35.30	B	C
ATOM	5446	CG	PHE	238	107.856	63.854	27.381	1.00	34.33	B	C
ATOM	5447	CD1	PHE	238	106.531	63.532	27.101	1.00	35.56	B	C
ATOM	5448	CD2	PHE	238	108.635	64.429	26.380	1.00	31.93	B	C
ATOM	5449	CE1	PHE	238	105.985	63.780	25.841	1.00	33.36	B	C
ATOM	5450	CE2	PHE	238	108.106	64.682	25.124	1.00	38.24	B	C
ATOM	5451	CZ	PHE	238	106.778	64.359	24.850	1.00	39.66	B	C
ATOM	5452	C	PHE	238	110.468	62.908	29.943	1.00	30.85	B	C
ATOM	5453	O	PHE	238	110.433	64.012	30.479	1.00	30.95	B	O
ATOM	5454	N	THR	239	111.303	61.951	30.325	1.00	29.27	B	N
ATOM	5455	CA	THR	239	112.266	62.182	31.391	1.00	33.21	B	C
ATOM	5456	CB	THR	239	112.113	61.150	32.520	1.00	23.55	B	C
ATOM	5457	OG1	THR	239	112.276	59.840	31.989	1.00	21.51	B	O
ATOM	5458	CG2	THR	239	110.745	61.242	33.153	1.00	26.46	B	C
ATOM	5459	C	THR	239	113.660	62.084	30.770	1.00	33.47	B	C
ATOM	5460	O	THR	239	113.930	61.177	29.980	1.00	33.97	B	O
ATOM	5461	N	GLU	240	114.531	63.030	31.117	1.00	17.24	B	N
ATOM	5462	CA	GLU	240	115.890	63.085	30.580	1.00	17.49	B	C
ATOM	5463	CB	GLU	240	116.748	64.003	31.444	1.00	74.12	B	C
ATOM	5464	CG	GLU	240	118.007	64.483	30.758	1.00	78.76	B	C
ATOM	5465	CD	GLU	240	118.634	65.654	31.479	1.00	81.67	B	C
ATOM	5466	OE1	GLU	240	117.904	66.627	31.774	1.00	81.77	B	O
ATOM	5467	OE2	GLU	240	119.853	65.605	31.746	1.00	81.74	B	O
ATOM	5468	C	GLU	240	116.555	61.712	30.465	1.00	18.84	B	C
ATOM	5469	O	GLU	240	117.323	61.444	29.530	1.00	20.05	B	O
ATOM	5470	N	ALA	241	116.234	60.839	31.415	1.00	54.75	B	N
ATOM	5471	CA	ALA	241	116.784	59.491	31.446	1.00	55.60	B	C
ATOM	5472	CB	ALA	241	116.331	58.783	32.723	1.00	26.00	B	C
ATOM	5473	C	ALA	241	116.387	58.678	30.212	1.00	55.07	B	C
ATOM	5474	O	ALA	241	117.093	57.751	29.823	1.00	56.53	B	O
ATOM	5475	N	ARG	242	115.259	59.024	29.598	1.00	25.17	B	N

Fig. 19: A-76

ATOM	5476	CA	ARG	242	114.805	58.305	28.417	1.00	24.91	B	C
ATOM	5477	CB	ARG	242	113.337	57.917	28.570	1.00	45.62	B	C
ATOM	5478	CG	ARG	242	113.136	56.644	29.392	1.00	45.82	B	C
ATOM	5479	CD	ARG	242	111.684	56.188	29.334	1.00	46.68	B	C
ATOM	5480	NE	ARG	242	111.525	54.733	29.424	1.00	47.88	B	N
ATOM	5481	CZ	ARG	242	111.348	54.055	30.557	1.00	47.08	B	C
ATOM	5482	NH1	ARG	242	111.307	54.695	31.721	1.00	46.13	B	N
ATOM	5483	NH2	ARG	242	111.187	52.738	30.526	1.00	49.10	B	N
ATOM	5484	C	ARG	242	115.039	59.088	27.120	1.00	26.11	B	C
ATOM	5485	O	ARG	242	114.450	58.796	26.076	1.00	29.12	B	O
ATOM	5486	N	GLY	243	115.919	60.079	27.194	1.00	41.48	B	N
ATOM	5487	CA	GLY	243	116.226	60.863	26.014	1.00	39.63	B	C
ATOM	5488	C	GLY	243	115.497	62.187	25.893	1.00	37.91	B	C
ATOM	5489	O	GLY	243	115.454	62.774	24.810	1.00	37.53	B	O
ATOM	5490	N	ALA	244	114.913	62.665	26.986	1.00	32.61	B	N
ATOM	5491	CA	ALA	244	114.209	63.941	26.939	1.00	30.61	B	C
ATOM	5492	CB	ALA	244	113.253	64.074	28.124	1.00	2.29	B	C
ATOM	5493	C	ALA	244	115.262	65.033	26.984	1.00	32.49	B	C
ATOM	5494	O	ALA	244	115.867	65.266	28.021	1.00	31.95	B	O
ATOM	5495	N	ARG	245	115.491	65.690	25.854	1.00	46.10	B	N
ATOM	5496	CA	ARG	245	116.482	66.760	25.768	1.00	46.93	B	C
ATOM	5497	CB	ARG	245	116.690	67.163	24.309	1.00	24.44	B	C
ATOM	5498	CG	ARG	245	117.460	66.126	23.503	1.00	26.91	B	C
ATOM	5499	CD	ARG	245	117.553	66.517	22.054	1.00	27.12	B	C
ATOM	5500	NE	ARG	245	116.229	66.560	21.457	1.00	21.54	B	N
ATOM	5501	CZ	ARG	245	115.999	66.826	20.179	1.00	21.36	B	C
ATOM	5502	NH1	ARG	245	117.016	67.074	19.370	1.00	20.56	B	N
ATOM	5503	NH2	ARG	245	114.756	66.834	19.708	1.00	18.65	B	N
ATOM	5504	C	ARG	245	116.101	67.986	26.585	1.00	45.30	B	C
ATOM	5505	O	ARG	245	114.975	68.480	26.496	1.00	41.41	B	O
ATOM	5506	N	ARG	246	117.051	68.476	27.376	1.00	48.54	B	N
ATOM	5507	CA	ARG	246	116.830	69.640	28.229	1.00	51.33	B	C
ATOM	5508	CB	ARG	246	118.096	69.982	29.012	1.00	83.48	B	C
ATOM	5509	CG	ARG	246	117.975	71.269	29.811	1.00	88.84	B	C
ATOM	5510	CD	ARG	246	119.295	71.647	30.449	1.00	94.76	B	C
ATOM	5511	NE	ARG	246	119.896	70.525	31.165	1.00	97.67	B	N
ATOM	5512	CZ	ARG	246	119.288	69.828	32.123	1.00	100.78	B	C
ATOM	5513	NH1	ARG	246	118.047	70.132	32.491	1.00	100.47	B	N
ATOM	5514	NH2	ARG	246	119.923	68.825	32.717	1.00	101.56	B	N
ATOM	5515	C	ARG	246	116.415	70.871	27.448	1.00	49.15	B	C
ATOM	5516	O	ARG	246	117.082	71.246	26.489	1.00	51.78	B	O
ATOM	5517	N	GLY	247	115.311	71.489	27.868	1.00	46.59	B	N
ATOM	5518	CA	GLY	247	114.825	72.705	27.233	1.00	49.17	B	C
ATOM	5519	C	GLY	247	114.381	72.609	25.787	1.00	49.24	B	C
ATOM	5520	O	GLY	247	114.531	73.560	25.019	1.00	52.20	B	O
ATOM	5521	N	VAL	248	113.836	71.462	25.407	1.00	57.57	B	N
ATOM	5522	CA	VAL	248	113.357	71.266	24.049	1.00	55.58	B	C
ATOM	5523	CB	VAL	248	114.012	70.043	23.407	1.00	22.85	B	C
ATOM	5524	CG1	VAL	248	113.384	69.765	22.056	1.00	20.50	B	C
ATOM	5525	CG2	VAL	248	115.499	70.287	23.266	1.00	14.62	B	C
ATOM	5526	C	VAL	248	111.855	71.056	24.094	1.00	58.60	B	C
ATOM	5527	O	VAL	248	111.343	70.403	25.005	1.00	62.65	B	O
ATOM	5528	N	LYS	249	111.147	71.607	23.115	1.00	37.34	B	N
ATOM	5529	CA	LYS	249	109.698	71.464	23.086	1.00	38.25	B	C
ATOM	5530	CB	LYS	249	109.115	72.122	21.832	1.00	57.29	B	C
ATOM	5531	CG	LYS	249	107.594	72.204	21.869	1.00	62.81	B	C
ATOM	5532	CD	LYS	249	107.103	72.892	23.155	1.00	63.88	B	C
ATOM	5533	CE	LYS	249	105.634	72.579	23.450	1.00	66.24	B	C
ATOM	5534	NZ	LYS	249	105.067	73.292	24.636	1.00	69.06	B	N
ATOM	5535	C	LYS	249	109.244	69.998	23.173	1.00	36.91	B	C
ATOM	5536	O	LYS	249	109.790	69.112	22.505	1.00	36.73	B	O
ATOM	5537	N	LYS	250	108.238	69.755	24.009	1.00	33.42	B	N
ATOM	5538	CA	LYS	250	107.706	68.419	24.208	1.00	33.07	B	C
ATOM	5539	CB	LYS	250	107.603	68.147	25.710	1.00	46.37	B	C
ATOM	5540	CG	LYS	250	108.970	68.151	26.374	1.00	44.97	B	C
ATOM	5541	CD	LYS	250	108.918	68.429	27.872	1.00	46.52	B	C
ATOM	5542	CE	LYS	250	108.389	67.256	28.686	1.00	45.68	B	C
ATOM	5543	NZ	LYS	250	108.578	67.474	30.157	1.00	47.50	B	N
ATOM	5544	C	LYS	250	106.355	68.263	23.506	1.00	32.42	B	C
ATOM	5545	O	LYS	250	105.380	68.931	23.842	1.00	32.10	B	O
ATOM	5546	N	VAL	251	106.320	67.372	22.519	1.00	37.83	B	N
ATOM	5547	CA	VAL	251	105.121	67.115	21.730	1.00	37.74	B	C
ATOM	5548	CB	VAL	251	105.403	67.373	20.248	1.00	28.71	B	C

Fig. 19: A-77

ATOM	5549	CG1	VAL	251	104.180	67.017	19.410	1.00	26.86	B	C
ATOM	5550	CG2	VAL	251	105.819	68.822	20.057	1.00	29.92	B	C
ATOM	5551	C	VAL	251	104.591	65.689	21.866	1.00	36.22	B	C
ATOM	5552	O	VAL	251	105.339	64.715	21.714	1.00	32.22	B	O
ATOM	5553	N	MET	252	103.289	65.572	22.122	1.00	42.57	B	N
ATOM	5554	CA	MET	252	102.651	64.269	22.275	1.00	43.55	B	C
ATOM	5555	CB	MET	252	102.013	64.160	23.660	1.00	27.32	B	C
ATOM	5556	CG	MET	252	101.440	62.787	23.998	1.00	26.01	B	C
ATOM	5557	SD	MET	252	100.740	62.725	25.675	1.00	30.06	B	S
ATOM	5558	CE	MET	252	102.222	63.011	26.691	1.00	21.37	B	C
ATOM	5559	C	MET	252	101.583	64.060	21.217	1.00	42.57	B	C
ATOM	5560	O	MET	252	100.761	64.937	20.982	1.00	44.94	B	O
ATOM	5561	N	VAL	253	101.604	62.900	20.573	1.00	21.89	B	N
ATOM	5562	CA	VAL	253	100.607	62.580	19.558	1.00	23.04	B	C
ATOM	5563	CB	VAL	253	101.267	62.281	18.187	1.00	9.79	B	C
ATOM	5564	CG1	VAL	253	100.191	61.900	17.168	1.00	11.21	B	C
ATOM	5565	CG2	VAL	253	102.044	63.490	17.701	1.00	9.43	B	C
ATOM	5566	C	VAL	253	99.819	61.353	20.015	1.00	22.61	B	C
ATOM	5567	O	VAL	253	100.383	60.276	20.161	1.00	21.05	B	O
ATOM	5568	N	ILE	254	98.522	61.516	20.252	1.00	29.50	B	N
ATOM	5569	CA	ILE	254	97.692	60.403	20.701	1.00	26.40	B	C
ATOM	5570	CB	ILE	254	96.820	60.777	21.925	1.00	25.01	B	C
ATOM	5571	CG2	ILE	254	96.017	59.564	22.369	1.00	21.48	B	C
ATOM	5572	CG1	ILE	254	97.697	61.256	23.089	1.00	23.59	B	C
ATOM	5573	CD1	ILE	254	98.231	62.661	22.921	1.00	23.22	B	C
ATOM	5574	C	ILE	254	96.757	59.905	19.611	1.00	24.49	B	C
ATOM	5575	O	ILE	254	96.163	60.692	18.876	1.00	26.36	B	O
ATOM	5576	N	VAL	255	96.628	58.587	19.516	1.00	26.63	B	N
ATOM	5577	CA	VAL	255	95.758	57.981	18.521	1.00	25.37	B	C
ATOM	5578	CB	VAL	255	96.553	57.259	17.428	1.00	15.78	B	C
ATOM	5579	CG1	VAL	255	95.672	57.064	16.198	1.00	14.23	B	C
ATOM	5580	CG2	VAL	255	97.805	58.036	17.089	1.00	16.42	B	C
ATOM	5581	C	VAL	255	94.907	56.947	19.221	1.00	23.12	B	C
ATOM	5582	O	VAL	255	95.444	56.089	19.916	1.00	25.12	B	O
ATOM	5583	N	THR	256	93.591	57.012	19.036	1.00	8.41	B	N
ATOM	5584	CA	THR	256	92.709	56.052	19.689	1.00	8.83	B	C
ATOM	5585	CB	THR	256	92.529	56.416	21.189	1.00	19.33	B	C
ATOM	5586	OG1	THR	256	91.459	55.645	21.755	1.00	15.37	B	O
ATOM	5587	CG2	THR	256	92.255	57.908	21.344	1.00	18.18	B	C
ATOM	5588	C	THR	256	91.353	55.955	18.992	1.00	12.31	B	C
ATOM	5589	O	THR	256	90.941	56.881	18.308	1.00	8.47	B	O
ATOM	5590	N	ASP	257	90.673	54.824	19.162	1.00	17.26	B	N
ATOM	5591	CA	ASP	257	89.375	54.601	18.530	1.00	17.64	B	C
ATOM	5592	CB	ASP	257	89.491	53.474	17.491	1.00	29.20	B	C
ATOM	5593	CG	ASP	257	89.534	52.074	18.122	1.00	34.56	B	C
ATOM	5594	OD1	ASP	257	89.894	51.957	19.313	1.00	35.03	B	O
ATOM	5595	OD2	ASP	257	89.220	51.084	17.421	1.00	39.83	B	O
ATOM	5596	C	ASP	257	88.267	54.259	19.535	1.00	14.23	B	C
ATOM	5597	O	ASP	257	87.243	53.660	19.169	1.00	13.47	B	O
ATOM	5598	N	GLY	258	88.462	54.634	20.798	1.00	26.33	B	N
ATOM	5599	CA	GLY	258	87.450	54.331	21.793	1.00	28.75	B	C
ATOM	5600	C	GLY	258	87.546	55.109	23.088	1.00	32.57	B	C
ATOM	5601	O	GLY	258	88.615	55.601	23.476	1.00	28.29	B	O
ATOM	5602	N	GLU	259	86.404	55.231	23.755	1.00	39.52	B	N
ATOM	5603	CA	GLU	259	86.335	55.931	25.025	1.00	41.40	B	C
ATOM	5604	CB	GLU	259	84.905	55.925	25.555	1.00	36.52	B	C
ATOM	5605	CG	GLU	259	83.950	56.783	24.749	1.00	44.30	B	C
ATOM	5606	CD	GLU	259	82.509	56.415	24.994	1.00	48.11	B	C
ATOM	5607	OE1	GLU	259	81.625	57.175	24.546	1.00	54.86	B	O
ATOM	5608	OE2	GLU	259	82.262	55.360	25.626	1.00	48.13	B	O
ATOM	5609	C	GLU	259	87.240	55.210	26.003	1.00	40.26	B	C
ATOM	5610	O	GLU	259	87.125	53.999	26.194	1.00	37.43	B	O
ATOM	5611	N	SER	260	88.155	55.953	26.610	1.00	34.06	B	N
ATOM	5612	CA	SER	260	89.067	55.369	27.576	1.00	37.22	B	C
ATOM	5613	CB	SER	260	90.041	56.432	28.083	1.00	50.00	B	C
ATOM	5614	OG	SER	260	89.341	57.516	28.666	1.00	50.51	B	O
ATOM	5615	C	SER	260	88.261	54.814	28.740	1.00	37.12	B	C
ATOM	5616	O	SER	260	87.177	55.300	29.043	1.00	33.15	B	O
ATOM	5617	N	HIS	261	88.781	53.787	29.392	1.00	36.47	B	N
ATOM	5618	CA	HIS	261	88.084	53.212	30.527	1.00	40.82	B	C
ATOM	5619	CB	HIS	261	88.509	51.755	30.728	1.00	21.13	B	C
ATOM	5620	CG	HIS	261	87.908	50.809	29.732	1.00	24.33	B	C
ATOM	5621	CD2	HIS	261	88.345	50.398	28.519	1.00	23.44	B	C

Fig. 19: A-78

ATOM	5622	ND1	HIS	261	86.688	50.197	29.925	1.00	25.81	B	N
ATOM	5623	CE1	HIS	261	86.400	49.448	28.876	1.00	25.88	B	C
ATOM	5624	NE2	HIS	261	87.390	49.554	28.009	1.00	23.15	B	N
ATOM	5625	C	HIS	261	88.394	54.045	31.761	1.00	41.88	B	C
ATOM	5626	O	HIS	261	87.711	53.940	32.779	1.00	39.10	B	O
ATOM	5627	N	ASP	262	89.425	54.880	31.657	1.00	49.36	B	N
ATOM	5628	CA	ASP	262	89.825	55.758	32.753	1.00	54.33	B	C
ATOM	5629	CB	ASP	262	91.343	55.676	32.985	1.00	33.92	B	C
ATOM	5630	CG	ASP	262	92.124	55.281	31.733	1.00	33.92	B	C
ATOM	5631	OD1	ASP	262	91.724	55.659	30.611	1.00	33.92	B	O
ATOM	5632	OD2	ASP	262	93.162	54.600	31.875	1.00	33.92	B	O
ATOM	5633	C	ASP	262	89.418	57.218	32.507	1.00	54.38	B	C
ATOM	5634	O	ASP	262	90.221	58.134	32.700	1.00	54.24	B	O
ATOM	5635	N	ASN	263	88.171	57.424	32.085	1.00	68.10	B	N
ATOM	5636	CA	ASN	263	87.646	58.765	31.813	1.00	69.27	B	C
ATOM	5637	CB	ASN	263	86.123	58.734	31.630	1.00	82.52	B	C
ATOM	5638	CG	ASN	263	85.660	57.631	30.707	1.00	86.89	B	C
ATOM	5639	OD1	ASN	263	85.981	57.626	29.519	1.00	88.39	B	O
ATOM	5640	ND2	ASN	263	84.893	56.686	31.249	1.00	81.39	B	N
ATOM	5641	C	ASN	263	87.948	59.670	32.998	1.00	69.91	B	C
ATOM	5642	O	ASN	263	88.360	60.822	32.841	1.00	68.81	B	O
ATOM	5643	N	TYR	264	87.732	59.122	34.187	1.00	59.82	B	N
ATOM	5644	CA	TYR	264	87.925	59.837	35.432	1.00	57.67	B	C
ATOM	5645	CB	TYR	264	87.914	58.853	36.590	1.00	108.49	B	C
ATOM	5646	CG	TYR	264	86.626	58.083	36.660	1.00	108.49	B	C
ATOM	5647	CD1	TYR	264	86.284	57.171	35.663	1.00	108.49	B	C
ATOM	5648	CE1	TYR	264	85.074	56.490	35.698	1.00	108.49	B	C
ATOM	5649	CD2	TYR	264	85.723	58.292	37.699	1.00	108.49	B	C
ATOM	5650	CE2	TYR	264	84.509	57.615	37.744	1.00	108.49	B	C
ATOM	5651	CZ	TYR	264	84.190	56.717	36.741	1.00	108.49	B	C
ATOM	5652	OH	TYR	264	82.987	56.052	36.783	1.00	108.49	B	O
ATOM	5653	C	TYR	264	89.156	60.710	35.512	1.00	56.32	B	C
ATOM	5654	O	TYR	264	89.047	61.935	35.549	1.00	53.45	B	O
ATOM	5655	N	ARG	265	90.331	60.098	35.527	1.00	41.74	B	N
ATOM	5656	CA	ARG	265	91.544	60.892	35.641	1.00	40.64	B	C
ATOM	5657	CB	ARG	265	92.610	60.127	36.427	1.00	58.89	B	C
ATOM	5658	CG	ARG	265	93.152	58.875	35.779	1.00	59.34	B	C
ATOM	5659	CD	ARG	265	94.501	58.614	36.400	1.00	61.17	B	C
ATOM	5660	NE	ARG	265	95.183	57.456	35.851	1.00	66.56	B	N
ATOM	5661	CZ	ARG	265	96.506	57.349	35.784	1.00	66.73	B	C
ATOM	5662	NH1	ARG	265	97.281	58.334	36.227	1.00	71.36	B	N
ATOM	5663	NH2	ARG	265	97.059	56.256	35.280	1.00	70.70	B	N
ATOM	5664	C	ARG	265	92.147	61.423	34.347	1.00	39.89	B	C
ATOM	5665	O	ARG	265	93.311	61.833	34.319	1.00	41.20	B	O
ATOM	5666	N	LEU	266	91.360	61.433	33.278	1.00	45.12	B	N
ATOM	5667	CA	LEU	266	91.855	61.947	32.007	1.00	46.69	B	C
ATOM	5668	CB	LEU	266	90.885	61.580	30.886	1.00	30.69	B	C
ATOM	5669	CG	LEU	266	91.357	61.919	29.480	1.00	29.90	B	C
ATOM	5670	CD1	LEU	266	92.760	61.369	29.232	1.00	32.24	B	C
ATOM	5671	CD2	LEU	266	90.347	61.344	28.500	1.00	26.36	B	C
ATOM	5672	C	LEU	266	91.989	63.466	32.139	1.00	49.51	B	C
ATOM	5673	O	LEU	266	92.861	64.093	31.541	1.00	49.39	B	O
ATOM	5674	N	LYS	267	91.107	64.041	32.945	1.00	50.12	B	N
ATOM	5675	CA	LYS	267	91.097	65.473	33.206	1.00	52.43	B	C
ATOM	5676	CB	LYS	267	89.927	65.807	34.136	1.00	99.33	B	C
ATOM	5677	CG	LYS	267	89.719	67.279	34.431	1.00	99.33	B	C
ATOM	5678	CD	LYS	267	88.623	67.863	33.558	1.00	99.33	B	C
ATOM	5679	CE	LYS	267	88.211	69.242	34.049	1.00	99.33	B	C
ATOM	5680	NZ	LYS	267	87.044	69.788	33.293	1.00	99.33	B	N
ATOM	5681	C	LYS	267	92.417	65.835	33.882	1.00	51.92	B	C
ATOM	5682	O	LYS	267	93.126	66.738	33.440	1.00	51.44	B	O
ATOM	5683	N	GLN	268	92.736	65.115	34.956	1.00	36.69	B	N
ATOM	5684	CA	GLN	268	93.968	65.338	35.709	1.00	35.66	B	C
ATOM	5685	CB	GLN	268	94.098	64.324	36.841	1.00	127.61	B	C
ATOM	5686	CG	GLN	268	93.032	64.387	37.906	1.00	127.61	B	C
ATOM	5687	CD	GLN	268	93.203	63.286	38.941	1.00	127.61	B	C
ATOM	5688	OE1	GLN	268	92.487	63.236	39.939	1.00	127.61	B	O
ATOM	5689	NE2	GLN	268	94.158	62.392	38.702	1.00	127.61	B	N
ATOM	5690	C	GLN	268	95.203	65.210	34.824	1.00	31.41	B	C
ATOM	5691	O	GLN	268	96.044	66.108	34.788	1.00	32.59	B	O
ATOM	5692	N	VAL	269	95.308	64.085	34.114	1.00	29.89	B	N
ATOM	5693	CA	VAL	269	96.457	63.831	33.256	1.00	27.64	B	C
ATOM	5694	CB	VAL	269	96.321	62.467	32.516	1.00	26.10	B	C

Fig. 19: A-79

ATOM	5695	CG1	VAL	269	97.551	62.215	31.663	1.00	21.75	B	C
ATOM	5696	CG2	VAL	269	96.161	61.338	33.520	1.00	23.96	B	C
ATOM	5697	C	VAL	269	96.683	64.956	32.246	1.00	27.23	B	C
ATOM	5698	O	VAL	269	97.784	65.502	32.174	1.00	30.07	B	O
ATOM	5699	N	ILE	270	95.658	65.306	31.471	1.00	16.50	B	N
ATOM	5700	CA	ILE	270	95.797	66.379	30.487	1.00	17.12	B	C
ATOM	5701	CB	ILE	270	94.459	66.696	29.777	1.00	35.19	B	C
ATOM	5702	CG2	ILE	270	94.594	67.973	28.937	1.00	29.81	B	C
ATOM	5703	CG1	ILE	270	94.060	65.520	28.885	1.00	32.75	B	C
ATOM	5704	CD1	ILE	270	95.062	65.231	27.778	1.00	33.87	B	C
ATOM	5705	C	ILE	270	96.275	67.631	31.210	1.00	20.99	B	C
ATOM	5706	O	ILE	270	97.060	68.413	30.670	1.00	19.77	B	O
ATOM	5707	N	GLN	271	95.802	67.796	32.444	1.00	57.05	B	N
ATOM	5708	CA	GLN	271	96.169	68.935	33.269	1.00	59.11	B	C
ATOM	5709	CB	GLN	271	95.440	68.865	34.610	1.00	85.78	B	C
ATOM	5710	CG	GLN	271	95.525	70.134	35.439	1.00	87.68	B	C
ATOM	5711	CD	GLN	271	94.967	71.338	34.708	1.00	90.18	B	C
ATOM	5712	OE1	GLN	271	95.614	71.898	33.822	1.00	90.51	B	O
ATOM	5713	NE2	GLN	271	93.752	71.735	35.065	1.00	91.75	B	N
ATOM	5714	C	GLN	271	97.673	68.932	33.495	1.00	61.57	B	C
ATOM	5715	O	GLN	271	98.359	69.896	33.172	1.00	64.26	B	O
ATOM	5716	N	ASP	272	98.184	67.837	34.042	1.00	39.03	B	N
ATOM	5717	CA	ASP	272	99.612	67.716	34.304	1.00	40.31	B	C
ATOM	5718	CB	ASP	272	99.922	66.338	34.890	1.00	54.12	B	C
ATOM	5719	CG	ASP	272	99.275	66.122	36.255	1.00	55.74	B	C
ATOM	5720	OD1	ASP	272	99.087.	64.949	36.647	1.00	57.81	B	O
ATOM	5721	OD2	ASP	272	98.961	67.123	36.939	1.00	62.00	B	O
ATOM	5722	C	ASP	272	100.420	67.937	33.033	1.00	41.11	B	C
ATOM	5723	O	ASP	272	101.550	68.418	33.083	1.00	38.56	B	O
ATOM	5724	N	CYS	273	99.843	67.587	31.891	1.00	49.56	B	N
ATOM	5725	CA	CYS	273	100.538	67.776	30.629	1.00	47.99	B	C
ATOM	5726	CB	CYS	273	99.824	67.028	29.503	1.00	39.07	B	C
ATOM	5727	SG	CYS	273	100.050	65.235	29.538	1.00	37.17	B	S
ATOM	5728	C	CYS	273	100.628	69.257	30.291	1.00	48.36	B	C
ATOM	5729	O	CYS	273	101.602	69.695	29.686	1.00	42.67	B	O
ATOM	5730	N	GLU	274	99.609	70.022	30.682	1.00	40.12	B	N
ATOM	5731	CA	GLU	274	99.584	71.467	30.425	1.00	42.92	B	C
ATOM	5732	CB	GLU	274	98.187	72.055	30.703	1.00	40.77	B	C
ATOM	5733	CG	GLU	274	97.285	72.151	29.470	1.00	45.89	B	C
ATOM	5734	CD	GLU	274	97.830	73.108	28.405	1.00	51.00	B	C
ATOM	5735	OE1	GLU	274	97.269	73.155	27.284	1.00	52.87	B	O
ATOM	5736	OE2	GLU	274	98.816	73.818	28.691	1.00	55.56	B	O
ATOM	5737	C	GLU	274	100.615	72.172	31.293	1.00	45.34	B	C
ATOM	5738	O	GLU	274	101.309	73.081	30.842	1.00	47.54	B	O
ATOM	5739	N	ASP	275	100.711	71.735	32.542	1.00	77.40	B	N
ATOM	5740	CA	ASP	275	101.656	72.302	33.495	1.00	76.14	B	C
ATOM	5741	CB	ASP	275	101.456	71.665	34.871	1.00	72.98	B	C
ATOM	5742	CG	ASP	275	100.070	71.900	35.432	1.00	74.25	B	C
ATOM	5743	OD1	ASP	275	99.160	72.258	34.656	1.00	77.95	B	O
ATOM	5744	OD2	ASP	275	99.887	71.712	36.652	1.00	75.91	B	O
ATOM	5745	C	ASP	275	103.093	72.050	33.046	1.00	75.13	B	C
ATOM	5746	O	ASP	275	104.021	72.707	33.512	1.00	70.68	B	O
ATOM	5747	N	GLU	276	103.275	71.091	32.146	1.00	44.46	B	N
ATOM	5748	CA	GLU	276	104.606	70.757	31.668	1.00	44.11	B	C
ATOM	5749	CB	GLU	276	104.846	69.258	31.847	1.00	54.99	B	C
ATOM	5750	CG	GLU	276	104.556	68.799	33.266	1.00	54.86	B	C
ATOM	5751	CD	GLU	276	105.018	67.383	33.547	1.00	55.96	B	C
ATOM	5752	OE1	GLU	276	104.861	66.934	34.705	1.00	56.67	B	O
ATOM	5753	OE2	GLU	276	105.538	66.724	32.616	1.00	52.90	B	O
ATOM	5754	C	GLU	276	104.843	71.175	30.222	1.00	42.94	B	C
ATOM	5755	O	GLU	276	105.823	70.759	29.597	1.00	44.05	B	O
ATOM	5756	N	ASN	277	103.938	71.997	29.700	1.00	43.81	B	N
ATOM	5757	CA	ASN	277	104.043	72.505	28.338	1.00	43.78	B	C
ATOM	5758	CB	ASN	277	105.229	73.464	28.233	1.00	55.27	B	C
ATOM	5759	CG	ASN	277	105.219	74.514	29.311	1.00	60.19	B	C
ATOM	5760	OD1	ASN	277	104.288	75.315	29.403	1.00	60.01	B	O
ATOM	5761	ND2	ASN	277	106.256	74.518	30.145	1.00	59.15	B	N
ATOM	5762	C	ASN	277	104.188	71.428	27.261	1.00	40.13	B	C
ATOM	5763	O	ASN	277	105.083	71.515	26.416	1.00	41.11	B	O
ATOM	5764	N	ILE	278	103.309	70.427	27.278	1.00	17.87	B	N
ATOM	5765	CA	ILE	278	103.366	69.361	26.289	1.00	18.32	B	C
ATOM	5766	CB	ILE	278	103.110	67.975	26.928	1.00	22.06	B	C
ATOM	5767	CG2	ILE	278	103.120	66.897	25.854	1.00	23.45	B	C

Fig. 19: A-80

ATOM	5768	CG1	ILE	278	104.172	67.675	27.987	1.00	19.51	B	C
ATOM	5769	CD1	ILE	278	103.941	66.373	28.707	1.00	21.79	B	C
ATOM	5770	C	ILE	278	102.316	69.579	25.213	1.00	18.92	B	C
ATOM	5771	O	ILE	278	101.132	69.378	25.463	1.00	19.26	B	O
ATOM	5772	N	GLN	279	102.749	69.994	24.024	1.00	49.21	B	N
ATOM	5773	CA	GLN	279	101.831	70.198	22.908	1.00	48.81	B	C
ATOM	5774	CB	GLN	279	102.579	70.633	21.652	1.00	63.04	B	C
ATOM	5775	CG	GLN	279	103.187	71.998	21.752	1.00	68.82	B	C
ATOM	5776	CD	GLN	279	102.173	73.043	22.155	1.00	72.74	B	C
ATOM	5777	OE1	GLN	279	101.233	73.328	21.410	1.00	66.98	B	O
ATOM	5778	NE2	GLN	279	102.352	73.618	23.345	1.00	72.33	B	N
ATOM	5779	C	GLN	279	101.175	68.864	22.640	1.00	46.68	B	C
ATOM	5780	O	GLN	279	101.861	67.859	22.467	1.00	43.60	B	O
ATOM	5781	N	ARG	280	99.851	68.848	22.595	1.00	28.30	B	N
ATOM	5782	CA	ARG	280	99.138	67.605	22.363	1.00	29.82	B	C
ATOM	5783	CB	ARG	280	98.276	67.277	23.575	1.00	38.67	B	C
ATOM	5784	CG	ARG	280	99.036	67.225	24.874	1.00	37.30	B	C
ATOM	5785	CD	ARG	280	98.068	67.012	26.018	1.00	36.97	B	C
ATOM	5786	NE	ARG	280	97.070	68.075	26.073	1.00	34.02	B	N
ATOM	5787	CZ	ARG	280	97.288	69.298	26.557	1.00	37.93	B	C
ATOM	5788	NH1	ARG	280	98.483	69.627	27.041	1.00	40.85	B	N
ATOM	5789	NH2	ARG	280	96.307	70.192	26.554	1.00	42.87	B	N
ATOM	5790	C	ARG	280	98.264	67.579	21.111	1.00	29.48	B	C
ATOM	5791	O	ARG	280	97.406	68.437	20.912	1.00	29.21	B	O
ATOM	5792	N	PHE	281	98.501	66.582	20.266	1.00	31.71	B	N
ATOM	5793	CA	PHE	281	97.713	66.392	19.066	1.00	33.70	B	C
ATOM	5794	CB	PHE	281	98.594	66.335	17.826	1.00	18.70	B	C
ATOM	5795	CG	PHE	281	99.324	67.604	17.555	1.00	21.73	B	C
ATOM	5796	CD1	PHE	281	100.438	67.950	18.308	1.00	25.58	B	C
ATOM	5797	CD2	PHE	281	98.887	68.469	16.551	1.00	23.46	B	C
ATOM	5798	CE1	PHE	281	101.111	69.136	18.070	1.00	25.64	B	C
ATOM	5799	CE2	PHE	281	99.554	69.665	16.301	1.00	21.19	B	C
ATOM	5800	CZ	PHE	281	100.669	69.999	17.064	1.00	22.62	B	C
ATOM	5801	C	PHE	281	97.025	65.060	19.266	1.00	34.41	B	C
ATOM	5802	O	PHE	281	97.677	64.053	19.509	1.00	36.78	B	O
ATOM	5803	N	SER	282	95.704	65.061	19.202	1.00	16.00	B	N
ATOM	5804	CA	SER	282	94.962	63.835	19.374	1.00	17.85	B	C
ATOM	5805	CB	SER	282	93.973	63.973	20.528	1.00	14.79	B	C
ATOM	5806	OG	SER	282	93.036	64.997	20.286	1.00	11.34	B	O
ATOM	5807	C	SER	282	94.231	63.507	18.093	1.00	19.73	B	C
ATOM	5808	O	SER	282	93.909	64.389	17.306	1.00	23.59	B	O
ATOM	5809	N	ILE	283	93.986	62.224	17.881	1.00	19.27	B	N
ATOM	5810	CA	ILE	283	93.288	61.779	16.693	1.00	17.19	B	C
ATOM	5811	CB	ILE	283	94.245	61.146	15.697	1.00	9.92	B	C
ATOM	5812	CG2	ILE	283	93.501	60.806	14.425	1.00	10.73	B	C
ATOM	5813	CG1	ILE	283	95.377	62.118	15.383	1.00	6.39	B	C
ATOM	5814	CD1	ILE	283	96.630	61.446	14.894	1.00	9.95	B	C
ATOM	5815	C	ILE	283	92.278	60.748	17.127	1.00	16.26	B	C
ATOM	5816	O	ILE	283	92.574	59.886	17.947	1.00	16.12	B	O
ATOM	5817	N	ALA	284	91.078	60.836	16.584	1.00	18.66	B	N
ATOM	5818	CA	ALA	284	90.050	59.896	16.955	1.00	18.68	B	C
ATOM	5819	CB	ALA	284	88.903	60.627	17.622	1.00	45.12	B	C
ATOM	5820	C	ALA	284	89.542	59.107	15.759	1.00	16.81	B	C
ATOM	5821	O	ALA	284	89.045	59.681	14.792	1.00	15.47	B	O
ATOM	5822	N	ILE	285	89.691	57.788	15.826	1.00	23.61	B	N
ATOM	5823	CA	ILE	285	89.205	56.922	14.772	1.00	17.81	B	C
ATOM	5824	CB	ILE	285	89.960	55.564	14.741	1.00	12.20	B	C
ATOM	5825	CG2	ILE	285	89.210	54.576	13.862	1.00	7.02	B	C
ATOM	5826	CG1	ILE	285	91.380	55.738	14.204	1.00	7.53	B	C
ATOM	5827	CD1	ILE	285	92.342	56.334	15.179	1.00	8.67	B	C
ATOM	5828	C	ILE	285	87.745	56.678	15.148	1.00	21.13	B	C
ATOM	5829	O	ILE	285	87.466	56.108	16.201	1.00	22.87	B	O
ATOM	5830	N	LEU	286	86.820	57.112	14.297	1.00	18.22	B	N
ATOM	5831	CA	LEU	286	85.399	56.937	14.581	1.00	18.70	B	C
ATOM	5832	CB	LEU	286	84.615	58.129	14.039	1.00	27.86	B	C
ATOM	5833	CG	LEU	286	85.105	59.512	14.456	1.00	30.68	B	C
ATOM	5834	CD1	LEU	286	84.112	60.536	13.961	1.00	33.24	B	C
ATOM	5835	CD2	LEU	286	85.249	59.599	15.963	1.00	32.35	B	C
ATOM	5836	C	LEU	286	84.774	55.645	14.044	1.00	19.15	B	C
ATOM	5837	O	LEU	286	83.552	55.458	14.122	1.00	19.99	B	O
ATOM	5838	N	GLY	287	85.609	54.752	13.520	1.00	37.37	B	N
ATOM	5839	CA	GLY	287	85.115	53.501	12.967	1.00	36.15	B	C
ATOM	5840	C	GLY	287	84.059	52.745	13.760	1.00	33.73	B	C

Fig. 19: A-81

ATOM	5841	O	GLY	287	82.899	52.681	13.367	1.00	37.83	B	O
ATOM	5842	N	HIS	288	84.464	52.162	14.878	1.00	34.79	B	N
ATOM	5843	CA	HIS	288	83.563	51.376	15.700	1.00	32.75	B	C
ATOM	5844	CB	HIS	288	84.272	51.016	16.996	1.00	68.63	B	C
ATOM	5845	CG	HIS	288	85.486	50.181	16.763	1.00	70.54	B	C
ATOM	5846	CD2	HIS	288	85.781	48.912	17.123	1.00	66.91	B	C
ATOM	5847	ND1	HIS	288	86.520	50.600	15.955	1.00	65.20	B	N
ATOM	5848	CE1	HIS	288	87.397	49.623	15.821	1.00	65.56	B	C
ATOM	5849	NE2	HIS	288	86.972	48.586	16.519	1.00	64.05	B	N
ATOM	5850	C	HIS	288	82.214	52.006	15.968	1.00	30.23	B	C
ATOM	5851	O	HIS	288	81.180	51.398	15.711	1.00	29.80	B	O
ATOM	5852	N	TYR	289	82.219	53.233	16.461	1.00	26.68	B	N
ATOM	5853	CA	TYR	289	80.982	53.912	16.754	1.00	27.59	B	C
ATOM	5854	CB	TYR	289	81.287	55.288	17.309	1.00	20.91	B	C
ATOM	5855	CG	TYR	289	81.803	55.203	18.717	1.00	23.71	B	C
ATOM	5856	CD1	TYR	289	83.163	55.293	18.997	1.00	24.30	B	C
ATOM	5857	CE1	TYR	289	83.633	55.127	20.281	1.00	27.49	B	C
ATOM	5858	CD2	TYR	289	80.928	54.947	19.764	1.00	26.60	B	C
ATOM	5859	CE2	TYR	289	81.381	54.776	21.047	1.00	21.41	B	C
ATOM	5860	CZ	TYR	289	82.733	54.866	21.303	1.00	23.14	B	C
ATOM	5861	OH	TYR	289	83.166	54.686	22.597	1.00	27.79	B	O
ATOM	5862	C	TYR	289	80.039	54.015	15.572	1.00	29.36	B	C
ATOM	5863	O	TYR	289	78.849	53.720	15.692	1.00	28.55	B	O
ATOM	5864	N	ASN	290	80.551	54.414	14.419	1.00	30.33	B	N
ATOM	5865	CA	ASN	290	79.681	54.538	13.264	1.00	29.82	B	C
ATOM	5866	CB	ASN	290	80.390	55.290	12.141	1.00	19.88	B	C
ATOM	5867	CG	ASN	290	80.582	56.750	12.466	1.00	23.09	B	C
ATOM	5868	OD1	ASN	290	79.681	57.395	13.005	1.00	24.51	B	O
ATOM	5869	ND2	ASN	290	81.748	57.286	12.133	1.00	26.61	B	N
ATOM	5870	C	ASN	290	79.142	53.214	12.746	1.00	28.65	B	C
ATOM	5871	O	ASN	290	78.008	53.153	12.264	1.00	35.25	B	O
ATOM	5872	N	ARG	291	79.944	52.155	12.842	1.00	46.80	B	N
ATOM	5873	CA	ARG	291	79.513	50.850	12.362	1.00	46.11	B	C
ATOM	5874	CB	ARG	291	80.694	49.867	12.337	1.00	45.84	B	C
ATOM	5875	CG	ARG	291	81.661	50.063	11.152	1.00	50.80	B	C
ATOM	5876	CD	ARG	291	82.722	48.943	11.054	1.00	54.88	B	C
ATOM	5877	NE	ARG	291	83.916	49.157	11.883	1.00	47.06	B	N
ATOM	5878	CZ	ARG	291	84.884	50.030	11.603	1.00	56.55	B	C
ATOM	5879	NH1	ARG	291	84.813	50.787	10.515	1.00	55.39	B	N
ATOM	5880	NH2	ARG	291	85.936	50.131	12.401	1.00	53.31	B	N
ATOM	5881	C	ARG	291	78.367	50.296	13.207	1.00	43.91	B	C
ATOM	5882	O	ARG	291	77.338	49.876	12.676	1.00	47.17	B	O
ATOM	5883	N	GLY	292	78.531	50.306	14.523	1.00	18.83	B	N
ATOM	5884	CA	GLY	292	77.476	49.795	15.374	1.00	19.08	B	C
ATOM	5885	C	GLY	292	76.427	50.857	15.628	1.00	26.45	B	C
ATOM	5886	O	GLY	292	75.874	50.947	16.722	1.00	32.58	B	O
ATOM	5887	N	ASN	293	76.151	51.664	14.610	1.00	32.56	B	N
ATOM	5888	CA	ASN	293	75.177	52.740	14.724	1.00	34.89	B	C
ATOM	5889	CB	ASN	293	73.785	52.239	14.339	1.00	18.98	B	C
ATOM	5890	CG	ASN	293	73.623	52.066	12.846	1.00	25.56	B	C
ATOM	5891	OD1	ASN	293	74.249	52.776	12.063	1.00	27.19	B	O
ATOM	5892	ND2	ASN	293	72.767	51.132	12.440	1.00	26.33	B	N
ATOM	5893	C	ASN	293	75.116	53.389	16.111	1.00	36.22	B	C
ATOM	5894	O	ASN	293	74.054	53.448	16.722	1.00	31.70	B	O
ATOM	5895	N	LEU	294	76.247	53.875	16.614	1.00	40.17	B	N
ATOM	5896	CA	LEU	294	76.260	54.525	17.921	1.00	39.32	B	C
ATOM	5897	CB	LEU	294	77.141	53.737	18.901	1.00	27.66	B	C
ATOM	5898	CG	LEU	294	76.633	52.343	19.291	1.00	26.48	B	C
ATOM	5899	CD1	LEU	294	77.463	51.781	20.440	1.00	27.02	B	C
ATOM	5900	CD2	LEU	294	75.175	52.437	19.714	1.00	27.39	B	C
ATOM	5901	C	LEU	294	76.730	55.985	17.823	1.00	41.69	B	C
ATOM	5902	O	LEU	294	77.579	56.314	16.984	1.00	40.35	B	O
ATOM	5903	N	SER	295	76.158	56.860	18.656	1.00	29.47	B	N
ATOM	5904	CA	SER	295	76.534	58.272	18.644	1.00	29.33	B	C
ATOM	5905	CB	SER	295	75.802	59.063	19.740	1.00	35.11	B	C
ATOM	5906	OG	SER	295	76.336	60.371	19.894	1.00	41.79	B	O
ATOM	5907	C	SER	295	78.022	58.329	18.890	1.00	25.45	B	C
ATOM	5908	O	SER	295	78.583	57.444	19.533	1.00	22.32	B	O
ATOM	5909	N	THR	296	78.661	59.379	18.401	1.00	28.05	B	N
ATOM	5910	CA	THR	296	80.096	59.500	18.559	1.00	28.09	B	C
ATOM	5911	CB	THR	296	80.786	59.452	17.191	1.00	44.94	B	C
ATOM	5912	OG1	THR	296	80.305	60.534	16.383	1.00	50.00	B	O
ATOM	5913	CG2	THR	296	80.485	58.150	16.487	1.00	44.81	B	C

Fig. 19: A-82

ATOM	5914	C	THR	296	80.519	60.792	19.227	1.00	29.07	B	C
ATOM	5915	O	THR	296	81.695	60.971	19.535	1.00	27.88	B	O
ATOM	5916	N	GLU	297	79.581	61.705	19.451	1.00	50.64	B	N
ATOM	5917	CA	GLU	297	79.970	62.978	20.038	1.00	54.10	B	C
ATOM	5918	CB	GLU	297	78.781	63.943	20.111	1.00	93.12	B	C
ATOM	5919	CG	GLU	297	77.787	63.695	21.213	1.00	100.15	B	C
ATOM	5920	CD	GLU	297	77.036	64.960	21.569	1.00	101.40	B	C
ATOM	5921	OE1	GLU	297	76.160	64.911	22.455	1.00	104.84	B	O
ATOM	5922	OE2	GLU	297	77.333	66.010	20.964	1.00	102.89	B	O
ATOM	5923	C	GLU	297	80.639	62.849	21.399	1.00	52.14	B	C
ATOM	5924	O	GLU	297	81.715	63.406	21.612	1.00	51.64	B	O
ATOM	5925	N	LYS	298	80.029	62.104	22.315	1.00	35.40	B	N
ATOM	5926	CA	LYS	298	80.622	61.942	23.636	1.00	35.40	B	C
ATOM	5927	CB	LYS	298	79.837	60.916	24.443	1.00	37.32	B	C
ATOM	5928	CG	LYS	298	80.199	60.902	25.910	1.00	46.03	B	C
ATOM	5929	CD	LYS	298	79.201	60.085	26.727	1.00	47.75	B	C
ATOM	5930	CE	LYS	298	77.777	60.625	26.578	1.00	51.57	B	C
ATOM	5931	NZ	LYS	298	77.676	62.075	26.908	1.00	55.89	B	N
ATOM	5932	C	LYS	298	82.087	61.518	23.514	1.00	33.00	B	C
ATOM	5933	O	LYS	298	82.939	61.933	24.310	1.00	33.88	B	O
ATOM	5934	N	PHE	299	82.371	60.699	22.505	1.00	29.00	B	N
ATOM	5935	CA	PHE	299	83.729	60.226	22.244	1.00	27.24	B	C
ATOM	5936	CB	PHE	299	83.701	59.054	21.263	1.00	39.15	B	C
ATOM	5937	CG	PHE	299	85.065	58.571	20.851	1.00	31.59	B	C
ATOM	5938	CD1	PHE	299	86.020	58.237	21.806	1.00	28.04	B	C
ATOM	5939	CD2	PHE	299	85.396	58.435	19.505	1.00	29.32	B	C
ATOM	5940	CE1	PHE	299	87.284	57.776	21.422	1.00	27.45	B	C
ATOM	5941	CE2	PHE	299	86.667	57.970	19.119	1.00	23.73	B	C
ATOM	5942	CZ	PHE	299	87.603	57.643	20.078	1.00	22.24	B	C
ATOM	5943	C	PHE	299	84.562	61.361	21.662	1.00	27.59	B	C
ATOM	5944	O	PHE	299	85.625	61.702	22.183	1.00	23.40	B	O
ATOM	5945	N	VAL	300	84.077	61.946	20.576	1.00	13.78	B	N
ATOM	5946	CA	VAL	300	84.791	63.050	19.944	1.00	18.73	B	C
ATOM	5947	CB	VAL	300	83.954	63.701	18.822	1.00	24.12	B	C
ATOM	5948	CG1	VAL	300	84.616	64.979	18.363	1.00	27.69	B	C
ATOM	5949	CG2	VAL	300	83.814	62.731	17.646	1.00	28.13	B	C
ATOM	5950	C	VAL	300	85.142	64.119	20.966	1.00	17.37	B	C
ATOM	5951	O	VAL	300	86.209	64.715	20.906	1.00	17.87	B	O
ATOM	5952	N	GLU	301	84.248	64.359	21.914	1.00	33.19	B	N
ATOM	5953	CA	GLU	301	84.520	65.377	22.915	1.00	33.85	B	C
ATOM	5954	CB	GLU	301	83.255	65.707	23.706	1.00	133.49	B	C
ATOM	5955	CG	GLU	301	83.426	66.851	24.703	1.00	135.76	B	C
ATOM	5956	CD	GLU	301	84.115	68.077	24.108	1.00	141.57	B	C
ATOM	5957	OE1	GLU	301	83.669	68.566	23.046	1.00	141.12	B	O
ATOM	5958	OE2	GLU	301	85.102	68.555	24.713	1.00	143.84	B	O
ATOM	5959	C	GLU	301	85.634	64.925	23.847	1.00	32.42	B	C
ATOM	5960	O	GLU	301	86.495	65.723	24.239	1.00	30.50	B	O
ATOM	5961	N	GLU	302	85.628	63.642	24.190	1.00	18.71	B	N
ATOM	5962	CA	GLU	302	86.663	63.091	25.060	1.00	18.52	B	C
ATOM	5963	CB	GLU	302	86.420	61.596	25.293	1.00	49.27	B	C
ATOM	5964	CG	GLU	302	87.438	60.934	26.207	1.00	49.02	B	C
ATOM	5965	CD	GLU	302	87.100	59.486	26.491	1.00	45.95	B	C
ATOM	5966	OE1	GLU	302	86.051	59.237	27.118	1.00	45.93	B	O
ATOM	5967	OE2	GLU	302	87.875	58.594	26.084	1.00	50.37	B	O
ATOM	5968	C	GLU	302	88.046	63.301	24.456	1.00	21.59	B	C
ATOM	5969	O	GLU	302	88.964	63.720	25.150	1.00	20.85	B	O
ATOM	5970	N	ILE	303	88.188	63.031	23.159	1.00	30.73	B	N
ATOM	5971	CA	ILE	303	89.479	63.175	22.472	1.00	30.78	B	C
ATOM	5972	CB	ILE	303	89.470	62.431	21.112	1.00	21.11	B	C
ATOM	5973	CG2	ILE	303	90.865	62.406	20.518	1.00	16.29	B	C
ATOM	5974	CG1	ILE	303	88.932	61.003	21.306	1.00	18.71	B	C
ATOM	5975	CD1	ILE	303	89.501	60.262	22.515	1.00	15.17	B	C
ATOM	5976	C	ILE	303	89.922	64.625	22.242	1.00	32.81	B	C
ATOM	5977	O	ILE	303	91.097	64.955	22.415	1.00	35.30	B	O
ATOM	5978	N	LYS	304	88.989	65.485	21.847	1.00	41.13	B	N
ATOM	5979	CA	LYS	304	89.321	66.881	21.624	1.00	41.93	B	C
ATOM	5980	CB	LYS	304	88.087	67.695	21.239	1.00	34.23	B	C
ATOM	5981	CG	LYS	304	87.578	67.484	19.837	1.00	40.90	B	C
ATOM	5982	CD	LYS	304	86.491	68.498	19.526	1.00	42.43	B	C
ATOM	5983	CE	LYS	304	85.937	68.312	18.122	1.00	45.16	B	C
ATOM	5984	NZ	LYS	304	84.893	69.323	17.799	1.00	47.34	B	N
ATOM	5985	C	LYS	304	89.892	67.455	22.906	1.00	38.02	B	C
ATOM	5986	O	LYS	304	90.833	68.240	22.871	1.00	42.10	B	O

Fig. 19: A-83

ATOM	5987	N	SER	305	89.322	67.066	24.043	1.00	21.53	B	N
ATOM	5988	CA	SER	305	89.788	67.571	25.335	1.00	18.69	B	C
ATOM	5989	CB	SER	305	88.872	67.096	26.460	1.00	39.18	B	C
ATOM	5990	OG	SER	305	89.039	65.715	26.696	1.00	35.86	B	O
ATOM	5991	C	SER	305	91.223	67.134	25.622	1.00	19.21	B	C
ATOM	5992	O	SER	305	91.935	67.754	26.418	1.00	21.78	B	O
ATOM	5993	N	ILE	306	91.652	66.063	24.969	1.00	47.39	B	N
ATOM	5994	CA	ILE	306	93.005	65.582	25.158	1.00	44.14	B	C
ATOM	5995	CB	ILE	306	93.129	64.131	24.682	1.00	20.56	B	C
ATOM	5996	CG2	ILE	306	94.584	63.769	24.454	1.00	21.29	B	C
ATOM	5997	CG1	ILE	306	92.479	63.210	25.713	1.00	23.19	B	C
ATOM	5998	CD1	ILE	306	92.459	61.762	25.302	1.00	20.90	B	C
ATOM	5999	C	ILE	306	93.966	66.469	24.378	1.00	41.90	B	C
ATOM	6000	O	ILE	306	95.146	66.583	24.717	1.00	42.43	B	O
ATOM	6001	N	ALA	307	93.445	67.103	23.334	1.00	47.34	B	N
ATOM	6002	CA	ALA	307	94.247	67.979	22.497	1.00	49.53	B	C
ATOM	6003	CB	ALA	307	93.538	68.236	21.181	1.00	34.34	B	C
ATOM	6004	C	ALA	307	94.526	69.296	23.200	1.00	49.19	B	C
ATOM	6005	O	ALA	307	93.952	69.595	24.253	1.00	48.18	B	O
ATOM	6006	N	SER	308	95.415	70.078	22.604	1.00	31.36	B	N
ATOM	6007	CA	SER	308	95.801	71.367	23.141	1.00	34.29	B	C
ATOM	6008	CB	SER	308	97.299	71.580	22.943	1.00	9.08	B	C
ATOM	6009	OG	SER	308	98.040	70.819	23.867	1.00	12.47	B	O
ATOM	6010	C	SER	308	95.054	72.489	22.446	1.00	37.94	B	C
ATOM	6011	O	SER	308	94.703	72.373	21.272	1.00	35.28	B	O
ATOM	6012	N	GLU	309	94.813	73.575	23.178	1.00	31.30	B	N
ATOM	6013	CA	GLU	309	94.137	74.735	22.614	1.00	34.79	B	C
ATOM	6014	CB	GLU	309	93.786	75.736	23.721	1.00	74.37	B	C
ATOM	6015	CG	GLU	309	92.834	75.203	24.787	1.00	79.74	B	C
ATOM	6016	CD	GLU	309	91.461	74.845	24.234	1.00	82.50	B	C
ATOM	6017	OE1	GLU	309	90.533	74.618	25.043	1.00	84.83	B	O
ATOM	6018	OE2	GLU	309	91.307	74.784	22.995	1.00	86.65	B	O
ATOM	6019	C	GLU	309	95.138	75.359	21.642	1.00	35.54	B	C
ATOM	6020	O	GLU	309	96.321	75.480	21.971	1.00	37.19	B	O
ATOM	6021	N	PRO	310	94.685	75.762	20.435	1.00	19.46	B	N
ATOM	6022	CD	PRO	310	95.588	76.399	19.457	1.00	19.32	B	C
ATOM	6023	CA	PRO	310	93.324	75.694	19.890	1.00	19.65	B	C
ATOM	6024	CB	PRO	310	93.362	76.729	18.770	1.00	21.15	B	C
ATOM	6025	CG	PRO	310	94.715	76.515	18.203	1.00	20.71	B	C
ATOM	6026	C	PRO	310	92.884	74.312	19.384	1.00	20.14	B	C
ATOM	6027	O	PRO	310	93.368	73.816	18.374	1.00	16.93	B	O
ATOM	6028	N	THR	311	91.945	73.714	20.101	1.00	34.98	B	N
ATOM	6029	CA	THR	311	91.410	72.410	19.764	1.00	35.85	B	C
ATOM	6030	CB	THR	311	89.985	72.276	20.321	1.00	54.06	B	C
ATOM	6031	OG1	THR	311	89.327	71.159	19.711	1.00	58.22	B	O
ATOM	6032	CG2	THR	311	89.195	73.556	20.052	1.00	57.14	B	C
ATOM	6033	C	THR	311	91.390	72.103	18.265	1.00	37.72	B	C
ATOM	6034	O	THR	311	91.801	71.022	17.847	1.00	38.89	B	O
ATOM	6035	N	GLU	312	90.929	73.049	17.451	1.00	45.13	B	N
ATOM	6036	CA	GLU	312	90.842	72.825	16.004	1.00	43.75	B	C
ATOM	6037	CB	GLU	312	90.160	74.008	15.309	1.00	94.13	B	C
ATOM	6038	CG	GLU	312	90.848	75.342	15.528	1.00	95.89	B	C
ATOM	6039	CD	GLU	312	90.633	76.309	14.376	1.00	95.00	B	C
ATOM	6040	OE1	GLU	312	90.998	77.496	14.516	1.00	98.35	B	O
ATOM	6041	OE2	GLU	312	90.109	75.880	13.327	1.00	95.87	B	O
ATOM	6042	C	GLU	312	92.168	72.547	15.310	1.00	42.37	B	C
ATOM	6043	O	GLU	312	92.219	71.771	14.367	1.00	42.33	B	O
ATOM	6044	N	LYS	313	93.240	73.180	15.763	1.00	62.67	B	N
ATOM	6045	CA	LYS	313	94.537	72.966	15.141	1.00	61.87	B	C
ATOM	6046	CB	LYS	313	95.368	74.255	15.192	1.00	80.35	B	C
ATOM	6047	CG	LYS	313	94.954	75.308	14.167	1.00	80.23	B	C
ATOM	6048	CD	LYS	313	95.351	74.917	12.745	1.00	76.53	B	C
ATOM	6049	CE	LYS	313	96.790	75.307	12.430	1.00	78.57	B	C
ATOM	6050	NZ	LYS	313	97.781	74.730	13.383	1.00	83.05	B	N
ATOM	6051	C	LYS	313	95.308	71.832	15.800	1.00	63.02	B	C
ATOM	6052	O	LYS	313	96.473	71.610	15.491	1.00	65.34	B	O
ATOM	6053	N	HIS	314	94.656	71.103	16.697	1.00	42.28	B	N
ATOM	6054	CA	HIS	314	95.326	70.011	17.391	1.00	43.13	B	C
ATOM	6055	CB	HIS	314	95.631	70.426	18.828	1.00	51.27	B	C
ATOM	6056	CG	HIS	314	96.611	71.551	18.938	1.00	48.13	B	C
ATOM	6057	CD2	HIS	314	96.423	72.880	19.111	1.00	47.60	B	C
ATOM	6058	ND1	HIS	314	97.973	71.364	18.847	1.00	47.71	B	N
ATOM	6059	CE1	HIS	314	98.582	72.530	18.960	1.00	47.00	B	C

Fig. 19: A-84

ATOM	6060	NE2	HIS	314	97.664	73.466	19.121	1.00	47.39	B	N
ATOM	6061	C	HIS	314	94.540	68.706	17.405	1.00	43.26	B	C
ATOM	6062	O	HIS	314	95.034	67.690	17.896	1.00	46.66	B	O
ATOM	6063	N	PHE	315	93.324	68.732	16.868	1.00	55.79	B	N
ATOM	6064	CA	PHE	315	92.475	67.546	16.835	1.00	55.59	B	C
ATOM	6065	CB	PHE	315	91.175	67.834	17.578	1.00	29.85	B	C
ATOM	6066	CG	PHE	315	90.175	66.731	17.499	1.00	24.83	B	C
ATOM	6067	CD1	PHE	315	90.445	65.490	18.057	1.00	26.67	B	C
ATOM	6068	CD2	PHE	315	88.944	66.942	16.890	1.00	22.91	B	C
ATOM	6069	CE1	PHE	315	89.503	64.473	18.016	1.00	21.62	B	C
ATOM	6070	CE2	PHE	315	87.989	65.939	16.838	1.00	23.61	B	C
ATOM	6071	CZ	PHE	315	88.268	64.700	17.404	1.00	25.28	B	C
ATOM	6072	C	PHE	315	92.172	67.086	15.412	1.00	56.31	B	C
ATOM	6073	O	PHE	315	91.948	67.903	14.516	1.00	57.71	B	O
ATOM	6074	N	PHE	316	92.170	65.772	15.212	1.00	44.89	B	N
ATOM	6075	CA	PHE	316	91.898	65.200	13.899	1.00	41.94	B	C
ATOM	6076	CB	PHE	316	93.175	64.621	13.282	1.00	20.23	B	C
ATOM	6077	CG	PHE	316	94.195	65.652	12.900	1.00	23.85	B	C
ATOM	6078	CD1	PHE	316	95.118	66.114	13.828	1.00	19.44	B	C
ATOM	6079	CD2	PHE	316	94.229	66.165	11.605	1.00	20.70	B	C
ATOM	6080	CE1	PHE	316	96.066	67.074	13.475	1.00	22.01	B	C
ATOM	6081	CE2	PHE	316	95.171	67.125	11.242	1.00	23.81	B	C
ATOM	6082	CZ	PHE	316	96.092	67.580	12.180	1.00	24.04	B	C
ATOM	6083	C	PHE	316	90.841	64.107	13.990	1.00	39.87	B	C
ATOM	6084	O	PHE	316	90.845	63.302	14.910	1.00	39.11	B	O
ATOM	6085	N	ASN	317	89.938	64.088	13.020	1.00	36.72	B	N
ATOM	6086	CA	ASN	317	88.863	63.110	12.978	1.00	37.94	B	C
ATOM	6087	CB	ASN	317	87.538	63.826	12.746	1.00	58.19	B	C
ATOM	6088	CG	ASN	317	86.496	63.443	13.752	1.00	61.18	B	C
ATOM	6089	OD1	ASN	317	86.408	62.284	14.144	1.00	63.11	B	O
ATOM	6090	ND2	ASN	317	85.688	64.411	14.176	1.00	59.44	B	N
ATOM	6091	C	ASN	317	89.102	62.140	11.831	1.00	38.90	B	C
ATOM	6092	O	ASN	317	89.519	62.549	10.757	1.00	39.76	B	O
ATOM	6093	N	VAL	318	88.840	60.858	12.045	1.00	40.86	B	N
ATOM	6094	CA	VAL	318	89.027	59.872	10.981	1.00	39.49	B	C
ATOM	6095	CB	VAL	318	90.348	59.096	11.156	1.00	59.32	B	C
ATOM	6096	CG1	VAL	318	90.497	58.075	10.065	1.00	59.45	B	C
ATOM	6097	CG2	VAL	318	91.519	60.052	11.111	1.00	59.30	B	C
ATOM	6098	C	VAL	318	87.861	58.894	10.987	1.00	34.64	B	C
ATOM	6099	O	VAL	318	87.363	58.523	12.050	1.00	35.31	B	O
ATOM	6100	N	SER	319	87.417	58.482	9.803	1.00	25.74	B	N
ATOM	6101	CA	SER	319	86.300	57.557	9.711	1.00	25.00	B	C
ATOM	6102	CB	SER	319	85.769	57.502	8.275	1.00	46.83	B	C
ATOM	6103	OG	SER	319	86.801	57.222	7.348	1.00	58.78	B	O
ATOM	6104	C	SER	319	86.672	56.161	10.195	1.00	23.60	B	C
ATOM	6105	O	SER	319	85.877	55.513	10.876	1.00	21.67	B	O
ATOM	6106	N	ASP	320	87.875	55.702	9.855	1.00	29.04	B	N
ATOM	6107	CA	ASP	320	88.342	54.377	10.272	1.00	29.02	B	C
ATOM	6108	CB	ASP	320	87.700	53.292	9.391	1.00	54.50	B	C
ATOM	6109	CG	ASP	320	88.036	53.455	7.907	1.00	52.95	B	C
ATOM	6110	OD1	ASP	320	87.708	54.505	7.318	1.00	51.63	B	O
ATOM	6111	OD2	ASP	320	88.628	52.525	7.324	1.00	53.50	B	O
ATOM	6112	C	ASP	320	89.878	54.249	10.227	1.00	27.39	B	C
ATOM	6113	O	ASP	320	90.574	55.142	9.734	1.00	27.17	B	O
ATOM	6114	N	GLU	321	90.403	53.140	10.745	1.00	32.71	B	N
ATOM	6115	CA	GLU	321	91.845	52.909	10.748	1.00	33.69	B	C
ATOM	6116	CB	GLU	321	92.152	51.430	11.018	1.00	76.40	B	C
ATOM	6117	CG	GLU	321	92.439	51.066	12.469	1.00	70.24	B	C
ATOM	6118	CD	GLU	321	91.229	51.194	13.373	1.00	69.99	B	C
ATOM	6119	OE1	GLU	321	90.159	50.621	13.053	1.00	71.42	B	O
ATOM	6120	OE2	GLU	321	91.357	51.862	14.418	1.00	74.03	B	O
ATOM	6121	C	GLU	321	92.476	53.300	9.412	1.00	37.68	B	C
ATOM	6122	O	GLU	321	93.529	53.943	9.369	1.00	34.44	B	O
ATOM	6123	N	LEU	322	91.820	52.905	8.323	1.00	34.24	B	N
ATOM	6124	CA	LEU	322	92.310	53.175	6.971	1.00	36.93	B	C
ATOM	6125	CB	LEU	322	91.345	52.598	5.937	1.00	67.00	B	C
ATOM	6126	CG	LEU	322	91.361	51.081	5.743	1.00	65.63	B	C
ATOM	6127	CD1	LEU	322	92.716	50.681	5.198	1.00	67.37	B	C
ATOM	6128	CD2	LEU	322	91.058	50.353	7.063	1.00	70.68	B	C
ATOM	6129	C	LEU	322	92.566	54.632	6.643	1.00	38.52	B	C
ATOM	6130	O	LEU	322	93.607	54.971	6.097	1.00	41.87	B	O
ATOM	6131	N	ALA	323	91.617	55.492	6.974	1.00	34.22	B	N
ATOM	6132	CA	ALA	323	91.759	56.908	6.687	1.00	34.65	B	C

Fig. 19: A-85

ATOM	6133	CB	ALA	323	90.420	57.600	6.897	1.00	1.87	B	C
ATOM	6134	C	ALA	323	92.859	57.644	7.476	1.00	35.06	B	C
ATOM	6135	O	ALA	323	93.171	58.804	7.181	1.00	35.08	B	O
ATOM	6136	N	LEU	324	93.447	56.995	8.476	1.00	26.80	B	N
ATOM	6137	CA	LEU	324	94.492	57.652	9.256	1.00	25.28	B	C
ATOM	6138	CB	LEU	324	95.221	56.640	10.146	1.00	29.36	B	C
ATOM	6139	CG	LEU	324	94.590	56.344	11.516	1.00	28.09	B	C
ATOM	6140	CD1	LEU	324	95.288	55.158	12.170	1.00	27.23	B	C
ATOM	6141	CD2	LEU	324	94.676	57.580	12.406	1.00	26.02	B	C
ATOM	6142	C	LEU	324	95.495	58.366	8.354	1.00	28.81	B	C
ATOM	6143	O	LEU	324	95.822	59.521	8.588	1.00	25.35	B	O
ATOM	6144	N	VAL	325	95.966	57.679	7.317	1.00	52.77	B	N
ATOM	6145	CA	VAL	325	96.934	58.246	6.378	1.00	56.30	B	C
ATOM	6146	CB	VAL	325	97.153	57.321	5.185	1.00	36.74	B	C
ATOM	6147	CG1	VAL	325	97.936	56.099	5.614	1.00	36.85	B	C
ATOM	6148	CG2	VAL	325	95.810	56.923	4.599	1.00	40.13	B	C
ATOM	6149	C	VAL	325	96.524	59.598	5.818	1.00	59.12	B	C
ATOM	6150	O	VAL	325	97.324	60.529	5.761	1.00	61.18	B	O
ATOM	6151	N	THR	326	95.277	59.694	5.384	1.00	40.34	B	N
ATOM	6152	CA	THR	326	94.743	60.925	4.818	1.00	41.75	B	C
ATOM	6153	CB	THR	326	93.298	60.706	4.344	1.00	81.94	B	C
ATOM	6154	OG1	THR	326	92.430	60.600	5.481	1.00	83.85	B	O
ATOM	6155	CG2	THR	326	93.206	59.417	3.534	1.00	84.31	B	C
ATOM	6156	C	THR	326	94.744	62.070	5.836	1.00	41.76	B	C
ATOM	6157	O	THR	326	93.885	62.952	5.785	1.00	40.58	B	O
ATOM	6158	N	ILE	327	95.705	62.052	6.755	1.00	36.65	B	N
ATOM	6159	CA	ILE	327	95.812	63.075	7.792	1.00	36.84	B	C
ATOM	6160	CB	ILE	327	95.078	62.604	9.085	1.00	16.25	B	C
ATOM	6161	CG2	ILE	327	95.934	62.757	10.328	1.00	17.02	B	C
ATOM	6162	CG1	ILE	327	93.807	63.408	9.260	1.00	16.61	B	C
ATOM	6163	CD1	ILE	327	92.943	62.878	10.372	1.00	16.28	B	C
ATOM	6164	C	ILE	327	97.272	63.402	8.093	1.00	37.35	B	C
ATOM	6165	O	ILE	327	97.590	64.494	8.559	1.00	37.60	B	O
ATOM	6166	N	VAL	328	98.158	62.455	7.804	1.00	43.89	B	N
ATOM	6167	CA	VAL	328	99.575	62.643	8.060	1.00	46.03	B	C
ATOM	6168	CB	VAL	328	100.407	61.469	7.510	1.00	54.81	B	C
ATOM	6169	CG1	VAL	328	99.871	60.157	8.061	1.00	56.76	B	C
ATOM	6170	CG2	VAL	328	100.381	61.480	5.997	1.00	56.08	B	C
ATOM	6171	C	VAL	328	100.121	63.943	7.481	1.00	45.95	B	C
ATOM	6172	O	VAL	328	100.998	64.563	8.075	1.00	45.23	B	O
ATOM	6173	N	LYS	329	99.611	64.366	6.331	1.00	44.51	B	N
ATOM	6174	CA	LYS	329	100.097	65.609	5.732	1.00	43.72	B	C
ATOM	6175	CB	LYS	329	99.471	65.824	4.356	1.00	45.34	B	C
ATOM	6176	CG	LYS	329	100.174	66.880	3.520	1.00	46.89	B	C
ATOM	6177	CD	LYS	329	99.423	67.129	2.220	1.00	49.21	B	C
ATOM	6178	CE	LYS	329	100.179	68.074	1.298	1.00	52.25	B	C
ATOM	6179	NZ	LYS	329	101.450	67.466	0.831	1.00	55.93	B	N
ATOM	6180	C	LYS	329	99.762	66.797	6.640	1.00	41.89	B	C
ATOM	6181	O	LYS	329	100.640	67.552	7.056	1.00	43.10	B	O
ATOM	6182	N	ALA	330	98.483	66.957	6.952	1.00	14.46	B	N
ATOM	6183	CA	ALA	330	98.053	68.043	7.814	1.00	14.49	B	C
ATOM	6184	CB	ALA	330	96.538	68.052	7.906	1.00	26.19	B	C
ATOM	6185	C	ALA	330	98.657	67.910	9.210	1.00	15.64	B	C
ATOM	6186	O	ALA	330	99.090	68.896	9.796	1.00	15.54	B	O
ATOM	6187	N	LEU	331	98.666	66.688	9.745	1.00	29.61	B	N
ATOM	6188	CA	LEU	331	99.200	66.447	11.078	1.00	27.25	B	C
ATOM	6189	CB	LEU	331	99.108	64.969	11.454	1.00	20.84	B	C
ATOM	6190	CG	LEU	331	99.086	64.642	12.958	1.00	17.26	B	C
ATOM	6191	CD1	LEU	331	99.332	63.152	13.131	1.00	18.89	B	C
ATOM	6192	CD2	LEU	331	100.130	65.436	13.722	1.00	12.95	B	C
ATOM	6193	C	LEU	331	100.647	66.860	11.070	1.00	27.28	B	C
ATOM	6194	O	LEU	331	101.090	67.613	11.931	1.00	26.63	B	O
ATOM	6195	N	GLY	332	101.374	66.358	10.079	1.00	36.12	B	N
ATOM	6196	CA	GLY	332	102.784	66.666	9.949	1.00	37.22	B	C
ATOM	6197	C	GLY	332	103.089	68.150	9.917	1.00	37.48	B	C
ATOM	6198	O	GLY	332	103.940	68.628	10.670	1.00	41.35	B	O
ATOM	6199	N	GLU	333	102.398	68.892	9.058	1.00	41.72	B	N
ATOM	6200	CA	GLU	333	102.653	70.317	8.967	1.00	39.78	B	C
ATOM	6201	CB	GLU	333	102.052	70.889	7.683	1.00	98.89	B	C
ATOM	6202	CG	GLU	333	100.546	70.988	7.678	1.00	97.26	B	C
ATOM	6203	CD	GLU	333	100.018	71.598	6.400	1.00	97.28	B	C
ATOM	6204	OE1	GLU	333	98.795	71.849	6.322	1.00	99.33	B	O
ATOM	6205	OE2	GLU	333	100.824	71.823	5.472	1.00	91.40	B	O

Fig. 19: A-86

ATOM	6206	C	GLU	333	102.120	71.069	10.179	1.00	38.76	B	C
ATOM	6207	O	GLU	333	102.747	72.010	10.650	1.00	38.38	B	O
ATOM	6208	N	ARG	334	100.969	70.659	10.695	1.00	43.09	B	N
ATOM	6209	CA	ARG	334	100.398	71.340	11.847	1.00	46.47	B	C
ATOM	6210	CB	ARG	334	99.089	70.667	12.265	1.00	41.05	B	C
ATOM	6211	CG	ARG	334	98.167	71.568	13.056	1.00	40.34	B	C
ATOM	6212	CD	ARG	334	96.722	71.432	12.592	1.00	39.10	B	C
ATOM	6213	NE	ARG	334	96.544	71.911	11.222	1.00	34.65	B	N
ATOM	6214	CZ	ARG	334	95.446	71.721	10.488	1.00	38.74	B	C
ATOM	6215	NH1	ARG	334	94.407	71.052	10.987	1.00	35.48	B	N
ATOM	6216	NH2	ARG	334	95.388	72.197	9.246	1.00	44.88	B	N
ATOM	6217	C	ARG	334	101.419	71.321	12.980	1.00	47.77	B	C
ATOM	6218	O	ARG	334	101.633	72.329	13.643	1.00	44.69	B	O
ATOM	6219	N	ILE	335	102.060	70.177	13.192	1.00	95.68	B	N
ATOM	6220	CA	ILE	335	103.084	70.066	14.227	1.00	95.61	B	C
ATOM	6221	CB	ILE	335	103.349	68.565	14.599	1.00	69.44	B	C
ATOM	6222	CG2	ILE	335	103.371	67.701	13.359	1.00	72.22	B	C
ATOM	6223	CG1	ILE	335	104.671	68.420	15.350	1.00	70.66	B	C
ATOM	6224	CD1	ILE	335	105.043	66.983	15.628	1.00	73.45	B	C
ATOM	6225	C	ILE	335	104.346	70.716	13.653	1.00	93.90	B	C
ATOM	6226	O	ILE	335	105.317	70.979	14.364	1.00	96.50	B	O
ATOM	6227	N	PHE	336	104.273	71.011	12.356	1.00	144.26	B	N
ATOM	6228	CA	PHE	336	105.347	71.604	11.560	1.00	143.89	B	C
ATOM	6229	CB	PHE	336	105.336	73.156	11.625	1.00	83.50	B	C
ATOM	6230	CG	PHE	336	105.600	73.748	12.992	1.00	79.82	B	C
ATOM	6231	CD1	PHE	336	106.696	73.355	13.760	1.00	79.24	B	C
ATOM	6232	CD2	PHE	336	104.783	74.762	13.479	1.00	77.77	B	C
ATOM	6233	CE1	PHE	336	106.973	73.966	14.988	1.00	69.57	B	C
ATOM	6234	CE2	PHE	336	105.053	75.377	14.702	1.00	72.13	B	C
ATOM	6235	CZ	PHE	336	106.152	74.977	15.457	1.00	72.59	B	C
ATOM	6236	C	PHE	336	106.737	71.068	11.853	1.00	143.92	B	C
ATOM	6237	O	PHE	336	106.889	70.255	12.788	1.00	123.54	B	O
ATOM	6238	OXT	PHE	336	107.658	71.461	11.111	1.00	66.99	B	O
ATOM	6239	CB	GLU	1	68.990	38.972	10.337	1.00	143.47	X	C
ATOM	6240	CG	GLU	1	68.785	37.653	11.053	1.00	143.47	X	C
ATOM	6241	CD	GLU	1	68.300	36.572	10.118	1.00	143.47	X	C
ATOM	6242	OE1	GLU	1	69.012	36.278	9.134	1.00	143.47	X	O
ATOM	6243	OE2	GLU	1	67.209	36.019	10.363	1.00	143.47	X	O
ATOM	6244	C	GLU	1	71.024	39.462	11.710	1.00	74.19	X	C
ATOM	6245	O	GLU	1	71.492	38.415	11.265	1.00	74.19	X	O
ATOM	6246	N	GLU	1	69.921	41.257	10.328	1.00	74.19	X	N
ATOM	6247	CA	GLU	1	69.711	40.037	11.162	1.00	74.19	X	C
ATOM	6248	N	VAL	2	71.613	40.151	12.681	1.00	55.61	X	N
ATOM	6249	CA	VAL	2	72.858	39.694	13.284	1.00	55.61	X	C
ATOM	6250	CB	VAL	2	73.533	40.812	14.089	1.00	66.95	X	C
ATOM	6251	CG1	VAL	2	74.850	40.323	14.647	1.00	66.95	X	C
ATOM	6252	CG2	VAL	2	73.752	42.021	13.210	1.00	66.95	X	C
ATOM	6253	C	VAL	2	72.566	38.543	14.232	1.00	55.61	X	C
ATOM	6254	O	VAL	2	71.728	38.673	15.127	1.00	55.61	X	O
ATOM	6255	N	GLN	3	73.258	37.421	14.045	1.00	39.72	X	N
ATOM	6256	CA	GLN	3	73.044	36.261	14.908	1.00	39.72	X	C
ATOM	6257	CB	GLN	3	71.807	35.502	14.455	1.00	102.66	X	C
ATOM	6258	CG	GLN	3	71.852	35.144	13.002	1.00	102.66	X	C
ATOM	6259	CD	GLN	3	70.688	34.291	12.604	1.00	102.66	X	C
ATOM	6260	OE1	GLN	3	69.537	34.635	12.873	1.00	102.66	X	O
ATOM	6261	NE2	GLN	3	70.972	33.168	11.955	1.00	102.66	X	N
ATOM	6262	C	GLN	3	74.213	35.288	15.002	1.00	39.72	X	C
ATOM	6263	O	GLN	3	75.064	35.207	14.108	1.00	39.72	X	O
ATOM	6264	N	LEU	4	74.231	34.553	16.109	1.00	34.59	X	N
ATOM	6265	CA	LEU	4	75.260	33.555	16.389	1.00	34.59	X	C
ATOM	6266	CB	LEU	4	76.043	33.931	17.653	1.00	34.08	X	C
ATOM	6267	CG	LEU	4	77.107	35.040	17.665	1.00	34.08	X	C
ATOM	6268	CD1	LEU	4	77.119	35.820	16.353	1.00	34.08	X	C
ATOM	6269	CD2	LEU	4	76.844	35.950	18.863	1.00	34.08	X	C
ATOM	6270	C	LEU	4	74.581	32.212	16.615	1.00	34.59	X	C
ATOM	6271	O	LEU	4	73.737	32.080	17.503	1.00	34.59	X	O
ATOM	6272	N	VAL	5	74.933	31.218	15.806	1.00	36.99	X	N
ATOM	6273	CA	VAL	5	74.350	29.889	15.961	1.00	36.99	X	C
ATOM	6274	CB	VAL	5	73.536	29.456	14.698	1.00	37.13	X	C
ATOM	6275	CG1	VAL	5	74.285	29.815	13.430	1.00	37.13	X	C
ATOM	6276	CG2	VAL	5	73.264	27.963	14.744	1.00	37.13	X	C
ATOM	6277	C	VAL	5	75.429	28.861	16.277	1.00	36.99	X	C
ATOM	6278	O	VAL	5	76.163	28.404	15.398	1.00	36.99	X	O

Fig. 19: A-87

ATOM	6279	N	GLU	6	75.519	28.517	17.555	1.00	44.32	X	N
ATOM	6280	CA	GLU	6	76.499	27.550	18.020	1.00	44.32	X	C
ATOM	6281	CB	GLU	6	76.924	27.884	19.457	1.00	53.96	X	C
ATOM	6282	CG	GLU	6	75.844	28.531	20.292	1.00	53.96	X	C
ATOM	6283	CD	GLU	6	76.340	28.943	21.659	1.00	53.96	X	C
ATOM	6284	OE1	GLU	6	75.590	29.646	22.368	1.00	53.96	X	O
ATOM	6285	OE2	GLU	6	77.472	28.561	22.028	1.00	53.96	X	O
ATOM	6286	C	GLU	6	76.029	26.095	17.930	1.00	44.32	X	C
ATOM	6287	O	GLU	6	74.856	25.813	17.668	1.00	44.32	X	O
ATOM	6288	N	SER	7	76.980	25.185	18.135	1.00	42.31	X	N
ATOM	6289	CA	SER	7	76.758	23.745	18.091	1.00	42.31	X	C
ATOM	6290	CB	SER	7	76.762	23.261	16.642	1.00	44.31	X	C
ATOM	6291	OG	SER	7	77.832	23.845	15.922	1.00	44.31	X	O
ATOM	6292	C	SER	7	77.919	23.123	18.848	1.00	42.31	X	C
ATOM	6293	O	SER	7	78.889	23.813	19.138	1.00	42.31	X	O
ATOM	6294	N	GLY	8	77.822	21.838	19.178	1.00	39.85	X	N
ATOM	6295	CA	GLY	8	78.908	21.177	19.893	1.00	39.85	X	C
ATOM	6296	C	GLY	8	78.569	20.747	21.313	1.00	39.85	X	C
ATOM	6297	O	GLY	8	79.330	20.016	21.962	1.00	39.85	X	O
ATOM	6298	N	GLY	9	77.417	21.199	21.795	1.00	54.13	X	N
ATOM	6299	CA	GLY	9	76.998	20.852	23.138	1.00	54.13	X	C
ATOM	6300	C	GLY	9	76.467	19.439	23.283	1.00	54.13	X	C
ATOM	6301	O	GLY	9	75.390	19.102	22.783	1.00	54.13	X	O
ATOM	6302	N	GLY	10	77.235	18.606	23.972	1.00	51.55	X	N
ATOM	6303	CA	GLY	10	76.825	17.236	24.195	1.00	51.55	X	C
ATOM	6304	C	GLY	10	77.359	16.807	25.544	1.00	51.55	X	C
ATOM	6305	O	GLY	10	77.723	17.651	26.370	1.00	51.55	X	O
ATOM	6306	N	LEU	11	77.409	15.500	25.776	1.00	54.73	X	N
ATOM	6307	CA	LEU	11	77.930	14.981	27.032	1.00	54.73	X	C
ATOM	6308	CB	LEU	11	76.994	13.903	27.583	1.00	40.69	X	C
ATOM	6309	CG	LEU	11	77.583	13.086	28.735	1.00	40.69	X	C
ATOM	6310	CD1	LEU	11	78.170	14.011	29.795	1.00	40.69	X	C
ATOM	6311	CD2	LEU	11	76.508	12.198	29.317	1.00	40.69	X	C
ATOM	6312	C	LEU	11	79.341	14.412	26.852	1.00	54.73	X	C
ATOM	6313	O	LEU	11	79.664	13.853	25.806	1.00	54.73	X	O
ATOM	6314	N	VAL	12	80.177	14.576	27.872	1.00	43.40	X	N
ATOM	6315	CA	VAL	12	81.552	14.079	27.848	1.00	43.40	X	C
ATOM	6316	CB	VAL	12	82.538	15.118	27.273	1.00	57.73	X	C
ATOM	6317	CG1	VAL	12	82.222	15.388	25.812	1.00	57.73	X	C
ATOM	6318	CG2	VAL	12	82.473	16.404	28.086	1.00	57.73	X	C
ATOM	6319	C	VAL	12	81.991	13.753	29.269	1.00	43.40	X	C
ATOM	6320	O	VAL	12	81.490	14.344	30.230	1.00	43.40	X	O
ATOM	6321	N	GLN	13	82.931	12.821	29.403	1.00	46.11	X	N
ATOM	6322	CA	GLN	13	83.404	12.420	30.720	1.00	46.11	X	C
ATOM	6323	CB	GLN	13	83.873	10.965	30.676	1.00	148.60	X	C
ATOM	6324	CG	GLN	13	82.843	10.015	30.094	1.00	148.60	X	C
ATOM	6325	CD	GLN	13	83.232	8.560	30.263	1.00	148.60	X	C
ATOM	6326	OE1	GLN	13	84.322	8.145	29.868	1.00	148.60	X	O
ATOM	6327	NE2	GLN	13	82.337	7.774	30.852	1.00	148.60	X	N
ATOM	6328	C	GLN	13	84.532	13.311	31.234	1.00	46.11	X	C
ATOM	6329	O	GLN	13	85.186	14.002	30.454	1.00	46.11	X	O
ATOM	6330	N	PRO	14	84.763	13.319	32.563	1.00	39.23	X	N
ATOM	6331	CD	PRO	14	83.989	12.657	33.630	1.00	55.62	X	C
ATOM	6332	CA	PRO	14	85.831	14.141	33.141	1.00	39.23	X	C
ATOM	6333	CB	PRO	14	85.902	13.648	34.581	1.00	55.62	X	C
ATOM	6334	CG	PRO	14	84.474	13.374	34.887	1.00	55.62	X	C
ATOM	6335	C	PRO	14	87.122	13.905	32.392	1.00	39.23	X	C
ATOM	6336	O	PRO	14	87.357	12.810	31.885	1.00	39.23	X	O
ATOM	6337	N	GLY	15	87.954	14.935	32.320	1.00	28.04	X	N
ATOM	6338	CA	GLY	15	89.220	14.816	31.616	1.00	28.04	X	C
ATOM	6339	C	GLY	15	89.037	14.807	30.109	1.00	28.04	X	C
ATOM	6340	O	GLY	15	89.990	14.979	29.352	1.00	28.04	X	O
ATOM	6341	N	GLY	16	87.801	14.613	29.672	1.00	22.75	X	N
ATOM	6342	CA	GLY	16	87.529	14.583	28.250	1.00	22.75	X	C
ATOM	6343	C	GLY	16	87.705	15.912	27.539	1.00	22.75	X	C
ATOM	6344	O	GLY	16	87.887	16.969	28.155	1.00	22.75	X	O
ATOM	6345	N	SER	17	87.633	15.845	26.217	1.00	36.95	X	N
ATOM	6346	CA	SER	17	87.789	17.014	25.371	1.00	36.95	X	C
ATOM	6347	CB	SER	17	88.962	16.795	24.417	1.00	47.78	X	C
ATOM	6348	OG	SER	17	89.203	17.952	23.645	1.00	47.78	X	O
ATOM	6349	C	SER	17	86.509	17.311	24.581	1.00	36.95	X	C
ATOM	6350	O	SER	17	85.817	16.402	24.106	1.00	36.95	X	O
ATOM	6351	N	LEU	18	86.199	18.593	24.429	1.00	50.75	X	N

Fig. 19: A-88

ATOM	6352	CA	LEU	18	84.995	18.978	23.719	1.00	50.75	X	C
ATOM	6353	CB	LEU	18	83.833	18.944	24.701	1.00	37.38	X	C
ATOM	6354	CG	LEU	18	82.463	19.285	24.146	1.00	37.38	X	C
ATOM	6355	CD1	LEU	18	82.177	18.476	22.874	1.00	37.38	X	C
ATOM	6356	CD2	LEU	18	81.442	19.012	25.239	1.00	37.38	X	C
ATOM	6357	C	LEU	18	85.107	20.355	23.069	1.00	50.75	X	C
ATOM	6358	O	LEU	18	85.530	21.313	23.714	1.00	50.75	X	O
ATOM	6359	N	ARG	19	84.737	20.454	21.792	1.00	27.07	X	N
ATOM	6360	CA	ARG	19	84.805	21.739	21.097	1.00	27.07	X	C
ATOM	6361	CB	ARG	19	85.774	21.708	19.924	1.00	43.18	X	C
ATOM	6362	CG	ARG	19	85.825	23.068	19.238	1.00	43.18	X	C
ATOM	6363	CD	ARG	19	86.689	23.075	18.015	1.00	43.18	X	C
ATOM	6364	NE	ARG	19	86.060	22.389	16.896	1.00	43.18	X	N
ATOM	6365	CZ	ARG	19	86.564	22.371	15.666	1.00	43.18	X	C
ATOM	6366	NH1	ARG	19	87.708	23.006	15.407	1.00	43.18	X	N
ATOM	6367	NH2	ARG	19	85.924	21.725	14.696	1.00	43.18	X	N
ATOM	6368	C	ARG	19	83.501	22.302	20.558	1.00	27.07	X	C
ATOM	6369	O	ARG	19	82.895	21.745	19.625	1.00	27.07	X	O
ATOM	6370	N	LEU	20	83.109	23.438	21.135	1.00	30.57	X	N
ATOM	6371	CA	LEU	20	81.908	24.150	20.731	1.00	30.57	X	C
ATOM	6372	CB	LEU	20	81.354	24.965	21.896	1.00	36.53	X	C
ATOM	6373	CG	LEU	20	80.981	24.196	23.159	1.00	36.53	X	C
ATOM	6374	CD1	LEU	20	80.415	25.142	24.218	1.00	36.53	X	C
ATOM	6375	CD2	LEU	20	79.964	23.135	22.802	1.00	36.53	X	C
ATOM	6376	C	LEU	20	82.304	25.098	19.618	1.00	30.57	X	C
ATOM	6377	O	LEU	20	83.313	25.784	19.723	1.00	30.57	X	O
ATOM	6378	N	SER	21	81.527	25.122	18.544	1.00	31.77	X	N
ATOM	6379	CA	SER	21	81.789	26.024	17.426	1.00	31.77	X	C
ATOM	6380	CB	SER	21	81.876	25.252	16.117	1.00	32.65	X	C
ATOM	6381	OG	SER	21	80.580	24.896	15.682	1.00	32.65	X	O
ATOM	6382	C	SER	21	80.593	26.971	17.383	1.00	31.77	X	C
ATOM	6383	O	SER	21	79.591	26.738	18.057	1.00	31.77	X	O
ATOM	6384	N	CYS	22	80.673	28.024	16.585	1.00	49.03	X	N
ATOM	6385	CA	CYS	22	79.580	28.981	16.526	1.00	49.03	X	C
ATOM	6386	C	CYS	22	79.725	29.812	15.272	1.00	49.03	X	C
ATOM	6387	O	CYS	22	80.743	30.484	15.096	1.00	49.03	X	O
ATOM	6388	CB	CYS	22	79.643	29.849	17.788	1.00	49.62	X	C
ATOM	6389	SG	CYS	22	78.993	31.555	17.774	1.00	49.62	X	S
ATOM	6390	N	ALA	23	78.724	29.744	14.389	1.00	43.82	X	N
ATOM	6391	CA	ALA	23	78.742	30.509	13.136	1.00	43.82	X	C
ATOM	6392	CB	ALA	23	78.022	29.768	12.021	1.00	1.87	X	C
ATOM	6393	C	ALA	23	78.093	31.854	13.329	1.00	43.82	X	C
ATOM	6394	O	ALA	23	77.118	31.999	14.070	1.00	43.82	X	O
ATOM	6395	N	ALA	24	78.644	32.843	12.645	1.00	28.70	X	N
ATOM	6396	CA	ALA	24	78.129	34.190	12.735	1.00	28.70	X	C
ATOM	6397	CB	ALA	24	79.199	35.129	13.323	1.00	18.49	X	C
ATOM	6398	C	ALA	24	77.725	34.659	11.356	1.00	28.70	X	C
ATOM	6399	O	ALA	24	78.213	34.160	10.345	1.00	28.70	X	O
ATOM	6400	N	SER	25	76.816	35.620	11.338	1.00	39.45	X	N
ATOM	6401	CA	SER	25	76.338	36.218	10.108	1.00	39.45	X	C
ATOM	6402	CB	SER	25	75.279	35.322	9.443	1.00	48.28	X	C
ATOM	6403	OG	SER	25	74.163	35.090	10.287	1.00	48.28	X	O
ATOM	6404	C	SER	25	75.751	37.575	10.486	1.00	39.45	X	C
ATOM	6405	O	SER	25	75.425	37.819	11.656	1.00	39.45	X	O
ATOM	6406	N	GLY	26	75.651	38.464	9.506	1.00	15.13	X	N
ATOM	6407	CA	GLY	26	75.093	39.773	9.767	1.00	15.13	X	C
ATOM	6408	C	GLY	26	76.061	40.808	10.313	1.00	15.13	X	C
ATOM	6409	O	GLY	26	75.650	41.692	11.070	1.00	15.13	X	O
ATOM	6410	N	PHE	27	77.336	40.697	9.941	1.00	51.25	X	N
ATOM	6411	CA	PHE	27	78.375	41.638	10.358	1.00	51.25	X	C
ATOM	6412	CB	PHE	27	78.322	41.921	11.860	1.00	33.43	X	C
ATOM	6413	CG	PHE	27	78.647	40.736	12.720	1.00	33.43	X	C
ATOM	6414	CD1	PHE	27	77.696	39.749	12.958	1.00	33.43	X	C
ATOM	6415	CD2	PHE	27	79.891	40.629	13.337	1.00	33.43	X	C
ATOM	6416	CE1	PHE	27	77.978	38.673	13.810	1.00	33.43	X	C
ATOM	6417	CE2	PHE	27	80.186	39.558	14.190	1.00	33.43	X	C
ATOM	6418	CZ	PHE	27	79.227	38.581	14.428	1.00	33.43	X	C
ATOM	6419	C	PHE	27	79.748	41.100	10.012	1.00	51.25	X	C
ATOM	6420	O	PHE	27	79.966	39.894	10.027	1.00	51.25	X	O
ATOM	6421	N	THR	28	80.671	42.006	9.707	1.00	31.93	X	N
ATOM	6422	CA	THR	28	82.031	41.637	9.348	1.00	31.93	X	C
ATOM	6423	CB	THR	28	82.821	42.872	8.910	1.00	48.89	X	C
ATOM	6424	OG1	THR	28	82.126	43.520	7.836	1.00	48.89	X	O

Fig. 19: A-89

ATOM	6425	CG2	THR	28	84.212	42.474	8.454	1.00	48.89	X	C
ATOM	6426	C	THR	28	82.744	40.981	10.519	1.00	31.93	X	C
ATOM	6427	O	THR	28	83.431	41.640	11.286	1.00	31.93	X	O
ATOM	6428	N	PHE	29	82.576	39.671	10.636	1.00	37.68	X	N
ATOM	6429	CA	PHE	29	83.166	38.876	11.712	1.00	37.68	X	C
ATOM	6430	CB	PHE	29	83.068	37.386	11.352	1.00	38.41	X	C
ATOM	6431	CG	PHE	29	83.484	36.454	12.462	1.00	38.41	X	C
ATOM	6432	CD1	PHE	29	82.795	36.440	13.676	1.00	38.41	X	C
ATOM	6433	CD2	PHE	29	84.570	35.587	12.296	1.00	38.41	X	C
ATOM	6434	CE1	PHE	29	83.183	35.577	14.709	1.00	38.41	X	C
ATOM	6435	CE2	PHE	29	84.967	34.718	13.324	1.00	38.41	X	C
ATOM	6436	CZ	PHE	29	84.272	34.715	14.530	1.00	38.41	X	C
ATOM	6437	C	PHE	29	84.616	39.225	12.021	1.00	37.68	X	C
ATOM	6438	O	PHE	29	84.958	39.552	13.160	1.00	37.68	X	O
ATOM	6439	N	SER	30	85.462	39.160	10.998	1.00	22.05	X	N
ATOM	6440	CA	SER	30	86.890	39.421	11.157	1.00	22.05	X	C
ATOM	6441	CB	SER	30	87.553	39.545	9.783	1.00	37.79	X	C
ATOM	6442	OG	SER	30	86.886	40.481	8.959	1.00	37.79	X	O
ATOM	6443	C	SER	30	87.270	40.622	12.014	1.00	22.05	X	C
ATOM	6444	O	SER	30	88.326	40.634	12.639	1.00	22.05	X	O
ATOM	6445	N	ARG	31	86.395	41.615	12.063	1.00	29.69	X	N
ATOM	6446	CA	ARG	31	86.651	42.846	12.801	1.00	29.69	X	C
ATOM	6447	CB	ARG	31	85.819	43.956	12.162	1.00	51.15	X	C
ATOM	6448	CG	ARG	31	86.068	45.323	12.719	1.00	51.15	X	C
ATOM	6449	CD	ARG	31	84.999	46.281	12.231	1.00	51.15	X	C
ATOM	6450	NE	ARG	31	84.964	46.383	10.772	1.00	51.15	X	N
ATOM	6451	CZ	ARG	31	85.899	46.974	10.038	1.00	51.15	X	C
ATOM	6452	NH1	ARG	31	86.959	47.523	10.621	1.00	51.15	X	N
ATOM	6453	NH2	ARG	31	85.764	47.027	8.722	1.00	51.15	X	N
ATOM	6454	C	ARG	31	86.425	42.833	14.329	1.00	29.69	X	C
ATOM	6455	O	ARG	31	87.226	43.399	15.080	1.00	29.69	X	O
ATOM	6456	N	TYR	32	85.352	42.185	14.785	1.00	39.46	X	N
ATOM	6457	CA	TYR	32	85.009	42.144	16.217	1.00	39.46	X	C
ATOM	6458	CB	TYR	32	83.506	41.880	16.409	1.00	51.56	X	C
ATOM	6459	CG	TYR	32	82.601	42.689	15.516	1.00	51.56	X	C
ATOM	6460	CD1	TYR	32	82.540	42.437	14.148	1.00	51.56	X	C
ATOM	6461	CE1	TYR	32	81.721	43.181	13.316	1.00	51.56	X	C
ATOM	6462	CD2	TYR	32	81.811	43.714	16.034	1.00	51.56	X	C
ATOM	6463	CE2	TYR	32	80.985	44.467	15.209	1.00	51.56	X	C
ATOM	6464	CZ	TYR	32	80.946	44.193	13.851	1.00	51.56	X	C
ATOM	6465	OH	TYR	32	80.135	44.929	13.015	1.00	51.56	X	O
ATOM	6466	C	TYR	32	85.761	41.108	17.037	1.00	39.46	X	C
ATOM	6467	O	TYR	32	86.159	40.072	16.515	1.00	39.46	X	O
ATOM	6468	N	THR	33	85.943	41.386	18.328	1.00	29.44	X	N
ATOM	6469	CA	THR	33	86.611	40.421	19.191	1.00	29.44	X	C
ATOM	6470	CB	THR	33	87.510	41.080	20.315	1.00	20.65	X	C
ATOM	6471	OG1	THR	33	86.749	41.242	21.514	1.00	20.65	X	O
ATOM	6472	CG2	THR	33	88.072	42.437	19.866	1.00	20.65	X	C
ATOM	6473	C	THR	33	85.483	39.614	19.835	1.00	29.44	X	C
ATOM	6474	O	THR	33	84.632	40.167	20.536	1.00	29.44	X	O
ATOM	6475	N	MET	34	85.484	38.307	19.568	1.00	30.35	X	N
ATOM	6476	CA	MET	34	84.474	37.391	20.084	1.00	30.35	X	C
ATOM	6477	CB	MET	34	84.235	36.284	19.067	1.00	43.39	X	C
ATOM	6478	CG	MET	34	84.070	36.798	17.652	1.00	43.39	X	C
ATOM	6479	SD	MET	34	82.775	38.029	17.525	1.00	43.39	X	S
ATOM	6480	CE	MET	34	81.376	37.024	17.198	1.00	43.39	X	C
ATOM	6481	C	MET	34	84.867	36.785	21.430	1.00	30.35	X	C
ATOM	6482	O	MET	34	86.049	36.761	21.790	1.00	30.35	X	O
ATOM	6483	N	SER	35	83.866	36.293	22.164	1.00	35.95	X	N
ATOM	6484	CA	SER	35	84.073	35.701	23.487	1.00	35.95	X	C
ATOM	6485	CB	SER	35	83.875	36.765	24.580	1.00	34.42	X	C
ATOM	6486	OG	SER	35	84.740	37.878	24.420	1.00	34.42	X	O
ATOM	6487	C	SER	35	83.105	34.548	23.761	1.00	35.95	X	C
ATOM	6488	O	SER	35	82.191	34.290	22.978	1.00	35.95	X	O
ATOM	6489	N	TRP	36	83.323	33.856	24.879	1.00	43.17	X	N
ATOM	6490	CA	TRP	36	82.457	32.758	25.309	1.00	43.17	X	C
ATOM	6491	CB	TRP	36	83.159	31.383	25.200	1.00	32.84	X	C
ATOM	6492	CG	TRP	36	83.355	30.875	23.782	1.00	32.84	X	C
ATOM	6493	CD2	TRP	36	82.419	30.118	22.998	1.00	32.84	X	C
ATOM	6494	CE2	TRP	36	82.982	29.957	21.711	1.00	32.84	X	C
ATOM	6495	CE3	TRP	36	81.153	29.564	23.257	1.00	32.84	X	C
ATOM	6496	CD1	TRP	36	84.419	31.124	22.962	1.00	32.84	X	C
ATOM	6497	NE1	TRP	36	84.201	30.579	21.716	1.00	32.84	X	N

Fig. 19: A-90

ATOM	6498	CZ2	TRP	36	82.324	29.267	20.681	1.00	32.84	X	C
ATOM	6499	CZ3	TRP	36	80.495	28.877	22.228	1.00	32.84	X	C
ATOM	6500	CH2	TRP	36	81.086	28.738	20.957	1.00	32.84	X	C
ATOM	6501	C	TRP	36	82.056	33.022	26.764	1.00	43.17	X	C
ATOM	6502	O	TRP	36	82.908	33.298	27.615	1.00	43.17	X	O
ATOM	6503	N	VAL	37	80.751	32.958	27.026	1.00	29.19	X	N
ATOM	6504	CA	VAL	37	80.177	33.175	28.360	1.00	29.19	X	C
ATOM	6505	CB	VAL	37	79.213	34.419	28.353	1.00	8.00	X	C
ATOM	6506	CG1	VAL	37	78.350	34.467	29.621	1.00	8.00	X	C
ATOM	6507	CG2	VAL	37	80.026	35.689	28.240	1.00	8.00	X	C
ATOM	6508	C	VAL	37	79.412	31.907	28.760	1.00	29.19	X	C
ATOM	6509	O	VAL	37	78.629	31.381	27.971	1.00	29.19	X	O
ATOM	6510	N	ARG	38	79.651	31.415	29.974	1.00	61.80	X	N
ATOM	6511	CA	ARG	38	78.992	30.198	30.454	1.00	61.80	X	C
ATOM	6512	CB	ARG	38	80.036	29.167	30.899	1.00	27.50	X	C
ATOM	6513	CG	ARG	38	80.926	29.688	32.011	1.00	27.50	X	C
ATOM	6514	CD	ARG	38	81.370	28.603	32.965	1.00	27.50	X	C
ATOM	6515	NE	ARG	38	82.222	27.579	32.364	1.00	27.50	X	N
ATOM	6516	CZ	ARG	38	83.391	27.181	32.874	1.00	27.50	X	C
ATOM	6517	NH1	ARG	38	83.862	27.725	33.992	1.00	27.50	X	N
ATOM	6518	NH2	ARG	38	84.087	26.217	32.281	1.00	27.50	X	N
ATOM	6519	C	ARG	38	78.053	30.468	31.628	1.00	61.80	X	C
ATOM	6520	O	ARG	38	78.104	31.528	32.245	1.00	61.80	X	O
ATOM	6521	N	GLN	39	77.204	29.491	31.934	1.00	39.46	X	N
ATOM	6522	CA	GLN	39	76.269	29.597	33.049	1.00	39.46	X	C
ATOM	6523	CB	GLN	39	74.982	30.269	32.588	1.00	44.48	X	C
ATOM	6524	CG	GLN	39	73.997	30.530	33.708	1.00	44.48	X	C
ATOM	6525	CD	GLN	39	72.916	31.497	33.294	1.00	44.48	X	C
ATOM	6526	OE1	GLN	39	72.269	31.320	32.252	1.00	44.48	X	O
ATOM	6527	NE2	GLN	39	72.709	32.532	34.106	1.00	44.48	X	N
ATOM	6528	C	GLN	39	75.955	28.224	33.663	1.00	39.46	X	C
ATOM	6529	O	GLN	39	75.233	27.404	33.076	1.00	39.46	X	O
ATOM	6530	N	ALA	40	76.514	27.984	34.846	1.00	47.11	X	N
ATOM	6531	CA	ALA	40	76.324	26.727	35.558	1.00	47.11	X	C
ATOM	6532	CB	ALA	40	77.241	26.678	36.773	1.00	19.87	X	C
ATOM	6533	C	ALA	40	74.875	26.592	35.995	1.00	47.11	X	C
ATOM	6534	O	ALA	40	74.296	27.542	36.512	1.00	47.11	X	O
ATOM	6535	N	PRO	41	74.271	25.403	35.802	1.00	63.91	X	N
ATOM	6536	CD	PRO	41	74.879	24.157	35.299	1.00	66.56	X	C
ATOM	6537	CA	PRO	41	72.875	25.168	36.187	1.00	63.91	X	C
ATOM	6538	CB	PRO	41	72.793	23.649	36.244	1.00	66.56	X	C
ATOM	6539	CG	PRO	41	73.667	23.254	35.115	1.00	66.56	X	C
ATOM	6540	C	PRO	41	72.507	25.826	37.508	1.00	63.91	X	C
ATOM	6541	O	PRO	41	73.186	25.637	38.522	1.00	63.91	X	O
ATOM	6542	N	GLY	42	71.432	26.608	37.478	1.00	63.56	X	N
ATOM	6543	CA	GLY	42	70.979	27.297	38.671	1.00	63.56	X	C
ATOM	6544	C	GLY	42	71.963	28.342	39.165	1.00	63.56	X	C
ATOM	6545	O	GLY	42	71.920	28.732	40.334	1.00	63.56	X	O
ATOM	6546	N	LYS	43	72.846	28.793	38.276	1.00	103.79	X	N
ATOM	6547	CA	LYS	43	73.852	29.802	38.607	1.00	103.79	X	C
ATOM	6548	CB	LYS	43	75.248	29.168	38.641	1.00	95.84	X	C
ATOM	6549	CG	LYS	43	75.752	28.830	40.037	1.00	95.84	X	C
ATOM	6550	CD	LYS	43	74.840	27.853	40.755	1.00	95.84	X	C
ATOM	6551	CE	LYS	43	75.225	27.734	42.222	1.00	95.84	X	C
ATOM	6552	NZ	LYS	43	75.138	29.048	42.920	1.00	95.84	X	N
ATOM	6553	C	LYS	43	73.848	30.984	37.634	1.00	103.79	X	C
ATOM	6554	O	LYS	43	73.085	31.013	36.668	1.00	103.79	X	O
ATOM	6555	N	GLY	44	74.714	31.956	37.899	1.00	36.05	X	N
ATOM	6556	CA	GLY	44	74.796	33.131	37.055	1.00	36.05	X	C
ATOM	6557	C	GLY	44	75.710	33.025	35.845	1.00	36.05	X	C
ATOM	6558	O	GLY	44	76.150	31.931	35.477	1.00	36.05	X	O
ATOM	6559	N	LEU	45	76.003	34.186	35.249	1.00	24.14	X	N
ATOM	6560	CA	LEU	45	76.832	34.316	34.046	1.00	24.14	X	C
ATOM	6561	CB	LEU	45	76.343	35.504	33.214	1.00	15.59	X	C
ATOM	6562	CG	LEU	45	74.932	35.346	32.638	1.00	15.59	X	C
ATOM	6563	CD1	LEU	45	74.470	36.606	31.917	1.00	15.59	X	C
ATOM	6564	CD2	LEU	45	74.942	34.179	31.677	1.00	15.59	X	C
ATOM	6565	C	LEU	45	78.316	34.474	34.311	1.00	24.14	X	C
ATOM	6566	O	LEU	45	78.732	35.324	35.095	1.00	24.14	X	O
ATOM	6567	N	GLU	46	79.110	33.661	33.624	1.00	56.59	X	N
ATOM	6568	CA	GLU	46	80.557	33.686	33.774	1.00	56.59	X	C
ATOM	6569	CB	GLU	46	81.034	32.373	34.412	1.00	46.99	X	C
ATOM	6570	CG	GLU	46	82.536	32.308	34.666	1.00	46.99	X	C

Fig. 19: A-91

ATOM	6571	CD	GLU	46	82.953	31.066	35.438	1.00	46.99	X	C
ATOM	6572	OE1	GLU	46	82.642	29.952	34.970	1.00	46.99	X	O
ATOM	6573	OE2	GLU	46	83.594	31.201	36.508	1.00	46.99	X	O
ATOM	6574	C	GLU	46	81.272	33.904	32.439	1.00	56.59	X	C
ATOM	6575	O	GLU	46	80.821	33.433	31.393	1.00	56.59	X	O
ATOM	6576	N	TRP	47	82.385	34.632	32.489	1.00	30.60	X	N
ATOM	6577	CA	TRP	47	83.188	34.910	31.300	1.00	30.60	X	C
ATOM	6578	CB	TRP	47	83.889	36.273	31.426	1.00	23.41	X	C
ATOM	6579	CG	TRP	47	84.944	36.481	30.385	1.00	23.41	X	C
ATOM	6580	CD2	TRP	47	86.358	36.500	30.601	1.00	23.41	X	C
ATOM	6581	CE2	TRP	47	86.971	36.591	29.328	1.00	23.41	X	C
ATOM	6582	CE3	TRP	47	87.170	36.441	31.746	1.00	23.41	X	C
ATOM	6583	CD1	TRP	47	84.759	36.570	29.031	1.00	23.41	X	C
ATOM	6584	NE1	TRP	47	85.969	36.633	28.392	1.00	23.41	X	N
ATOM	6585	CZ2	TRP	47	88.365	36.622	29.165	1.00	23.41	X	C
ATOM	6586	CZ3	TRP	47	88.553	36.470	31.587	1.00	23.41	X	C
ATOM	6587	CH2	TRP	47	89.137	36.560	30.304	1.00	23.41	X	C
ATOM	6588	C	TRP	47	84.231	33.810	31.153	1.00	30.60	X	C
ATOM	6589	O	TRP	47	84.965	33.516	32.097	1.00	30.60	X	O
ATOM	6590	N	VAL	48	84.317	33.219	29.967	1.00	24.17	X	N
ATOM	6591	CA	VAL	48	85.270	32.128	29.755	1.00	24.17	X	C
ATOM	6592	CB	VAL	48	84.589	30.924	29.011	1.00	22.03	X	C
ATOM	6593	CG1	VAL	48	85.589	29.786	28.790	1.00	22.03	X	C
ATOM	6594	CG2	VAL	48	83.408	30.436	29.805	1.00	22.03	X	C
ATOM	6595	C	VAL	48	86.550	32.490	29.006	1.00	24.17	X	C
ATOM	6596	O	VAL	48	87.640	32.477	29.579	1.00	24.17	X	O
ATOM	6597	N	ALA	49	86.407	32.800	27.724	1.00	21.43	X	N
ATOM	6598	CA	ALA	49	87.550	33.118	26.885	1.00	21.43	X	C
ATOM	6599	CB	ALA	49	87.953	31.884	26.094	1.00	38.48	X	C
ATOM	6600	C	ALA	49	87.228	34.257	25.934	1.00	21.43	X	C
ATOM	6601	O	ALA	49	86.066	34.661	25.825	1.00	21.43	X	O
ATOM	6602	N	THR	50	88.257	34.745	25.235	1.00	24.70	X	N
ATOM	6603	CA	THR	50	88.115	35.856	24.286	1.00	24.70	X	C
ATOM	6604	CB	THR	50	87.952	37.202	25.048	1.00	38.80	X	C
ATOM	6605	OG1	THR	50	86.711	37.215	25.763	1.00	38.80	X	O
ATOM	6606	CG2	THR	50	87.981	38.369	24.087	1.00	38.80	X	C
ATOM	6607	C	THR	50	89.298	36.039	23.324	1.00	24.70	X	C
ATOM	6608	O	THR	50	90.456	35.935	23.738	1.00	24.70	X	O
ATOM	6609	N	ILE	51	89.010	36.300	22.047	1.00	32.54	X	N
ATOM	6610	CA	ILE	51	90.075	36.599	21.074	1.00	32.54	X	C
ATOM	6611	CB	ILE	51	90.333	35.495	19.998	1.00	54.98	X	C
ATOM	6612	CG2	ILE	51	90.567	34.178	20.661	1.00	54.98	X	C
ATOM	6613	CG1	ILE	51	89.180	35.415	18.997	1.00	54.98	X	C
ATOM	6614	CD1	ILE	51	87.893	34.921	19.582	1.00	54.98	X	C
ATOM	6615	C	ILE	51	89.674	37.865	20.335	1.00	32.54	X	C
ATOM	6616	O	ILE	51	88.516	38.024	19.937	1.00	32.54	X	O
ATOM	6617	N	SER	52	90.628	38.774	20.167	1.00	43.61	X	N
ATOM	6618	CA	SER	52	90.361	40.024	19.477	1.00	43.61	X	C
ATOM	6619	CB	SER	52	91.374	41.081	19.910	1.00	24.33	X	C
ATOM	6620	OG	SER	52	92.684	40.702	19.528	1.00	24.33	X	O
ATOM	6621	C	SER	52	90.450	39.789	17.973	1.00	43.61	X	C
ATOM	6622	O	SER	52	90.677	38.663	17.533	1.00	43.61	X	O
ATOM	6623	N	GLY	53	90.243	40.843	17.187	1.00	34.59	X	N
ATOM	6624	CA	GLY	53	90.336	40.707	15.747	1.00	34.59	X	C
ATOM	6625	C	GLY	53	91.800	40.559	15.381	1.00	34.59	X	C
ATOM	6626	O	GLY	53	92.152	40.020	14.332	1.00	34.59	X	O
ATOM	6627	N	GLY	54	92.658	41.047	16.266	1.00	29.30	X	N
ATOM	6628	CA	GLY	54	94.079	40.949	16.033	1.00	29.30	X	C
ATOM	6629	C	GLY	54	94.555	39.550	16.359	1.00	29.30	X	C
ATOM	6630	O	GLY	54	95.642	39.135	15.954	1.00	29.30	X	O
ATOM	6631	N	GLY	55	93.747	38.811	17.103	1.00	15.27	X	N
ATOM	6632	CA	GLY	55	94.139	37.465	17.437	1.00	15.27	X	C
ATOM	6633	C	GLY	55	94.596	37.254	18.867	1.00	15.27	X	C
ATOM	6634	O	GLY	55	94.878	36.105	19.231	1.00	15.27	X	O
ATOM	6635	N	HIS	56	94.676	38.319	19.675	1.00	13.76	X	N
ATOM	6636	CA	HIS	56	95.101	38.181	21.076	1.00	13.76	X	C
ATOM	6637	CB	HIS	56	95.268	39.543	21.741	1.00	60.58	X	C
ATOM	6638	CG	HIS	56	96.115	40.490	20.957	1.00	60.58	X	C
ATOM	6639	CD2	HIS	56	97.417	40.838	21.087	1.00	60.58	X	C
ATOM	6640	ND1	HIS	56	95.638	41.180	19.862	1.00	60.58	X	N
ATOM	6641	CE1	HIS	56	96.611	41.913	19.351	1.00	60.58	X	C
ATOM	6642	NE2	HIS	56	97.701	41.724	20.075	1.00	60.58	X	N
ATOM	6643	C	HIS	56	94.071	37.383	21.857	1.00	13.76	X	C

Fig. 19: A-92

ATOM	6644	O	HIS	56	92.864	37.621	21.736	1.00	13.76	X	O
ATOM	6645	N	THR	57	94.529	36.438	22.671	1.00	20.05	X	N
ATOM	6646	CA	THR	57	93.583	35.632	23.436	1.00	20.05	X	C
ATOM	6647	CB	THR	57	93.759	34.123	23.096	1.00	15.53	X	C
ATOM	6648	OG1	THR	57	95.015	33.651	23.587	1.00	15.53	X	O
ATOM	6649	CG2	THR	57	93.734	33.929	21.593	1.00	15.53	X	C
ATOM	6650	C	THR	57	93.655	35.876	24.952	1.00	20.05	X	C
ATOM	6651	O	THR	57	94.716	36.142	25.512	1.00	20.05	X	O
ATOM	6652	N	TYR	58	92.500	35.808	25.603	1.00	19.06	X	N
ATOM	6653	CA	TYR	58	92.410	36.037	27.040	1.00	19.06	X	C
ATOM	6654	CB	TYR	58	91.829	37.428	27.304	1.00	22.48	X	C
ATOM	6655	CG	TYR	58	92.614	38.542	26.661	1.00	22.48	X	C
ATOM	6656	CD1	TYR	58	93.565	39.252	27.384	1.00	22.48	X	C
ATOM	6657	CE1	TYR	58	94.308	40.265	26.788	1.00	22.48	X	C
ATOM	6658	CD2	TYR	58	92.423	38.871	25.316	1.00	22.48	X	C
ATOM	6659	CE2	TYR	58	93.167	39.886	24.703	1.00	22.48	X	C
ATOM	6660	CZ	TYR	58	94.105	40.580	25.447	1.00	22.48	X	C
ATOM	6661	OH	TYR	58	94.828	41.611	24.876	1.00	22.48	X	O
ATOM	6662	C	TYR	58	91.513	34.973	27.656	1.00	19.06	X	C
ATOM	6663	O	TYR	58	90.442	34.660	27.123	1.00	19.06	X	O
ATOM	6664	N	TYR	59	91.945	34.437	28.792	1.00	29.06	X	N
ATOM	6665	CA	TYR	59	91.199	33.378	29.456	1.00	29.06	X	C
ATOM	6666	CB	TYR	59	91.988	32.080	29.371	1.00	21.37	X	C
ATOM	6667	CG	TYR	59	92.252	31.641	27.969	1.00	21.37	X	C
ATOM	6668	CD1	TYR	59	91.352	30.813	27.303	1.00	21.37	X	C
ATOM	6669	CE1	TYR	59	91.573	30.428	25.988	1.00	21.37	X	C
ATOM	6670	CD2	TYR	59	93.382	32.076	27.286	1.00	21.37	X	C
ATOM	6671	CE2	TYR	59	93.608	31.698	25.968	1.00	21.37	X	C
ATOM	6672	CZ	TYR	59	92.697	30.874	25.330	1.00	21.37	X	C
ATOM	6673	OH	TYR	59	92.897	30.495	24.027	1.00	21.37	X	O
ATOM	6674	C	TYR	59	90.857	33.605	30.910	1.00	29.06	X	C
ATOM	6675	O	TYR	59	91.575	34.287	31.648	1.00	29.06	X	O
ATOM	6676	N	LEU	60	89.745	33.002	31.308	1.00	26.45	X	N
ATOM	6677	CA	LEU	60	89.309	33.048	32.689	1.00	26.45	X	C
ATOM	6678	CB	LEU	60	87.927	32.397	32.826	1.00	24.21	X	C
ATOM	6679	CG	LEU	60	87.411	32.193	34.252	1.00	24.21	X	C
ATOM	6680	CD1	LEU	60	87.173	33.538	34.911	1.00	24.21	X	C
ATOM	6681	CD2	LEU	60	86.135	31.380	34.223	1.00	24.21	X	C
ATOM	6682	C	LEU	60	90.382	32.189	33.360	1.00	26.45	X	C
ATOM	6683	O	LEU	60	90.822	31.191	32.781	1.00	26.45	X	O
ATOM	6684	N	ASP	61	90.822	32.570	34.553	1.00	64.06	X	N
ATOM	6685	CA	ASP	61	91.865	31.810	35.240	1.00	64.06	X	C
ATOM	6686	CB	ASP	61	92.297	32.556	36.502	1.00	60.41	X	C
ATOM	6687	CG	ASP	61	92.984	33.865	36.183	1.00	60.41	X	C
ATOM	6688	OD1	ASP	61	93.262	34.650	37.114	1.00	60.41	X	O
ATOM	6689	OD2	ASP	61	93.250	34.106	34.986	1.00	60.41	X	O
ATOM	6690	C	ASP	61	91.477	30.371	35.576	1.00	64.06	X	C
ATOM	6691	O	ASP	61	92.337	29.503	35.701	1.00	64.06	X	O
ATOM	6692	N	SER	62	90.181	30.122	35.707	1.00	57.78	X	N
ATOM	6693	CA	SER	62	89.681	28.791	36.028	1.00	57.78	X	C
ATOM	6694	CB	SER	62	88.196	28.868	36.386	1.00	42.55	X	C
ATOM	6695	OG	SER	62	87.643	27.575	36.556	1.00	42.55	X	O
ATOM	6696	C	SER	62	89.872	27.787	34.894	1.00	57.78	X	C
ATOM	6697	O	SER	62	90.000	26.590	35.142	1.00	57.78	X	O
ATOM	6698	N	VAL	63	89.890	28.269	33.655	1.00	47.11	X	N
ATOM	6699	CA	VAL	63	90.047	27.383	32.504	1.00	47.11	X	C
ATOM	6700	CB	VAL	63	88.796	27.464	31.555	1.00	39.29	X	C
ATOM	6701	CG1	VAL	63	87.513	27.472	32.375	1.00	39.29	X	C
ATOM	6702	CG2	VAL	63	88.863	28.700	30.679	1.00	39.29	X	C
ATOM	6703	C	VAL	63	91.318	27.660	31.686	1.00	47.11	X	C
ATOM	6704	O	VAL	63	91.504	27.093	30.603	1.00	47.11	X	O
ATOM	6705	N	LYS	64	92.200	28.511	32.208	1.00	47.01	X	N
ATOM	6706	CA	LYS	64	93.424	28.843	31.483	1.00	47.01	X	C
ATOM	6707	CB	LYS	64	94.116	30.063	32.107	1.00	84.46	X	C
ATOM	6708	CG	LYS	64	95.038	30.797	31.135	1.00	84.46	X	C
ATOM	6709	CD	LYS	64	95.670	32.025	31.766	1.00	84.46	X	C
ATOM	6710	CE	LYS	64	96.370	32.907	30.725	1.00	84.46	X	C
ATOM	6711	NZ	LYS	64	95.419	33.654	29.833	1.00	84.46	X	N
ATOM	6712	C	LYS	64	94.388	27.666	31.441	1.00	47.01	X	C
ATOM	6713	O	LYS	64	94.757	27.113	32.479	1.00	47.01	X	O
ATOM	6714	N	GLY	65	94.795	27.289	30.231	1.00	35.35	X	N
ATOM	6715	CA	GLY	65	95.704	26.167	30.073	1.00	35.35	X	C
ATOM	6716	C	GLY	65	94.953	24.919	29.652	1.00	35.35	X	C

Fig. 19: A-93

ATOM	6717	O	GLY	65	95.547	23.945	29.195	1.00	35.35	X	O
ATOM	6718	N	ARG	66	93.634	24.956	29.809	1.00	33.32	X	N
ATOM	6719	CA	ARG	66	92.791	23.833	29.450	1.00	33.32	X	C
ATOM	6720	CB	ARG	66	91.881	23.470	30.616	1.00	43.17	X	C
ATOM	6721	CG	ARG	66	92.594	23.386	31.958	1.00	43.17	X	C
ATOM	6722	CD	ARG	66	91.684	22.813	33.050	1.00	43.17	X	C
ATOM	6723	NE	ARG	66	90.548	23.679	33.367	1.00	43.17	X	N
ATOM	6724	CZ	ARG	66	89.277	23.296	33.305	1.00	43.17	X	C
ATOM	6725	NH1	ARG	66	88.973	22.061	32.932	1.00	43.17	X	N
ATOM	6726	NH2	ARG	66	88.309	24.144	33.630	1.00	43.17	X	N
ATOM	6727	C	ARG	66	91.945	24.169	28.232	1.00	33.32	X	C
ATOM	6728	O	ARG	66	91.775	23.336	27.346	1.00	33.32	X	O
ATOM	6729	N	PHE	67	91.411	25.389	28.191	1.00	33.69	X	N
ATOM	6730	CA	PHE	67	90.567	25.834	27.074	1.00	33.69	X	C
ATOM	6731	CB	PHE	67	89.444	26.750	27.587	1.00	42.44	X	C
ATOM	6732	CG	PHE	67	88.346	26.030	28.330	1.00	42.44	X	C
ATOM	6733	CD1	PHE	67	88.573	24.802	28.943	1.00	42.44	X	C
ATOM	6734	CD2	PHE	67	87.074	26.594	28.426	1.00	42.44	X	C
ATOM	6735	CE1	PHE	67	87.547	24.145	29.637	1.00	42.44	X	C
ATOM	6736	CE2	PHE	67	86.038	25.940	29.122	1.00	42.44	X	C
ATOM	6737	CZ	PHE	67	86.278	24.717	29.724	1.00	42.44	X	C
ATOM	6738	C	PHE	67	91.393	26.578	26.027	1.00	33.69	X	C
ATOM	6739	O	PHE	67	92.405	27.194	26.344	1.00	33.69	X	O
ATOM	6740	N	THR	68	90.949	26.526	24.779	1.00	56.59	X	N
ATOM	6741	CA	THR	68	91.646	27.201	23.689	1.00	56.59	X	C
ATOM	6742	CB	THR	68	92.454	26.193	22.846	1.00	46.98	X	C
ATOM	6743	OG1	THR	68	93.611	25.781	23.578	1.00	46.98	X	O
ATOM	6744	CG2	THR	68	92.870	26.808	21.512	1.00	46.98	X	C
ATOM	6745	C	THR	68	90.661	27.913	22.768	1.00	56.59	X	C
ATOM	6746	O	THR	68	89.899	27.270	22.047	1.00	56.59	X	O
ATOM	6747	N	ILE	69	90.672	29.239	22.781	1.00	20.15	X	N
ATOM	6748	CA	ILE	69	89.760	29.975	21.918	1.00	20.15	X	C
ATOM	6749	CB	ILE	69	89.287	31.289	22.607	1.00	31.46	X	C
ATOM	6750	CG2	ILE	69	90.480	32.153	22.953	1.00	31.46	X	C
ATOM	6751	CG1	ILE	69	88.283	32.028	21.722	1.00	31.46	X	C
ATOM	6752	CD1	ILE	69	87.574	33.159	22.446	1.00	31.46	X	C
ATOM	6753	C	ILE	69	90.464	30.262	20.591	1.00	20.15	X	C
ATOM	6754	O	ILE	69	91.672	30.481	20.559	1.00	20.15	X	O
ATOM	6755	N	SER	70	89.724	30.223	19.489	1.00	21.14	X	N
ATOM	6756	CA	SER	70	90.319	30.482	18.182	1.00	21.14	X	C
ATOM	6757	CB	SER	70	91.105	29.263	17.693	1.00	37.41	X	C
ATOM	6758	OG	SER	70	90.228	28.236	17.253	1.00	37.41	X	O
ATOM	6759	C	SER	70	89.242	30.824	17.163	1.00	21.14	X	C
ATOM	6760	O	SER	70	88.045	30.637	17.413	1.00	21.14	X	O
ATOM	6761	N	ARG	71	89.673	31.322	16.009	1.00	30.73	X	N
ATOM	6762	CA	ARG	71	88.734	31.687	14.966	1.00	30.73	X	C
ATOM	6763	CB	ARG	71	88.369	33.178	15.073	1.00	24.51	X	C
ATOM	6764	CG	ARG	71	89.546	34.139	14.901	1.00	24.51	X	C
ATOM	6765	CD	ARG	71	89.071	35.503	14.453	1.00	24.51	X	C
ATOM	6766	NE	ARG	71	88.464	36.278	15.534	1.00	24.51	X	N
ATOM	6767	CZ	ARG	71	87.604	37.283	15.351	1.00	24.51	X	C
ATOM	6768	NH1	ARG	71	87.229	37.643	14.131	1.00	24.51	X	N
ATOM	6769	NH2	ARG	71	87.132	37.948	16.391	1.00	24.51	X	N
ATOM	6770	C	ARG	71	89.259	31.393	13.560	1.00	30.73	X	C
ATOM	6771	O	ARG	71	90.464	31.415	13.301	1.00	30.73	X	O
ATOM	6772	N	ASP	72	88.326	31.106	12.663	1.00	55.72	X	N
ATOM	6773	CA	ASP	72	88.619	30.836	11.268	1.00	55.72	X	C
ATOM	6774	CB	ASP	72	88.219	29.405	10.902	1.00	83.09	X	C
ATOM	6775	CG	ASP	72	88.255	29.153	9.409	1.00	83.09	X	C
ATOM	6776	OD1	ASP	72	89.282	29.466	8.773	1.00	83.09	X	O
ATOM	6777	OD2	ASP	72	87.256	28.637	8.870	1.00	83.09	X	O
ATOM	6778	C	ASP	72	87.749	31.837	10.528	1.00	55.72	X	C
ATOM	6779	O	ASP	72	86.613	31.539	10.162	1.00	55.72	X	O
ATOM	6780	N	ASN	73	88.284	33.036	10.340	1.00	57.89	X	N
ATOM	6781	CA	ASN	73	87.552	34.098	9.673	1.00	57.89	X	C
ATOM	6782	CB	ASN	73	88.426	35.345	9.558	1.00	43.96	X	C
ATOM	6783	CG	ASN	73	88.777	35.928	10.912	1.00	43.96	X	C
ATOM	6784	OD1	ASN	73	88.021	35.794	11.879	1.00	43.96	X	O
ATOM	6785	ND2	ASN	73	89.919	36.593	10.986	1.00	43.96	X	N
ATOM	6786	C	ASN	73	87.020	33.715	8.306	1.00	57.89	X	C
ATOM	6787	O	ASN	73	85.949	34.173	7.903	1.00	57.89	X	O
ATOM	6788	N	SER	74	87.756	32.870	7.594	1.00	50.09	X	N
ATOM	6789	CA	SER	74	87.324	32.451	6.268	1.00	50.09	X	C

Fig. 19: A-94

ATOM	6790	CB	SER	74	88.277	31.398	5.705	1.00	34.87	X	C
ATOM	6791	OG	SER	74	88.179	30.197	6.441	1.00	34.87	X	O
ATOM	6792	C	SER	74	85.910	31.880	6.303	1.00	50.09	X	C
ATOM	6793	O	SER	74	85.141	32.050	5.356	1.00	50.09	X	O
ATOM	6794	N	LYS	75	85.572	31.209	7.400	1.00	50.16	X	N
ATOM	6795	CA	LYS	75	84.257	30.597	7.551	1.00	50.16	X	C
ATOM	6796	CB	LYS	75	84.418	29.097	7.814	1.00	60.89	X	C
ATOM	6797	CG	LYS	75	85.206	28.372	6.729	1.00	60.89	X	C
ATOM	6798	CD	LYS	75	85.356	26.884	7.009	1.00	60.89	X	C
ATOM	6799	CE	LYS	75	86.046	26.195	5.840	1.00	60.89	X	C
ATOM	6800	NZ	LYS	75	85.341	26.459	4.551	1.00	60.89	X	N
ATOM	6801	C	LYS	75	83.423	31.226	8.663	1.00	50.16	X	C
ATOM	6802	O	LYS	75	82.470	30.618	9.142	1.00	50.16	X	O
ATOM	6803	N	ASN	76	83.786	32.441	9.066	1.00	54.49	X	N
ATOM	6804	CA	ASN	76	83.075	33.165	10.117	1.00	54.49	X	C
ATOM	6805	CB	ASN	76	81.812	33.818	9.559	1.00	41.29	X	C
ATOM	6806	CG	ASN	76	82.116	34.956	8.620	1.00	41.29	X	C
ATOM	6807	OD1	ASN	76	81.399	35.956	8.592	1.00	41.29	X	O
ATOM	6808	ND2	ASN	76	83.181	34.812	7.839	1.00	41.29	X	N
ATOM	6809	C	ASN	76	82.684	32.285	11.286	1.00	54.49	X	C
ATOM	6810	O	ASN	76	81.523	32.278	11.706	1.00	54.49	X	O
ATOM	6811	N	THR	77	83.645	31.550	11.827	1.00	48.88	X	N
ATOM	6812	CA	THR	77	83.325	30.675	12.938	1.00	48.88	X	C
ATOM	6813	CB	THR	77	83.321	29.215	12.481	1.00	67.62	X	C
ATOM	6814	OG1	THR	77	82.318	29.048	11.469	1.00	67.62	X	O
ATOM	6815	CG2	THR	77	83.028	28.284	13.653	1.00	67.62	X	C
ATOM	6816	C	THR	77	84.245	30.817	14.132	1.00	48.88	X	C
ATOM	6817	O	THR	77	85.463	30.858	13.990	1.00	48.88	X	O
ATOM	6818	N	LEU	78	83.641	30.900	15.313	1.00	25.08	X	N
ATOM	6819	CA	LEU	78	84.387	31.014	16.562	1.00	25.08	X	C
ATOM	6820	CB	LEU	78	83.739	32.047	17.488	1.00	24.57	X	C
ATOM	6821	CG	LEU	78	84.362	32.022	18.881	1.00	24.57	X	C
ATOM	6822	CD1	LEU	78	85.757	32.625	18.789	1.00	24.57	X	C
ATOM	6823	CD2	LEU	78	83.507	32.770	19.868	1.00	24.57	X	C
ATOM	6824	C	LEU	78	84.370	29.653	17.250	1.00	25.08	X	C
ATOM	6825	O	LEU	78	83.312	29.041	17.389	1.00	25.08	X	O
ATOM	6826	N	TYR	79	85.530	29.179	17.687	1.00	41.94	X	N
ATOM	6827	CA	TYR	79	85.595	27.880	18.344	1.00	41.94	X	C
ATOM	6828	CB	TYR	79	86.608	26.963	17.657	1.00	47.62	X	C
ATOM	6829	CG	TYR	79	86.328	26.619	16.226	1.00	47.62	X	C
ATOM	6830	CD1	TYR	79	85.264	25.794	15.887	1.00	47.62	X	C
ATOM	6831	CE1	TYR	79	85.008	25.460	14.559	1.00	47.62	X	C
ATOM	6832	CD2	TYR	79	87.139	27.108	15.207	1.00	47.62	X	C
ATOM	6833	CE2	TYR	79	86.896	26.784	13.878	1.00	47.62	X	C
ATOM	6834	CZ	TYR	79	85.826	25.959	13.559	1.00	47.62	X	C
ATOM	6835	OH	TYR	79	85.564	25.640	12.245	1.00	47.62	X	O
ATOM	6836	C	TYR	79	86.043	27.991	19.779	1.00	41.94	X	C
ATOM	6837	O	TYR	79	86.890	28.824	20.100	1.00	41.94	X	O
ATOM	6838	N	LEU	80	85.470	27.160	20.642	1.00	19.15	X	N
ATOM	6839	CA	LEU	80	85.917	27.110	22.022	1.00	19.15	X	C
ATOM	6840	CB	LEU	80	84.809	27.382	23.047	1.00	21.08	X	C
ATOM	6841	CG	LEU	80	85.271	27.127	24.510	1.00	21.08	X	C
ATOM	6842	CD1	LEU	80	86.500	27.981	24.840	1.00	21.08	X	C
ATOM	6843	CD2	LEU	80	84.142	27.412	25.503	1.00	21.08	X	C
ATOM	6844	C	LEU	80	86.342	25.671	22.129	1.00	19.15	X	C
ATOM	6845	O	LEU	80	85.517	24.769	21.941	1.00	19.15	X	O
ATOM	6846	N	GLN	81	87.631	25.455	22.395	1.00	31.28	X	N
ATOM	6847	CA	GLN	81	88.193	24.111	22.530	1.00	31.28	X	C
ATOM	6848	CB	GLN	81	89.497	24.015	21.738	1.00	68.87	X	C
ATOM	6849	CG	GLN	81	90.141	22.647	21.783	1.00	68.87	X	C
ATOM	6850	CD	GLN	81	89.318	21.580	21.075	1.00	68.87	X	C
ATOM	6851	OE1	GLN	81	89.101	21.648	19.864	1.00	68.87	X	O
ATOM	6852	NE2	GLN	81	88.857	20.588	21.831	1.00	68.87	X	N
ATOM	6853	C	GLN	81	88.448	23.775	24.001	1.00	31.28	X	C
ATOM	6854	O	GLN	81	89.402	24.260	24.604	1.00	31.28	X	O
ATOM	6855	N	MET	82	87.589	22.935	24.569	1.00	32.50	X	N
ATOM	6856	CA	MET	82	87.701	22.541	25.975	1.00	32.50	X	C
ATOM	6857	CB	MET	82	86.297	22.429	26.589	1.00	41.50	X	C
ATOM	6858	CG	MET	82	85.537	23.752	26.653	1.00	41.50	X	C
ATOM	6859	SD	MET	82	83.790	23.594	27.062	1.00	41.50	X	S
ATOM	6860	CE	MET	82	83.088	23.391	25.452	1.00	41.50	X	C
ATOM	6861	C	MET	82	88.463	21.230	26.188	1.00	32.50	X	C
ATOM	6862	O	MET	82	88.239	20.250	25.487	1.00	32.50	X	O

Fig. 19: A-95

ATOM	6863	N	ASN	83	89.369	21.224	27.160	1.00	43.69	X	N
ATOM	6864	CA	ASN	83	90.155	20.032	27.459	1.00	43.69	X	C
ATOM	6865	CB	ASN	83	91.574	20.157	26.883	1.00	34.50	X	C
ATOM	6866	CG	ASN	83	91.574	20.391	25.383	1.00	34.50	X	C
ATOM	6867	OD1	ASN	83	90.920	19.670	24.636	1.00	34.50	X	O
ATOM	6868	ND2	ASN	83	92.313	21.401	24.937	1.00	34.50	X	N
ATOM	6869	C	ASN	83	90.225	19.855	28.967	1.00	43.69	X	C
ATOM	6870	O	ASN	83	90.054	20.822	29.705	1.00	43.69	X	O
ATOM	6871	N	SER	84	90.480	18.625	29.416	1.00	47.01	X	N
ATOM	6872	CA	SER	84	90.560	18.322	30.843	1.00	47.01	X	C
ATOM	6873	CB	SER	84	91.748	19.045	31.482	1.00	36.84	X	C
ATOM	6874	OG	SER	84	92.963	18.623	30.892	1.00	36.84	X	O
ATOM	6875	C	SER	84	89.270	18.757	31.516	1.00	47.01	X	C
ATOM	6876	O	SER	84	89.272	19.261	32.644	1.00	47.01	X	O
ATOM	6877	N	LEU	85	88.170	18.548	30.804	1.00	35.88	X	N
ATOM	6878	CA	LEU	85	86.842	18.920	31.273	1.00	35.88	X	C
ATOM	6879	CB	LEU	85	85.800	18.466	30.250	1.00	45.16	X	C
ATOM	6880	CG	LEU	85	85.854	19.211	28.921	1.00	45.16	X	C
ATOM	6881	CD1	LEU	85	84.875	18.608	27.936	1.00	45.16	X	C
ATOM	6882	CD2	LEU	85	85.536	20.672	29.178	1.00	45.16	X	C
ATOM	6883	C	LEU	85	86.450	18.396	32.652	1.00	35.88	X	C
ATOM	6884	O	LEU	85	86.175	17.208	32.818	1.00	35.88	X	O
ATOM	6885	N	ARG	86	86.415	19.290	33.636	1.00	55.90	X	N
ATOM	6886	CA	ARG	86	86.022	18.907	34.985	1.00	55.90	X	C
ATOM	6887	CB	ARG	86	86.606	19.864	36.023	1.00	50.18	X	C
ATOM	6888	CG	ARG	86	88.108	20.015	35.994	1.00	50.18	X	C
ATOM	6889	CD	ARG	86	88.620	20.357	37.385	1.00	50.18	X	C
ATOM	6890	NE	ARG	86	89.970	20.904	37.355	1.00	50.18	X	N
ATOM	6891	CZ	ARG	86	90.256	22.185	37.133	1.00	50.18	X	C
ATOM	6892	NH1	ARG	86	89.280	23.066	36.926	1.00	50.18	X	N
ATOM	6893	NH2	ARG	86	91.524	22.587	37.109	1.00	50.18	X	N
ATOM	6894	C	ARG	86	84.501	18.954	35.069	1.00	55.90	X	C
ATOM	6895	O	ARG	86	83.818	19.086	34.055	1.00	55.90	X	O
ATOM	6896	N	ALA	87	83.974	18.856	36.282	1.00	39.09	X	N
ATOM	6897	CA	ALA	87	82.533	18.893	36.485	1.00	39.09	X	C
ATOM	6898	CB	ALA	87	82.164	18.133	37.750	1.00	69.79	X	C
ATOM	6899	C	ALA	87	82.028	20.325	36.578	1.00	39.09	X	C
ATOM	6900	O	ALA	87	80.885	20.607	36.219	1.00	39.09	X	O
ATOM	6901	N	GLU	88	82.876	21.228	37.066	1.00	49.44	X	N
ATOM	6902	CA	GLU	88	82.492	22.628	37.197	1.00	49.44	X	C
ATOM	6903	CB	GLU	88	83.586	23.435	37.899	1.00	57.40	X	C
ATOM	6904	CG	GLU	88	84.189	22.765	39.107	1.00	57.40	X	C
ATOM	6905	CD	GLU	88	85.178	21.691	38.724	1.00	57.40	X	C
ATOM	6906	OE1	GLU	88	86.227	22.035	38.146	1.00	57.40	X	O
ATOM	6907	OE2	GLU	88	84.906	20.504	38.993	1.00	57.40	X	O
ATOM	6908	C	GLU	88	82.242	23.242	35.824	1.00	49.44	X	C
ATOM	6909	O	GLU	88	81.474	24.195	35.687	1.00	49.44	X	O
ATOM	6910	N	ASP	89	82.892	22.698	34.803	1.00	49.12	X	N
ATOM	6911	CA	ASP	89	82.720	23.229	33.464	1.00	49.12	X	C
ATOM	6912	CB	ASP	89	83.818	22.698	32.549	1.00	52.75	X	C
ATOM	6913	CG	ASP	89	85.194	22.903	33.124	1.00	52.75	X	C
ATOM	6914	OD1	ASP	89	85.430	23.960	33.752	1.00	52.75	X	O
ATOM	6915	OD2	ASP	89	86.043	22.011	32.936	1.00	52.75	X	O
ATOM	6916	C	ASP	89	81.348	22.914	32.871	1.00	49.12	X	C
ATOM	6917	O	ASP	89	80.981	23.459	31.834	1.00	49.12	X	O
ATOM	6918	N	THR	90	80.590	22.034	33.517	1.00	33.14	X	N
ATOM	6919	CA	THR	90	79.265	21.686	33.012	1.00	33.14	X	C
ATOM	6920	CB	THR	90	78.652	20.480	33.766	1.00	40.77	X	C
ATOM	6921	OG1	THR	90	78.585	20.770	35.162	1.00	40.77	X	O
ATOM	6922	CG2	THR	90	79.498	19.257	33.590	1.00	40.77	X	C
ATOM	6923	C	THR	90	78.361	22.899	33.174	1.00	33.14	X	C
ATOM	6924	O	THR	90	78.260	23.486	34.263	1.00	33.14	X	O
ATOM	6925	N	ALA	91	77.718	23.276	32.076	1.00	55.37	X	N
ATOM	6926	CA	ALA	91	76.832	24.428	32.058	1.00	55.37	X	C
ATOM	6927	CB	ALA	91	77.527	25.625	32.692	1.00	7.95	X	C
ATOM	6928	C	ALA	91	76.504	24.732	30.609	1.00	55.37	X	C
ATOM	6929	O	ALA	91	77.073	24.128	29.698	1.00	55.37	X	O
ATOM	6930	N	VAL	92	75.579	25.656	30.387	1.00	44.83	X	N
ATOM	6931	CA	VAL	92	75.243	26.017	29.021	1.00	44.83	X	C
ATOM	6932	CB	VAL	92	73.747	26.429	28.878	1.00	41.51	X	C
ATOM	6933	CG1	VAL	92	73.210	26.967	30.198	1.00	41.51	X	C
ATOM	6934	CG2	VAL	92	73.596	27.460	27.769	1.00	41.51	X	C
ATOM	6935	C	VAL	92	76.182	27.145	28.591	1.00	44.83	X	C

Fig. 19: A-96

ATOM	6936	O	VAL	92	76.446	28.085	29.354	1.00	44.83	X	O
ATOM	6937	N	TYR	93	76.701	27.019	27.371	1.00	51.76	X	N
ATOM	6938	CA	TYR	93	77.642	27.978	26.811	1.00	51.76	X	C
ATOM	6939	CB	TYR	93	78.838	27.241	26.227	1.00	15.58	X	C
ATOM	6940	CG	TYR	93	79.743	26.693	27.287	1.00	15.58	X	C
ATOM	6941	CD1	TYR	93	79.520	25.443	27.841	1.00	15.58	X	C
ATOM	6942	CE1	TYR	93	80.339	24.959	28.860	1.00	15.58	X	C
ATOM	6943	CD2	TYR	93	80.802	27.454	27.777	1.00	15.58	X	C
ATOM	6944	CE2	TYR	93	81.618	26.983	28.797	1.00	15.58	X	C
ATOM	6945	CZ	TYR	93	81.384	25.735	29.328	1.00	15.58	X	C
ATOM	6946	OH	TYR	93	82.223	25.253	30.297	1.00	15.58	X	O
ATOM	6947	C	TYR	93	77.091	28.908	25.757	1.00	51.76	X	C
ATOM	6948	O	TYR	93	76.223	28.534	24.972	1.00	51.76	X	O
ATOM	6949	N	TYR	94	77.633	30.121	25.729	1.00	29.82	X	N
ATOM	6950	CA	TYR	94	77.210	31.143	24.774	1.00	29.82	X	C
ATOM	6951	CB	TYR	94	76.448	32.267	25.489	1.00	45.66	X	C
ATOM	6952	CG	TYR	94	75.282	31.829	26.343	1.00	45.66	X	C
ATOM	6953	CD1	TYR	94	74.053	31.494	25.771	1.00	45.66	X	C
ATOM	6954	CE1	TYR	94	72.979	31.108	26.564	1.00	45.66	X	C
ATOM	6955	CD2	TYR	94	75.405	31.763	27.733	1.00	45.66	X	C
ATOM	6956	CE2	TYR	94	74.342	31.376	28.532	1.00	45.66	X	C
ATOM	6957	CZ	TYR	94	73.132	31.051	27.943	1.00	45.66	X	C
ATOM	6958	OH	TYR	94	72.082	30.665	28.743	1.00	45.66	X	O
ATOM	6959	C	TYR	94	78.389	31.799	24.074	1.00	29.82	X	C
ATOM	6960	O	TYR	94	79.360	32.174	24.727	1.00	29.82	X	O
ATOM	6961	N	CYS	95	78.332	31.923	22.752	1.00	22.64	X	N
ATOM	6962	CA	CYS	95	79.394	32.659	22.091	1.00	22.64	X	C
ATOM	6963	C	CYS	95	78.871	34.094	22.103	1.00	22.64	X	C
ATOM	6964	O	CYS	95	77.656	34.337	22.170	1.00	22.64	X	O
ATOM	6965	CB	CYS	95	79.660	32.185	20.660	1.00	55.79	X	C
ATOM	6966	SG	CYS	95	78.222	31.748	19.650	1.00	55.79	X	S
ATOM	6967	N	THR	96	79.778	35.057	22.067	1.00	43.77	X	N
ATOM	6968	CA	THR	96	79.337	36.435	22.107	1.00	43.77	X	C
ATOM	6969	CB	THR	96	79.387	36.985	23.556	1.00	38.47	X	C
ATOM	6970	OG1	THR	96	80.723	36.865	24.069	1.00	38.47	X	O
ATOM	6971	CG2	THR	96	78.421	36.220	24.453	1.00	38.47	X	C
ATOM	6972	C	THR	96	80.130	37.370	21.220	1.00	43.77	X	C
ATOM	6973	O	THR	96	81.328	37.174	20.987	1.00	43.77	X	O
ATOM	6974	N	ARG	97	79.432	38.379	20.709	1.00	52.60	X	N
ATOM	6975	CA	ARG	97	80.068	39.400	19.899	1.00	52.60	X	C
ATOM	6976	CB	ARG	97	79.237	39.799	18.689	1.00	26.06	X	C
ATOM	6977	CG	ARG	97	80.052	40.645	17.733	1.00	26.06	X	C
ATOM	6978	CD	ARG	97	79.235	41.249	16.624	1.00	26.06	X	C
ATOM	6979	NE	ARG	97	78.494	42.412	17.074	1.00	26.06	X	N
ATOM	6980	CZ	ARG	97	77.853	43.231	16.255	1.00	26.06	X	C
ATOM	6981	NH1	ARG	97	77.873	43.004	14.948	1.00	26.06	X	N
ATOM	6982	NH2	ARG	97	77.187	44.271	16.742	1.00	26.06	X	N
ATOM	6983	C	ARG	97	80.142	40.590	20.820	1.00	52.60	X	C
ATOM	6984	O	ARG	97	79.116	41.100	21.260	1.00	52.60	X	O
ATOM	6985	N	GLY	98	81.353	41.020	21.129	1.00	31.82	X	N
ATOM	6986	CA	GLY	98	81.505	42.162	22.004	1.00	31.82	X	C
ATOM	6987	C	GLY	98	81.635	43.450	21.225	1.00	31.82	X	C
ATOM	6988	O	GLY	98	81.903	43.452	20.020	1.00	31.82	X	O
ATOM	6989	N	PHE	99	81.416	44.558	21.913	1.00	20.36	X	N
ATOM	6990	CA	PHE	99	81.554	45.859	21.289	1.00	20.36	X	C
ATOM	6991	CB	PHE	99	80.358	46.753	21.621	1.00	37.93	X	C
ATOM	6992	CG	PHE	99	80.633	48.214	21.431	1.00	37.93	X	C
ATOM	6993	CD1	PHE	99	80.968	49.015	22.517	1.00	37.93	X	C
ATOM	6994	CD2	PHE	99	80.606	48.783	20.158	1.00	37.93	X	C
ATOM	6995	CE1	PHE	99	81.276	50.355	22.339	1.00	37.93	X	C
ATOM	6996	CE2	PHE	99	80.913	50.127	19.967	1.00	37.93	X	C
ATOM	6997	CZ	PHE	99	81.250	50.914	21.058	1.00	37.93	X	C
ATOM	6998	C	PHE	99	82.836	46.468	21.835	1.00	20.36	X	C
ATOM	6999	O	PHE	99	83.239	46.164	22.969	1.00	20.36	X	O
ATOM	7000	N	GLY	100	83.480	47.309	21.030	1.00	25.28	X	N
ATOM	7001	CA	GLY	100	84.704	47.954	21.469	1.00	25.28	X	C
ATOM	7002	C	GLY	100	85.850	46.983	21.672	1.00	25.28	X	C
ATOM	7003	O	GLY	100	86.390	46.466	20.700	1.00	25.28	X	O
ATOM	7004	N	ASP	101	86.231	46.744	22.926	1.00	27.39	X	N
ATOM	7005	CA	ASP	101	87.315	45.814	23.233	1.00	27.39	X	C
ATOM	7006	CB	ASP	101	88.175	46.338	24.396	1.00	32.17	X	C
ATOM	7007	CG	ASP	101	89.037	47.540	24.013	1.00	32.17	X	C
ATOM	7008	OD1	ASP	101	89.287	47.744	22.812	1.00	32.17	X	O

Fig. 19: A-97

ATOM	7009	OD2	ASP	101	89.483	48.274	24.920	1.00	32.17	X	O
ATOM	7010	C	ASP	101	86.773	44.418	23.596	1.00	27.39	X	C
ATOM	7011	O	ASP	101	87.549	43.518	23.929	1.00	27.39	X	O
ATOM	7012	N	GLY	102	85.449	44.250	23.538	1.00	18.22	X	N
ATOM	7013	CA	GLY	102	84.822	42.973	23.861	1.00	18.22	X	C
ATOM	7014	C	GLY	102	83.925	42.948	25.100	1.00	18.22	X	C
ATOM	7015	O	GLY	102	83.031	42.113	25.198	1.00	18.22	X	O
ATOM	7016	N	GLY	103	84.147	43.870	26.034	1.00	34.16	X	N
ATOM	7017	CA	GLY	103	83.370	43.915	27.268	1.00	34.16	X	C
ATOM	7018	C	GLY	103	81.850	43.964	27.216	1.00	34.16	X	C
ATOM	7019	O	GLY	103	81.182	43.416	28.087	1.00	34.16	X	O
ATOM	7020	N	TYR	104	81.290	44.649	26.230	1.00	25.31	X	N
ATOM	7021	CA	TYR	104	79.839	44.732	26.096	1.00	25.31	X	C
ATOM	7022	CB	TYR	104	79.433	46.131	25.639	1.00	26.21	X	C
ATOM	7023	CG	TYR	104	77.989	46.260	25.234	1.00	26.21	X	C
ATOM	7024	CD1	TYR	104	77.635	46.980	24.087	1.00	26.21	X	C
ATOM	7025	CE1	TYR	104	76.309	47.079	23.677	1.00	26.21	X	C
ATOM	7026	CD2	TYR	104	76.972	45.646	25.972	1.00	26.21	X	C
ATOM	7027	CE2	TYR	104	75.639	45.742	25.573	1.00	26.21	X	C
ATOM	7028	CZ	TYR	104	75.323	46.456	24.422	1.00	26.21	X	C
ATOM	7029	OH	TYR	104	74.025	46.523	23.995	1.00	26.21	X	O
ATOM	7030	C	TYR	104	79.484	43.700	25.037	1.00	25.31	X	C
ATOM	7031	O	TYR	104	79.905	43.810	23.886	1.00	25.31	X	O
ATOM	7032	N	PHE	105	78.728	42.686	25.432	1.00	17.54	X	N
ATOM	7033	CA	PHE	105	78.354	41.616	24.518	1.00	17.54	X	C
ATOM	7034	CB	PHE	105	78.088	40.337	25.309	1.00	20.12	X	C
ATOM	7035	CG	PHE	105	79.154	40.010	26.312	1.00	20.12	X	C
ATOM	7036	CD1	PHE	105	80.478	39.817	25.908	1.00	20.12	X	C
ATOM	7037	CD2	PHE	105	78.832	39.891	27.661	1.00	20.12	X	C
ATOM	7038	CE1	PHE	105	81.472	39.511	26.836	1.00	20.12	X	C
ATOM	7039	CE2	PHE	105	79.808	39.586	28.594	1.00	20.12	X	C
ATOM	7040	CZ	PHE	105	81.136	39.395	28.183	1.00	20.12	X	C
ATOM	7041	C	PHE	105	77.127	41.938	23.669	1.00	17.54	X	C
ATOM	7042	O	PHE	105	75.989	41.689	24.080	1.00	17.54	X	O
ATOM	7043	N	ASP	106	77.376	42.488	22.482	1.00	46.21	X	N
ATOM	7044	CA	ASP	106	76.327	42.840	21.532	1.00	46.21	X	C
ATOM	7045	CB	ASP	106	76.908	43.074	20.143	1.00	54.80	X	C
ATOM	7046	CG	ASP	106	77.456	44.442	19.976	1.00	54.80	X	C
ATOM	7047	OD1	ASP	106	76.774	45.384	20.429	1.00	54.80	X	O
ATOM	7048	OD2	ASP	106	78.552	44.576	19.387	1.00	54.80	X	O
ATOM	7049	C	ASP	106	75.355	41.705	21.399	1.00	46.21	X	C
ATOM	7050	O	ASP	106	74.281	41.707	21.974	1.00	46.21	X	O
ATOM	7051	N	VAL	107	75.769	40.732	20.603	1.00	33.04	X	N
ATOM	7052	CA	VAL	107	74.979	39.559	20.312	1.00	33.04	X	C
ATOM	7053	CB	VAL	107	75.180	39.152	18.858	1.00	31.62	X	C
ATOM	7054	CG1	VAL	107	74.156	38.100	18.457	1.00	31.62	X	C
ATOM	7055	CG2	VAL	107	75.092	40.388	17.980	1.00	31.62	X	C
ATOM	7056	C	VAL	107	75.322	38.379	21.197	1.00	33.04	X	C
ATOM	7057	O	VAL	107	76.413	38.296	21.763	1.00	33.04	X	O
ATOM	7058	N	TRP	108	74.359	37.474	21.306	1.00	37.95	X	N
ATOM	7059	CA	TRP	108	74.501	36.266	22.092	1.00	37.95	X	C
ATOM	7060	CB	TRP	108	73.674	36.351	23.372	1.00	32.89	X	C
ATOM	7061	CG	TRP	108	74.212	37.315	24.368	1.00	32.89	X	C
ATOM	7062	CD2	TRP	108	74.712	37.004	25.668	1.00	32.89	X	C
ATOM	7063	CE2	TRP	108	75.114	38.216	26.261	1.00	32.89	X	C
ATOM	7064	CE3	TRP	108	74.861	35.816	26.390	1.00	32.89	X	C
ATOM	7065	CD1	TRP	108	74.327	38.664	24.225	1.00	32.89	X	C
ATOM	7066	NE1	TRP	108	74.867	39.216	25.358	1.00	32.89	X	N
ATOM	7067	CZ2	TRP	108	75.655	38.278	27.543	1.00	32.89	X	C
ATOM	7068	CZ3	TRP	108	75.402	35.878	27.670	1.00	32.89	X	C
ATOM	7069	CH2	TRP	108	75.792	37.103	28.231	1.00	32.89	X	C
ATOM	7070	C	TRP	108	73.984	35.119	21.260	1.00	37.95	X	C
ATOM	7071	O	TRP	108	73.067	35.296	20.451	1.00	37.95	X	O
ATOM	7072	N	GLY	109	74.568	33.942	21.460	1.00	75.91	X	N
ATOM	7073	CA	GLY	109	74.124	32.770	20.732	1.00	75.91	X	C
ATOM	7074	C	GLY	109	72.791	32.307	21.288	1.00	75.91	X	C
ATOM	7075	O	GLY	109	71.997	33.114	21.780	1.00	75.91	X	O
ATOM	7076	N	GLN	110	72.537	31.007	21.207	1.00	35.37	X	N
ATOM	7077	CA	GLN	110	71.291	30.457	21.724	1.00	35.37	X	C
ATOM	7078	CB	GLN	110	70.652	29.498	20.714	1.00	98.79	X	C
ATOM	7079	CG	GLN	110	71.443	28.228	20.442	1.00	98.79	X	C
ATOM	7080	CD	GLN	110	72.597	28.441	19.485	1.00	98.79	X	C
ATOM	7081	OE1	GLN	110	73.318	27.502	19.152	1.00	98.79	X	O

Fig. 19: A-98

ATOM	7082	NE2	GLN	110	72.775	29.675	19.031	1.00	98.79	X	N
ATOM	7083	C	GLN	110	71.610	29.708	23.004	1.00	35.37	X	C
ATOM	7084	O	GLN	110	70.793	29.626	23.918	1.00	35.37	X	O
ATOM	7085	N	GLY	111	72.831	29.194	23.067	1.00	45.85	X	N
ATOM	7086	CA	GLY	111	73.257	28.430	24.219	1.00	45.85	X	C
ATOM	7087	C	GLY	111	73.349	26.981	23.781	1.00	45.85	X	C
ATOM	7088	O	GLY	111	72.596	26.540	22.913	1.00	45.85	X	O
ATOM	7089	N	THR	112	74.281	26.243	24.369	1.00	30.06	X	N
ATOM	7090	CA	THR	112	74.480	24.840	24.040	1.00	30.06	X	C
ATOM	7091	CB	THR	112	75.550	24.696	22.962	1.00	24.67	X	C
ATOM	7092	OG1	THR	112	75.636	23.327	22.562	1.00	24.67	X	O
ATOM	7093	CG2	THR	112	76.903	25.177	23.487	1.00	24.67	X	C
ATOM	7094	C	THR	112	74.944	24.184	25.328	1.00	30.06	X	C
ATOM	7095	O	THR	112	75.883	24.658	25.960	1.00	30.06	X	O
ATOM	7096	N	LEU	113	74.292	23.102	25.725	1.00	42.99	X	N
ATOM	7097	CA	LEU	113	74.646	22.449	26.981	1.00	42.99	X	C
ATOM	7098	CB	LEU	113	73.434	21.652	27.499	1.00	32.90	X	C
ATOM	7099	CG	LEU	113	73.366	21.006	28.896	1.00	32.90	X	C
ATOM	7100	CD1	LEU	113	73.914	19.580	28.860	1.00	32.90	X	C
ATOM	7101	CD2	LEU	113	74.109	21.884	29.889	1.00	32.90	X	C
ATOM	7102	C	LEU	113	75.890	21.560	26.932	1.00	42.99	X	C
ATOM	7103	O	LEU	113	76.190	20.899	25.929	1.00	42.99	X	O
ATOM	7104	N	VAL	114	76.621	21.561	28.037	1.00	35.21	X	N
ATOM	7105	CA	VAL	114	77.815	20.754	28.141	1.00	35.21	X	C
ATOM	7106	CB	VAL	114	79.070	21.592	27.837	1.00	43.74	X	C
ATOM	7107	CG1	VAL	114	80.324	20.909	28.384	1.00	43.74	X	C
ATOM	7108	CG2	VAL	114	79.189	21.774	26.331	1.00	43.74	X	C
ATOM	7109	C	VAL	114	77.906	20.141	29.529	1.00	35.21	X	C
ATOM	7110	O	VAL	114	78.064	20.845	30.529	1.00	35.21	X	O
ATOM	7111	N	THR	115	77.788	18.819	29.575	1.00	58.81	X	N
ATOM	7112	CA	THR	115	77.855	18.099	30.829	1.00	58.81	X	C
ATOM	7113	CB	THR	115	76.717	17.098	30.956	1.00	63.66	X	C
ATOM	7114	OG1	THR	115	75.549	17.620	30.311	1.00	63.66	X	O
ATOM	7115	CG2	THR	115	76.412	16.849	32.422	1.00	63.66	X	C
ATOM	7116	C	THR	115	79.161	17.337	30.903	1.00	58.81	X	C
ATOM	7117	O	THR	115	79.831	17.121	29.893	1.00	58.81	X	O
ATOM	7118	N	VAL	116	79.516	16.933	32.114	1.00	73.79	X	N
ATOM	7119	CA	VAL	116	80.741	16.191	32.352	1.00	73.79	X	C
ATOM	7120	CB	VAL	116	81.899	17.135	32.747	1.00	46.90	X	C
ATOM	7121	CG1	VAL	116	83.172	16.339	32.941	1.00	46.90	X	C
ATOM	7122	CG2	VAL	116	82.101	18.194	31.667	1.00	46.90	X	C
ATOM	7123	C	VAL	116	80.478	15.202	33.482	1.00	73.79	X	C
ATOM	7124	O	VAL	116	80.382	15.584	34.649	1.00	73.79	X	O
ATOM	7125	N	SER	117	80.349	13.931	33.114	1.00	65.98	X	N
ATOM	7126	CA	SER	117	80.088	12.858	34.066	1.00	65.98	X	C
ATOM	7127	CB	SER	117	78.608	12.861	34.458	1.00	62.16	X	C
ATOM	7128	OG	SER	117	77.776	12.825	33.308	1.00	62.16	X	O
ATOM	7129	C	SER	117	80.454	11.521	33.427	1.00	65.98	X	C
ATOM	7130	O	SER	117	81.498	11.396	32.789	1.00	65.98	X	O
ATOM	7131	N	SER	118	79.587	10.524	33.594	1.00	80.64	X	N
ATOM	7132	CA	SER	118	79.828	9.208	33.014	1.00	80.64	X	C
ATOM	7133	CB	SER	118	80.556	8.329	34.031	1.00	66.12	X	C
ATOM	7134	OG	SER	118	81.771	8.944	34.438	1.00	66.12	X	O
ATOM	7135	C	SER	118	78.524	8.543	32.563	1.00	80.64	X	C
ATOM	7136	O	SER	118	77.445	9.021	32.973	1.00	79.69	X	O
ATOM	7137	OXT	SER	118	78.594	7.553	31.804	1.00	65.17	X	O
ATOM	7138	CB	ILE	2	85.629	44.767	39.417	1.00	24.34	Y	C
ATOM	7139	CG2	ILE	2	84.329	45.456	39.830	1.00	24.34	Y	C
ATOM	7140	CG1	ILE	2	86.754	45.793	39.275	1.00	24.34	Y	C
ATOM	7141	CD1	ILE	2	86.473	46.861	38.237	1.00	24.34	Y	C
ATOM	7142	C	ILE	2	84.812	42.776	40.634	1.00	29.24	Y	C
ATOM	7143	O	ILE	2	84.508	41.962	39.756	1.00	29.24	Y	O
ATOM	7144	N	ILE	2	87.254	42.972	40.068	1.00	29.24	Y	N
ATOM	7145	CA	ILE	2	86.011	43.705	40.462	1.00	29.24	Y	C
ATOM	7146	N	GLN	3	84.122	42.926	41.761	1.00	42.94	Y	N
ATOM	7147	CA	GLN	3	82.960	42.107	42.070	1.00	42.94	Y	C
ATOM	7148	CB	GLN	3	83.156	41.435	43.434	1.00	85.86	Y	C
ATOM	7149	CG	GLN	3	82.045	40.492	43.850	1.00	85.86	Y	C
ATOM	7150	CD	GLN	3	82.371	39.747	45.131	1.00	85.86	Y	C
ATOM	7151	OE1	GLN	3	81.534	39.028	45.670	1.00	85.86	Y	O
ATOM	7152	NE2	GLN	3	83.597	39.911	45.621	1.00	85.86	Y	N
ATOM	7153	C	GLN	3	81.684	42.943	42.059	1.00	42.94	Y	C
ATOM	7154	O	GLN	3	81.626	44.026	42.645	1.00	42.94	Y	O

Fig. 19: A-99

ATOM	7155	N	LEU	4	80.666	42.426	41.380	1.00	33.35	Y	N
ATOM	7156	CA	LEU	4	79.378	43.098	41.269	1.00	33.35	Y	C
ATOM	7157	CB	LEU	4	78.954	43.160	39.800	1.00	47.12	Y	C
ATOM	7158	CG	LEU	4	79.344	44.389	38.979	1.00	47.12	Y	C
ATOM	7159	CD1	LEU	4	80.683	44.945	39.443	1.00	47.12	Y	C
ATOM	7160	CD2	LEU	4	79.370	44.008	37.512	1.00	47.12	Y	C
ATOM	7161	C	LEU	4	78.296	42.395	42.073	1.00	33.35	Y	C
ATOM	7162	O	LEU	4	78.012	41.215	41.852	1.00	33.35	Y	O
ATOM	7163	N	THR	5	77.691	43.129	43.001	1.00	42.53	Y	N
ATOM	7164	CA	THR	5	76.628	42.586	43.833	1.00	42.53	Y	C
ATOM	7165	CB	THR	5	77.100	42.482	45.315	1.00	37.95	Y	C
ATOM	7166	OG1	THR	5	75.992	42.697	46.196	1.00	37.95	Y	O
ATOM	7167	CG2	THR	5	78.209	43.479	45.604	1.00	37.95	Y	C
ATOM	7168	C	THR	5	75.348	43.426	43.699	1.00	42.53	Y	C
ATOM	7169	O	THR	5	75.306	44.593	44.089	1.00	42.53	Y	O
ATOM	7170	N	GLN	6	74.318	42.806	43.119	1.00	44.79	Y	N
ATOM	7171	CA	GLN	6	73.009	43.423	42.877	1.00	44.79	Y	C
ATOM	7172	CB	GLN	6	72.340	42.791	41.641	1.00	23.30	Y	C
ATOM	7173	CG	GLN	6	73.239	42.643	40.421	1.00	23.30	Y	C
ATOM	7174	CD	GLN	6	72.520	42.055	39.195	1.00	23.30	Y	C
ATOM	7175	OE1	GLN	6	73.163	41.628	38.231	1.00	23.30	Y	O
ATOM	7176	NE2	GLN	6	71.193	42.046	39.226	1.00	23.30	Y	N
ATOM	7177	C	GLN	6	72.050	43.274	44.061	1.00	44.79	Y	C
ATOM	7178	O	GLN	6	72.195	42.370	44.883	1.00	44.79	Y	O
ATOM	7179	N	SER	7	71.057	44.156	44.128	1.00	78.31	Y	N
ATOM	7180	CA	SER	7	70.069	44.113	45.201	1.00	78.31	Y	C
ATOM	7181	CB	SER	7	70.640	44.715	46.480	1.00	85.46	Y	C
ATOM	7182	OG	SER	7	71.028	46.058	46.262	1.00	85.46	Y	O
ATOM	7183	C	SER	7	68.797	44.855	44.824	1.00	78.31	Y	C
ATOM	7184	O	SER	7	68.847	45.923	44.220	1.00	78.31	Y	O
ATOM	7185	N	PRO	8	67.633	44.283	45.165	1.00	83.70	Y	N
ATOM	7186	CD	PRO	8	66.277	44.777	44.863	1.00	54.81	Y	C
ATOM	7187	CA	PRO	8	67.571	43.000	45.865	1.00	83.70	Y	C
ATOM	7188	CB	PRO	8	66.097	42.880	46.226	1.00	54.81	Y	C
ATOM	7189	CG	PRO	8	65.427	43.534	45.054	1.00	54.81	Y	C
ATOM	7190	C	PRO	8	68.015	41.895	44.925	1.00	83.70	Y	C
ATOM	7191	O	PRO	8	68.274	42.136	43.745	1.00	83.70	Y	O
ATOM	7192	N	SER	9	68.111	40.685	45.455	1.00	47.38	Y	N
ATOM	7193	CA	SER	9	68.504	39.541	44.651	1.00	47.38	Y	C
ATOM	7194	CB	SER	9	69.145	38.481	45.543	1.00	74.91	Y	C
ATOM	7195	OG	SER	9	70.214	39.045	46.283	1.00	74.91	Y	O
ATOM	7196	C	SER	9	67.232	39.002	44.025	1.00	47.38	Y	C
ATOM	7197	O	SER	9	67.237	38.434	42.936	1.00	47.38	Y	O
ATOM	7198	N	SER	10	66.134	39.214	44.736	1.00	60.45	Y	N
ATOM	7199	CA	SER	10	64.819	38.770	44.305	1.00	60.45	Y	C
ATOM	7200	CB	SER	10	64.476	37.449	44.991	1.00	51.82	Y	C
ATOM	7201	OG	SER	10	63.252	36.935	44.504	1.00	51.82	Y	O
ATOM	7202	C	SER	10	63.797	39.840	44.691	1.00	60.45	Y	C
ATOM	7203	O	SER	10	63.976	40.552	45.683	1.00	60.45	Y	O
ATOM	7204	N	LEU	11	62.730	39.964	43.910	1.00	65.48	Y	N
ATOM	7205	CA	LEU	11	61.710	40.964	44.206	1.00	65.48	Y	C
ATOM	7206	CB	LEU	11	62.206	42.366	43.830	1.00	51.28	Y	C
ATOM	7207	CG	LEU	11	62.310	42.727	42.342	1.00	51.28	Y	C
ATOM	7208	CD1	LEU	11	60.949	43.139	41.803	1.00	51.28	Y	C
ATOM	7209	CD2	LEU	11	63.294	43.877	42.168	1.00	51.28	Y	C
ATOM	7210	C	LEU	11	60.413	40.680	43.473	1.00	65.48	Y	C
ATOM	7211	O	LEU	11	60.412	40.363	42.282	1.00	65.48	Y	O
ATOM	7212	N	SER	12	59.305	40.803	44.189	1.00	84.56	Y	N
ATOM	7213	CA	SER	12	58.004	40.567	43.595	1.00	84.56	Y	C
ATOM	7214	CB	SER	12	57.209	39.578	44.445	1.00	71.89	Y	C
ATOM	7215	OG	SER	12	56.137	39.026	43.705	1.00	71.89	Y	O
ATOM	7216	C	SER	12	57.273	41.902	43.507	1.00	84.56	Y	C
ATOM	7217	O	SER	12	57.232	42.666	44.471	1.00	84.56	Y	O
ATOM	7218	N	ALA	13	56.713	42.192	42.341	1.00	109.71	Y	N
ATOM	7219	CA	ALA	13	55.997	43.442	42.152	1.00	109.71	Y	C
ATOM	7220	CB	ALA	13	56.947	44.509	41.632	1.00	88.46	Y	C
ATOM	7221	C	ALA	13	54.838	43.244	41.186	1.00	109.71	Y	C
ATOM	7222	O	ALA	13	54.869	42.347	40.341	1.00	109.71	Y	O
ATOM	7223	N	SER	14	53.816	44.084	41.315	1.00	66.55	Y	N
ATOM	7224	CA	SER	14	52.632	44.000	40.461	1.00	66.55	Y	C
ATOM	7225	CB	SER	14	51.370	44.265	41.290	1.00	62.23	Y	C
ATOM	7226	OG	SER	14	51.506	45.449	42.059	1.00	62.23	Y	O
ATOM	7227	C	SER	14	52.699	44.984	39.299	1.00	66.55	Y	C

Fig. 19: A-100

ATOM	7228	O	SER	14	53.362	46.015	39.394	1.00	66.55	Y	O
ATOM	7229	N	VAL	15	52.018	44.660	38.202	1.00	56.27	Y	N
ATOM	7230	CA	VAL	15	52.017	45.540	37.037	1.00	56.27	Y	C
ATOM	7231	CB	VAL	15	50.922	45.156	36.016	1.00	42.35	Y	C
ATOM	7232	CG1	VAL	15	51.449	44.089	35.066	1.00	42.35	Y	C
ATOM	7233	CG2	VAL	15	49.679	44.644	36.750	1.00	42.35	Y	C
ATOM	7234	C	VAL	15	51.773	46.964	37.492	1.00	56.27	Y	C
ATOM	7235	O	VAL	15	50.948	47.208	38.369	1.00	56.27	Y	O
ATOM	7236	N	GLY	16	52.509	47.903	36.911	1.00	54.44	Y	N
ATOM	7237	CA	GLY	16	52.343	49.296	37.280	1.00	54.44	Y	C
ATOM	7238	C	GLY	16	53.284	49.795	38.359	1.00	54.44	Y	C
ATOM	7239	O	GLY	16	53.419	51.000	38.542	1.00	54.44	Y	O
ATOM	7240	N	ASP	17	53.931	48.885	39.082	1.00	75.77	Y	N
ATOM	7241	CA	ASP	17	54.863	49.283	40.134	1.00	75.77	Y	C
ATOM	7242	CB	ASP	17	55.212	48.091	41.034	1.00	114.73	Y	C
ATOM	7243	CG	ASP	17	54.035	47.608	41.849	1.00	114.73	Y	C
ATOM	7244	OD1	ASP	17	54.208	46.639	42.623	1.00	114.73	Y	O
ATOM	7245	OD2	ASP	17	52.942	48.198	41.716	1.00	114.73	Y	O
ATOM	7246	C	ASP	17	56.149	49.824	39.525	1.00	75.77	Y	C
ATOM	7247	O	ASP	17	56.476	49.533	38.373	1.00	75.77	Y	O
ATOM	7248	N	ARG	18	56.873	50.616	40.304	1.00	69.15	Y	N
ATOM	7249	CA	ARG	18	58.139	51.161	39.844	1.00	69.15	Y	C
ATOM	7250	CB	ARG	18	58.263	52.634	40.225	1.00	52.23	Y	C
ATOM	7251	CG	ARG	18	59.557	53.291	39.779	1.00	52.23	Y	C
ATOM	7252	CD	ARG	18	59.365	54.788	39.625	1.00	52.23	Y	C
ATOM	7253	NE	ARG	18	60.622	55.478	39.370	1.00	52.23	Y	N
ATOM	7254	CZ	ARG	18	61.621	55.550	40.246	1.00	52.23	Y	C
ATOM	7255	NH1	ARG	18	61.506	54.968	41.436	1.00	52.23	Y	N
ATOM	7256	NH2	ARG	18	62.733	56.209	39.933	1.00	52.23	Y	N
ATOM	7257	C	ARG	18	59.232	50.346	40.514	1.00	69.15	Y	C
ATOM	7258	O	ARG	18	59.318	50.293	41.744	1.00	69.15	Y	O
ATOM	7259	N	VAL	19	60.064	49.706	39.701	1.00	58.62	Y	N
ATOM	7260	CA	VAL	19	61.132	48.871	40.221	1.00	58.62	Y	C
ATOM	7261	CB	VAL	19	61.068	47.477	39.567	1.00	74.00	Y	C
ATOM	7262	CG1	VAL	19	62.050	46.531	40.235	1.00	74.00	Y	C
ATOM	7263	CG2	VAL	19	59.651	46.938	39.664	1.00	74.00	Y	C
ATOM	7264	C	VAL	19	62.518	49.477	40.003	1.00	58.62	Y	C
ATOM	7265	O	VAL	19	62.782	50.096	38.975	1.00	58.62	Y	O
ATOM	7266	N	THR	20	63.399	49.297	40.978	1.00	54.75	Y	N
ATOM	7267	CA	THR	20	64.753	49.815	40.878	1.00	54.75	Y	C
ATOM	7268	CB	THR	20	64.883	51.148	41.639	1.00	56.43	Y	C
ATOM	7269	OG1	THR	20	64.132	52.154	40.955	1.00	56.43	Y	O
ATOM	7270	CG2	THR	20	66.337	51.586	41.726	1.00	56.43	Y	C
ATOM	7271	C	THR	20	65.806	48.834	41.401	1.00	54.75	Y	C
ATOM	7272	O	THR	20	65.963	48.663	42.611	1.00	54.75	Y	O
ATOM	7273	N	ILE	21	66.526	48.194	40.484	1.00	38.23	Y	N
ATOM	7274	CA	ILE	21	67.572	47.250	40.855	1.00	38.23	Y	C
ATOM	7275	CB	ILE	21	67.775	46.182	39.765	1.00	34.57	Y	C
ATOM	7276	CG2	ILE	21	68.753	45.112	40.252	1.00	34.57	Y	C
ATOM	7277	CG1	ILE	21	66.427	45.547	39.426	1.00	34.57	Y	C
ATOM	7278	CD1	ILE	21	66.496	44.426	38.415	1.00	34.57	Y	C
ATOM	7279	C	ILE	21	68.877	48.006	41.047	1.00	38.23	Y	C
ATOM	7280	O	ILE	21	69.215	48.885	40.256	1.00	38.23	Y	O
ATOM	7281	N	THR	22	69.610	47.660	42.100	1.00	41.70	Y	N
ATOM	7282	CA	THR	22	70.880	48.312	42.396	1.00	41.70	Y	C
ATOM	7283	CB	THR	22	70.919	48.826	43.856	1.00	62.77	Y	C
ATOM	7284	OG1	THR	22	69.986	49.903	44.017	1.00	62.77	Y	O
ATOM	7285	CG2	THR	22	72.322	49.303	44.222	1.00	62.77	Y	C
ATOM	7286	C	THR	22	72.052	47.370	42.199	1.00	41.70	Y	C
ATOM	7287	O	THR	22	72.028	46.237	42.674	1.00	41.70	Y	O
ATOM	7288	N	CYS	23	73.077	47.852	41.500	1.00	52.46	Y	N
ATOM	7289	CA	CYS	23	74.289	47.076	41.247	1.00	52.46	Y	C
ATOM	7290	C	CYS	23	75.446	47.833	41.875	1.00	52.46	Y	C
ATOM	7291	O	CYS	23	75.749	48.957	41.476	1.00	52.46	Y	O
ATOM	7292	CB	CYS	23	74.522	46.938	39.744	1.00	61.15	Y	C
ATOM	7293	SG	CYS	23	75.983	45.982	39.184	1.00	61.15	Y	S
ATOM	7294	N	SER	24	76.079	47.219	42.866	1.00	43.95	Y	N
ATOM	7295	CA	SER	24	77.200	47.837	43.556	1.00	43.95	Y	C
ATOM	7296	CB	SER	24	76.992	47.751	45.072	1.00	58.07	Y	C
ATOM	7297	OG	SER	24	75.782	48.379	45.462	1.00	58.07	Y	O
ATOM	7298	C	SER	24	78.495	47.138	43.177	1.00	43.95	Y	C
ATOM	7299	O	SER	24	78.582	45.912	43.222	1.00	43.95	Y	O
ATOM	7300	N	ALA	25	79.503	47.924	42.814	1.00	35.63	Y	N

Fig. 19: A-101

ATOM	7301	CA	ALA	25	80.796	47.373	42.427	1.00	35.63	Y	C
ATOM	7302	CB	ALA	25	81.214	47.920	41.068	1.00	50.18	Y	C
ATOM	7303	C	ALA	25	81.894	47.635	43.454	1.00	35.63	Y	C
ATOM	7304	O	ALA	25	82.050	48.754	43.959	1.00	35.63	Y	O
ATOM	7305	N	SER	26	82.650	46.579	43.742	1.00	37.44	Y	N
ATOM	7306	CA	SER	26	83.746	46.616	44.697	1.00	37.44	Y	C
ATOM	7307	CB	SER	26	84.492	45.280	44.672	1.00	31.41	Y	C
ATOM	7308	OG	SER	26	85.018	45.005	43.381	1.00	31.41	Y	O
ATOM	7309	C	SER	26	84.718	47.745	44.393	1.00	37.44	Y	C
ATOM	7310	O	SER	26	85.358	48.286	45.297	1.00	37.44	Y	O
ATOM	7311	N	SER	27	84.835	48.088	43.116	1.00	70.39	Y	N
ATOM	7312	CA	SER	27	85.726	49.157	42.687	1.00	70.39	Y	C
ATOM	7313	CB	SER	27	86.941	48.581	41.954	1.00	53.81	Y	C
ATOM	7314	OG	SER	27	87.574	47.567	42.716	1.00	53.81	Y	O
ATOM	7315	C	SER	27	84.922	50.023	41.736	1.00	70.39	Y	C
ATOM	7316	O	SER	27	83.960	49.545	41.139	1.00	70.39	Y	O
ATOM	7317	N	SER	28	85.306	51.290	41.595	1.00	30.73	Y	N
ATOM	7318	CA	SER	28	84.598	52.194	40.695	1.00	30.73	Y	C
ATOM	7319	CB	SER	28	85.060	53.628	40.920	1.00	55.81	Y	C
ATOM	7320	OG	SER	28	86.448	53.723	40.688	1.00	55.81	Y	O
ATOM	7321	C	SER	28	84.824	51.813	39.230	1.00	30.73	Y	C
ATOM	7322	O	SER	28	85.873	51.287	38.863	1.00	30.73	Y	O
ATOM	7323	N	VAL	29	83.832	52.092	38.398	1.00	34.83	Y	N
ATOM	7324	CA	VAL	29	83.909	51.780	36.983	1.00	34.83	Y	C
ATOM	7325	CB	VAL	29	83.173	50.443	36.682	1.00	24.96	Y	C
ATOM	7326	CG1	VAL	29	83.891	49.286	37.382	1.00	24.96	Y	C
ATOM	7327	CG2	VAL	29	81.717	50.518	37.153	1.00	24.96	Y	C
ATOM	7328	C	VAL	29	83.267	52.929	36.208	1.00	34.83	Y	C
ATOM	7329	O	VAL	29	82.397	53.621	36.738	1.00	34.83	Y	O
ATOM	7330	N	ASN	30	83.689	53.134	34.963	1.00	19.83	Y	N
ATOM	7331	CA	ASN	30	83.152	54.225	34.145	1.00	19.83	Y	C
ATOM	7332	CB	ASN	30	84.086	54.517	32.963	1.00	44.92	Y	C
ATOM	7333	CG	ASN	30	84.524	53.261	32.254	1.00	44.92	Y	C
ATOM	7334	OD1	ASN	30	85.235	52.431	32.832	1.00	44.92	Y	O
ATOM	7335	ND2	ASN	30	84.097	53.099	31.001	1.00	44.92	Y	N
ATOM	7336	C	ASN	30	81.740	53.976	33.634	1.00	19.83	Y	C
ATOM	7337	O	ASN	30	80.998	54.926	33.381	1.00	19.83	Y	O
ATOM	7338	N	HIS	31	81.367	52.708	33.475	1.00	24.55	Y	N
ATOM	7339	CA	HIS	31	80.031	52.373	32.991	1.00	24.55	Y	C
ATOM	7340	CB	HIS	31	80.003	52.259	31.459	1.00	41.70	Y	C
ATOM	7341	CG	HIS	31	80.061	53.572	30.737	1.00	41.70	Y	C
ATOM	7342	CD2	HIS	31	79.124	54.233	30.016	1.00	41.70	Y	C
ATOM	7343	ND1	HIS	31	81.196	54.351	30.692	1.00	41.70	Y	N
ATOM	7344	CE1	HIS	31	80.958	55.435	29.973	1.00	41.70	Y	C
ATOM	7345	NE2	HIS	31	79.708	55.387	29.551	1.00	41.70	Y	N
ATOM	7346	C	HIS	31	79.548	51.058	33.567	1.00	24.55	Y	C
ATOM	7347	O	HIS	31	80.274	50.392	34.305	1.00	24.55	Y	O
ATOM	7348	N	MET	32	78.312	50.698	33.227	1.00	16.59	Y	N
ATOM	7349	CA	MET	32	77.719	49.440	33.664	1.00	16.59	Y	C
ATOM	7350	CB	MET	32	76.944	49.624	34.971	1.00	29.77	Y	C
ATOM	7351	CG	MET	32	76.606	48.310	35.684	1.00	29.77	Y	C
ATOM	7352	SD	MET	32	78.097	47.369	36.143	1.00	29.77	Y	S
ATOM	7353	CE	MET	32	78.855	48.463	37.337	1.00	29.77	Y	C
ATOM	7354	C	MET	32	76.779	48.941	32.563	1.00	16.59	Y	C
ATOM	7355	O	MET	32	76.138	49.734	31.871	1.00	16.59	Y	O
ATOM	7356	N	PHE	33	76.706	47.629	32.383	1.00	41.04	Y	N
ATOM	7357	CA	PHE	33	75.830	47.089	31.358	1.00	41.04	Y	C
ATOM	7358	CB	PHE	33	76.639	46.329	30.315	1.00	16.08	Y	C
ATOM	7359	CG	PHE	33	77.695	47.161	29.657	1.00	16.08	Y	C
ATOM	7360	CD1	PHE	33	78.846	47.528	30.354	1.00	16.08	Y	C
ATOM	7361	CD2	PHE	33	77.524	47.609	28.350	1.00	16.08	Y	C
ATOM	7362	CE1	PHE	33	79.810	48.328	29.763	1.00	16.08	Y	C
ATOM	7363	CE2	PHE	33	78.484	48.414	27.745	1.00	16.08	Y	C
ATOM	7364	CZ	PHE	33	79.634	48.776	28.456	1.00	16.08	Y	C
ATOM	7365	C	PHE	33	74.803	46.175	31.985	1.00	41.04	Y	C
ATOM	7366	O	PHE	33	75.036	45.622	33.057	1.00	41.04	Y	O
ATOM	7367	N	TRP	34	73.664	46.020	31.322	1.00	26.10	Y	N
ATOM	7368	CA	TRP	34	72.604	45.168	31.843	1.00	26.10	Y	C
ATOM	7369	CB	TRP	34	71.438	46.009	32.364	1.00	47.27	Y	C
ATOM	7370	CG	TRP	34	71.807	46.935	33.466	1.00	47.27	Y	C
ATOM	7371	CD2	TRP	34	71.660	46.692	34.868	1.00	47.27	Y	C
ATOM	7372	CE2	TRP	34	72.145	47.836	35.542	1.00	47.27	Y	C
ATOM	7373	CE3	TRP	34	71.167	45.621	35.622	1.00	47.27	Y	C

Fig. 19: A-102

ATOM	7374	CD1	TRP	34	72.360	48.175	33.346	1.00	47.27	Y	C
ATOM	7375	NE1	TRP	34	72.567	48.725	34.589	1.00	47.27	Y	N
ATOM	7376	CZ2	TRP	34	72.150	47.939	36.940	1.00	47.27	Y	C
ATOM	7377	CZ3	TRP	34	71.172	45.725	37.013	1.00	47.27	Y	C
ATOM	7378	CH2	TRP	34	71.661	46.879	37.655	1.00	47.27	Y	C
ATOM	7379	C	TRP	34	72.067	44.187	30.812	1.00	26.10	Y	C
ATOM	7380	O	TRP	34	71.904	44.513	29.630	1.00	26.10	Y	O
ATOM	7381	N	TYR	35	71.793	42.972	31.267	1.00	43.42	Y	N
ATOM	7382	CA	TYR	35	71.248	41.964	30.381	1.00	43.42	Y	C
ATOM	7383	CB	TYR	35	72.230	40.808	30.189	1.00	22.29	Y	C
ATOM	7384	CG	TYR	35	73.549	41.240	29.596	1.00	22.29	Y	C
ATOM	7385	CD1	TYR	35	74.645	41.535	30.417	1.00	22.29	Y	C
ATOM	7386	CE1	TYR	35	75.841	41.962	29.881	1.00	22.29	Y	C
ATOM	7387	CD2	TYR	35	73.697	41.385	28.216	1.00	22.29	Y	C
ATOM	7388	CE2	TYR	35	74.898	41.808	27.670	1.00	22.29	Y	C
ATOM	7389	CZ	TYR	35	75.960	42.094	28.510	1.00	22.29	Y	C
ATOM	7390	OH	TYR	35	77.148	42.516	27.972	1.00	22.29	Y	O
ATOM	7391	C	TYR	35	69.966	41.449	30.991	1.00	43.42	Y	C
ATOM	7392	O	TYR	35	69.826	41.393	32.214	1.00	43.42	Y	O
ATOM	7393	N	GLN	36	69.015	41.107	30.136	1.00	45.64	Y	N
ATOM	7394	CA	GLN	36	67.760	40.567	30.607	1.00	45.64	Y	C
ATOM	7395	CB	GLN	36	66.574	41.346	30.054	1.00	37.71	Y	C
ATOM	7396	CG	GLN	36	65.259	40.610	30.277	1.00	37.71	Y	C
ATOM	7397	CD	GLN	36	64.189	41.002	29.287	1.00	37.71	Y	C
ATOM	7398	OE1	GLN	36	63.601	42.072	29.391	1.00	37.71	Y	O
ATOM	7399	NE2	GLN	36	63.936	40.137	28.314	1.00	37.71	Y	N
ATOM	7400	C	GLN	36	67.664	39.138	30.118	1.00	45.64	Y	C
ATOM	7401	O	GLN	36	67.725	38.881	28.910	1.00	45.64	Y	O
ATOM	7402	N	GLN	37	67.522	38.205	31.050	1.00	50.28	Y	N
ATOM	7403	CA	GLN	37	67.390	36.809	30.670	1.00	50.28	Y	C
ATOM	7404	CB	GLN	37	68.522	35.961	31.265	1.00	34.85	Y	C
ATOM	7405	CG	GLN	37	68.392	34.487	30.904	1.00	34.85	Y	C
ATOM	7406	CD	GLN	37	69.543	33.645	31.388	1.00	34.85	Y	C
ATOM	7407	OE1	GLN	37	69.925	33.699	32.565	1.00	34.85	Y	O
ATOM	7408	NE2	GLN	37	70.098	32.842	30.484	1.00	34.85	Y	N
ATOM	7409	C	GLN	37	66.042	36.248	31.108	1.00	50.28	Y	C
ATOM	7410	O	GLN	37	65.690	36.272	32.293	1.00	50.28	Y	O
ATOM	7411	N	LYS	38	65.284	35.763	30.133	1.00	68.24	Y	N
ATOM	7412	CA	LYS	38	63.983	35.175	30.403	1.00	68.24	Y	C
ATOM	7413	CB	LYS	38	62.991	35.530	29.291	1.00	55.54	Y	C
ATOM	7414	CG	LYS	38	62.893	37.031	29.023	1.00	55.54	Y	C
ATOM	7415	CD	LYS	38	61.764	37.382	28.056	1.00	55.54	Y	C
ATOM	7416	CE	LYS	38	60.394	37.298	28.726	1.00	55.54	Y	C
ATOM	7417	NZ	LYS	38	60.290	38.166	29.943	1.00	55.54	Y	N
ATOM	7418	C	LYS	38	64.198	33.667	30.473	1.00	68.24	Y	C
ATOM	7419	O	LYS	38	64.971	33.104	29.696	1.00	68.24	Y	O
ATOM	7420	N	PRO	39	63.520	32.994	31.412	1.00	67.87	Y	N
ATOM	7421	CD	PRO	39	62.478	33.563	32.282	1.00	58.47	Y	C
ATOM	7422	CA	PRO	39	63.621	31.546	31.614	1.00	67.87	Y	C
ATOM	7423	CB	PRO	39	62.368	31.234	32.417	1.00	58.47	Y	C
ATOM	7424	CG	PRO	39	62.247	32.446	33.271	1.00	58.47	Y	C
ATOM	7425	C	PRO	39	63.717	30.714	30.338	1.00	67.87	Y	C
ATOM	7426	O	PRO	39	62.898	30.859	29.425	1.00	67.87	Y	O
ATOM	7427	N	GLY	40	64.730	29.847	30.288	1.00	54.98	Y	N
ATOM	7428	CA	GLY	40	64.925	28.977	29.137	1.00	54.98	Y	C
ATOM	7429	C	GLY	40	65.488	29.625	27.882	1.00	54.98	Y	C
ATOM	7430	O	GLY	40	65.625	28.957	26.855	1.00	54.98	Y	O
ATOM	7431	N	LYS	41	65.801	30.918	27.955	1.00	83.28	Y	N
ATOM	7432	CA	LYS	41	66.364	31.641	26.816	1.00	83.28	Y	C
ATOM	7433	CB	LYS	41	65.414	32.754	26.354	1.00	72.06	Y	C
ATOM	7434	CG	LYS	41	64.045	32.271	25.882	1.00	72.06	Y	C
ATOM	7435	CD	LYS	41	63.316	33.311	25.008	1.00	72.06	Y	C
ATOM	7436	CE	LYS	41	63.035	34.642	25.726	1.00	72.06	Y	C
ATOM	7437	NZ	LYS	41	64.229	35.536	25.855	1.00	72.06	Y	N
ATOM	7438	C	LYS	41	67.727	32.245	27.160	1.00	83.28	Y	C
ATOM	7439	O	LYS	41	68.110	32.327	28.331	1.00	83.28	Y	O
ATOM	7440	N	ALA	42	68.458	32.666	26.133	1.00	55.60	Y	N
ATOM	7441	CA	ALA	42	69.776	33.261	26.326	1.00	55.60	Y	C
ATOM	7442	CB	ALA	42	70.561	33.194	25.041	1.00	1.87	Y	C
ATOM	7443	C	ALA	42	69.623	34.707	26.754	1.00	55.60	Y	C
ATOM	7444	O	ALA	42	68.607	35.337	26.462	1.00	55.60	Y	O
ATOM	7445	N	PRO	43	70.628	35.259	27.455	1.00	54.21	Y	N
ATOM	7446	CD	PRO	43	71.849	34.627	27.983	1.00	18.24	Y	C

Fig. 19: A-103

ATOM	7447	CA	PRO	43	70.537	36.656	27.889	1.00	54.21	Y	C
ATOM	7448	CB	PRO	43	71.875	36.890	28.594	1.00	18.24	Y	C
ATOM	7449	CG	PRO	43	72.202	35.544	29.149	1.00	18.24	Y	C
ATOM	7450	C	PRO	43	70.349	37.584	26.689	1.00	54.21	Y	C
ATOM	7451	O	PRO	43	70.660	37.219	25.555	1.00	54.21	Y	O
ATOM	7452	N	LYS	44	69.837	38.782	26.946	1.00	55.44	Y	N
ATOM	7453	CA	LYS	44	69.618	39.764	25.892	1.00	55.44	Y	C
ATOM	7454	CB	LYS	44	68.120	39.894	25.601	1.00	46.11	Y	C
ATOM	7455	CG	LYS	44	67.705	39.473	24.199	1.00	46.11	Y	C
ATOM	7456	CD	LYS	44	66.189	39.520	24.018	1.00	46.11	Y	C
ATOM	7457	CE	LYS	44	65.457	38.464	24.865	1.00	46.11	Y	C
ATOM	7458	NZ	LYS	44	65.564	38.665	26.354	1.00	46.11	Y	N
ATOM	7459	C	LYS	44	70.172	41.117	26.328	1.00	55.44	Y	C
ATOM	7460	O	LYS	44	69.930	41.554	27.454	1.00	55.44	Y	O
ATOM	7461	N	PRO	45	70.946	41.785	25.451	1.00	21.39	Y	N
ATOM	7462	CD	PRO	45	71.303	41.365	24.085	1.00	11.37	Y	C
ATOM	7463	CA	PRO	45	71.523	43.103	25.772	1.00	21.39	Y	C
ATOM	7464	CB	PRO	45	72.159	43.539	24.457	1.00	11.37	Y	C
ATOM	7465	CG	PRO	45	72.485	42.234	23.795	1.00	11.37	Y	C
ATOM	7466	C	PRO	45	70.361	44.010	26.138	1.00	21.39	Y	C
ATOM	7467	O	PRO	45	69.407	44.103	25.383	1.00	21.39	Y	O
ATOM	7468	N	TRP	46	70.434	44.676	27.281	1.00	48.64	Y	N
ATOM	7469	CA	TRP	46	69.333	45.532	27.704	1.00	48.64	Y	C
ATOM	7470	CB	TRP	46	68.783	45.038	29.043	1.00	23.18	Y	C
ATOM	7471	CG	TRP	46	67.316	45.220	29.143	1.00	23.18	Y	C
ATOM	7472	CD2	TRP	46	66.330	44.620	28.299	1.00	23.18	Y	C
ATOM	7473	CE2	TRP	46	65.070	45.075	28.739	1.00	23.18	Y	C
ATOM	7474	CE3	TRP	46	66.391	43.736	27.206	1.00	23.18	Y	C
ATOM	7475	CD1	TRP	46	66.637	45.997	30.038	1.00	23.18	Y	C
ATOM	7476	NE1	TRP	46	65.282	45.914	29.803	1.00	23.18	Y	N
ATOM	7477	CZ2	TRP	46	63.881	44.679	28.126	1.00	23.18	Y	C
ATOM	7478	CZ3	TRP	46	65.212	43.342	26.599	1.00	23.18	Y	C
ATOM	7479	CH2	TRP	46	63.973	43.814	27.059	1.00	23.18	Y	C
ATOM	7480	C	TRP	46	69.694	47.007	27.826	1.00	48.64	Y	C
ATOM	7481	O	TRP	46	68.986	47.877	27.324	1.00	48.64	Y	O
ATOM	7482	N	ILE	47	70.785	47.283	28.523	1.00	42.06	Y	N
ATOM	7483	CA	ILE	47	71.238	48.644	28.717	1.00	42.06	Y	C
ATOM	7484	CB	ILE	47	70.801	49.172	30.099	1.00	37.03	Y	C
ATOM	7485	CG2	ILE	47	71.345	50.580	30.325	1.00	37.03	Y	C
ATOM	7486	CG1	ILE	47	69.275	49.168	30.198	1.00	37.03	Y	C
ATOM	7487	CD1	ILE	47	68.749	49.670	31.538	1.00	37.03	Y	C
ATOM	7488	C	ILE	47	72.758	48.641	28.638	1.00	42.06	Y	C
ATOM	7489	O	ILE	47	73.417	47.951	29.414	1.00	42.06	Y	O
ATOM	7490	N	TYR	48	73.310	49.387	27.684	1.00	17.47	Y	N
ATOM	7491	CA	TYR	48	74.753	49.467	27.532	1.00	17.47	Y	C
ATOM	7492	CB	TYR	48	75.189	49.145	26.106	1.00	20.64	Y	C
ATOM	7493	CG	TYR	48	74.613	50.048	25.046	1.00	20.64	Y	C
ATOM	7494	CD1	TYR	48	73.267	49.988	24.710	1.00	20.64	Y	C
ATOM	7495	CE1	TYR	48	72.743	50.792	23.704	1.00	20.64	Y	C
ATOM	7496	CD2	TYR	48	75.425	50.940	24.353	1.00	20.64	Y	C
ATOM	7497	CE2	TYR	48	74.916	51.750	23.347	1.00	20.64	Y	C
ATOM	7498	CZ	TYR	48	73.573	51.671	23.028	1.00	20.64	Y	C
ATOM	7499	OH	TYR	48	73.051	52.476	22.045	1.00	20.64	Y	O
ATOM	7500	C	TYR	48	75.193	50.861	27.892	1.00	17.47	Y	C
ATOM	7501	O	TYR	48	74.365	51.754	28.021	1.00	17.47	Y	O
ATOM	7502	N	LEU	49	76.497	51.044	28.054	1.00	31.07	Y	N
ATOM	7503	CA	LEU	49	77.042	52.337	28.429	1.00	31.07	Y	C
ATOM	7504	CB	LEU	49	77.200	53.247	27.205	1.00	20.44	Y	C
ATOM	7505	CG	LEU	49	78.368	53.044	26.236	1.00	20.44	Y	C
ATOM	7506	CD1	LEU	49	79.662	52.870	27.019	1.00	20.44	Y	C
ATOM	7507	CD2	LEU	49	78.121	51.836	25.385	1.00	20.44	Y	C
ATOM	7508	C	LEU	49	76.173	53.037	29.475	1.00	31.07	Y	C
ATOM	7509	O	LEU	49	75.769	54.178	29.293	1.00	31.07	Y	O
ATOM	7510	N	THR	50	75.861	52.329	30.555	1.00	28.24	Y	N
ATOM	7511	CA	THR	50	75.083	52.870	31.670	1.00	28.24	Y	C
ATOM	7512	CB	THR	50	75.754	54.128	32.230	1.00	41.62	Y	C
ATOM	7513	OG1	THR	50	77.134	53.847	32.495	1.00	41.62	Y	O
ATOM	7514	CG2	THR	50	75.066	54.568	33.522	1.00	41.62	Y	C
ATOM	7515	C	THR	50	73.605	53.187	31.485	1.00	28.24	Y	C
ATOM	7516	O	THR	50	72.761	52.603	32.158	1.00	28.24	Y	O
ATOM	7517	N	SER	51	73.283	54.114	30.595	1.00	28.33	Y	N
ATOM	7518	CA	SER	51	71.889	54.496	30.402	1.00	28.33	Y	C
ATOM	7519	CB	SER	51	71.729	55.981	30.714	1.00	81.44	Y	C

Fig. 19: A-104

ATOM	7520	OG	SER	51	72.714	56.738	30.034	1.00	81.44	Y	O
ATOM	7521	C	SER	51	71.312	54.190	29.019	1.00	28.33	Y	C
ATOM	7522	O	SER	51	70.092	54.174	28.831	1.00	28.33	Y	O
ATOM	7523	N	ASN	52	72.184	53.941	28.053	1.00	27.44	Y	N
ATOM	7524	CA	ASN	52	71.736	53.648	26.704	1.00	27.44	Y	C
ATOM	7525	CB	ASN	52	72.942	53.523	25.779	1.00	42.81	Y	C
ATOM	7526	CG	ASN	52	73.623	54.849	25.546	1.00	42.81	Y	C
ATOM	7527	OD1	ASN	52	73.059	55.733	24.907	1.00	42.81	Y	O
ATOM	7528	ND2	ASN	52	74.829	55.006	26.076	1.00	42.81	Y	N
ATOM	7529	C	ASN	52	70.896	52.390	26.623	1.00	27.44	Y	C
ATOM	7530	O	ASN	52	71.336	51.320	27.027	1.00	27.44	Y	O
ATOM	7531	N	LEU	53	69.682	52.519	26.100	1.00	46.42	Y	N
ATOM	7532	CA	LEU	53	68.805	51.367	25.954	1.00	46.42	Y	C
ATOM	7533	CB	LEU	53	67.349	51.803	25.887	1.00	19.90	Y	C
ATOM	7534	CG	LEU	53	66.763	52.595	27.051	1.00	19.90	Y	C
ATOM	7535	CD1	LEU	53	65.255	52.685	26.846	1.00	19.90	Y	C
ATOM	7536	CD2	LEU	53	67.071	51.918	28.382	1.00	19.90	Y	C
ATOM	7537	C	LEU	53	69.136	50.610	24.676	1.00	46.42	Y	C
ATOM	7538	O	LEU	53	69.414	51.220	23.644	1.00	46.42	Y	O
ATOM	7539	N	ALA	54	69.101	49.281	24.744	1.00	35.05	Y	N
ATOM	7540	CA	ALA	54	69.378	48.447	23.583	1.00	35.05	Y	C
ATOM	7541	CB	ALA	54	69.220	46.994	23.930	1.00	27.54	Y	C
ATOM	7542	C	ALA	54	68.373	48.829	22.530	1.00	35.05	Y	C
ATOM	7543	O	ALA	54	67.680	49.834	22.666	1.00	35.05	Y	O
ATOM	7544	N	SER	55	68.259	48.026	21.486	1.00	47.40	Y	N
ATOM	7545	CA	SER	55	67.319	48.376	20.443	1.00	47.40	Y	C
ATOM	7546	CB	SER	55	67.689	47.681	19.140	1.00	36.06	Y	C
ATOM	7547	OG	SER	55	67.083	48.359	18.051	1.00	36.06	Y	O
ATOM	7548	C	SER	55	65.866	48.073	20.801	1.00	47.40	Y	C
ATOM	7549	O	SER	55	64.993	48.921	20.631	1.00	47.40	Y	O
ATOM	7550	N	GLY	56	65.599	46.878	21.312	1.00	54.09	Y	N
ATOM	7551	CA	GLY	56	64.225	46.531	21.647	1.00	54.09	Y	C
ATOM	7552	C	GLY	56	63.650	47.071	22.948	1.00	54.09	Y	C
ATOM	7553	O	GLY	56	62.457	47.370	23.025	1.00	54.09	Y	O
ATOM	7554	N	VAL	57	64.497	47.197	23.965	1.00	63.10	Y	N
ATOM	7555	CA	VAL	57	64.082	47.667	25.282	1.00	63.10	Y	C
ATOM	7556	CB	VAL	57	65.311	48.113	26.120	1.00	46.15	Y	C
ATOM	7557	CG1	VAL	57	64.923	48.248	27.588	1.00	46.15	Y	C
ATOM	7558	CG2	VAL	57	66.446	47.118	25.961	1.00	46.15	Y	C
ATOM	7559	C	VAL	57	63.071	48.817	25.251	1.00	63.10	Y	C
ATOM	7560	O	VAL	57	63.363	49.898	24.747	1.00	63.10	Y	O
ATOM	7561	N	PRO	58	61.862	48.594	25.791	1.00	51.01	Y	N
ATOM	7562	CD	PRO	58	61.362	47.365	26.426	1.00	31.12	Y	C
ATOM	7563	CA	PRO	58	60.834	49.639	25.815	1.00	51.01	Y	C
ATOM	7564	CB	PRO	58	59.634	48.929	26.433	1.00	31.12	Y	C
ATOM	7565	CG	PRO	58	60.258	47.899	27.300	1.00	31.12	Y	C
ATOM	7566	C	PRO	58	61.305	50.829	26.643	1.00	51.01	Y	C
ATOM	7567	O	PRO	58	61.992	50.660	27.653	1.00	51.01	Y	O
ATOM	7568	N	SER	59	60.918	52.027	26.216	1.00	33.61	Y	N
ATOM	7569	CA	SER	59	61.330	53.267	26.874	1.00	33.61	Y	C
ATOM	7570	CB	SER	59	60.780	54.482	26.113	1.00	61.12	Y	C
ATOM	7571	OG	SER	59	59.368	54.481	26.096	1.00	61.12	Y	O
ATOM	7572	C	SER	59	61.023	53.411	28.359	1.00	33.61	Y	C
ATOM	7573	O	SER	59	61.495	54.353	28.990	1.00	33.61	Y	O
ATOM	7574	N	ARG	60	60.244	52.500	28.928	1.00	39.70	Y	N
ATOM	7575	CA	ARG	60	59.963	52.599	30.359	1.00	39.70	Y	C
ATOM	7576	CB	ARG	60	58.764	51.731	30.751	1.00	42.51	Y	C
ATOM	7577	CG	ARG	60	58.846	50.293	30.287	1.00	42.51	Y	C
ATOM	7578	CD	ARG	60	57.798	49.425	30.971	1.00	42.51	Y	C
ATOM	7579	NE	ARG	60	57.683	48.120	30.333	1.00	42.51	Y	N
ATOM	7580	CZ	ARG	60	57.277	47.939	29.079	1.00	42.51	Y	C
ATOM	7581	NH1	ARG	60	56.943	48.979	28.324	1.00	42.51	Y	N
ATOM	7582	NH2	ARG	60	57.210	46.718	28.569	1.00	42.51	Y	N
ATOM	7583	C	ARG	60	61.202	52.180	31.158	1.00	39.70	Y	C
ATOM	7584	O	ARG	60	61.311	52.451	32.357	1.00	39.70	Y	O
ATOM	7585	N	PHE	61	62.136	51.522	30.480	1.00	40.60	Y	N
ATOM	7586	CA	PHE	61	63.372	51.086	31.109	1.00	40.60	Y	C
ATOM	7587	CB	PHE	61	63.965	49.886	30.370	1.00	38.42	Y	C
ATOM	7588	CG	PHE	61	63.416	48.563	30.811	1.00	38.42	Y	C
ATOM	7589	CD1	PHE	61	62.493	47.881	30.028	1.00	38.42	Y	C
ATOM	7590	CD2	PHE	61	63.830	47.997	32.010	1.00	38.42	Y	C
ATOM	7591	CE1	PHE	61	61.990	46.652	30.434	1.00	38.42	Y	C
ATOM	7592	CE2	PHE	61	63.332	46.770	32.423	1.00	38.42	Y	C

Fig. 19: A-105

ATOM	7593	CZ	PHE	61	62.410	46.096	31.634	1.00	38.42	Y	C
ATOM	7594	C	PHE	61	64.399	52.209	31.097	1.00	40.60	Y	C
ATOM	7595	O	PHE	61	64.470	52.989	30.144	1.00	40.60	Y	O
ATOM	7596	N	SER	62	65.202	52.284	32.152	1.00	26.58	Y	N
ATOM	7597	CA	SER	62	66.238	53.306	32.247	1.00	26.58	Y	C
ATOM	7598	CB	SER	62	65.658	54.604	32.802	1.00	47.08	Y	C
ATOM	7599	OG	SER	62	65.071	54.395	34.076	1.00	47.08	Y	O
ATOM	7600	C	SER	62	67.376	52.828	33.145	1.00	26.58	Y	C
ATOM	7601	O	SER	62	67.160	52.123	34.125	1.00	26.58	Y	O
ATOM	7602	N	GLY	63	68.595	53.208	32.797	1.00	30.78	Y	N
ATOM	7603	CA	GLY	63	69.738	52.810	33.591	1.00	30.78	Y	C
ATOM	7604	C	GLY	63	70.426	54.067	34.056	1.00	30.78	Y	C
ATOM	7605	O	GLY	63	70.266	55.122	33.442	1.00	30.78	Y	O
ATOM	7606	N	SER	64	71.195	53.964	35.130	1.00	54.48	Y	N
ATOM	7607	CA	SER	64	71.884	55.130	35.652	1.00	54.48	Y	C
ATOM	7608	CB	SER	64	70.869	56.075	36.290	1.00	25.06	Y	C
ATOM	7609	OG	SER	64	71.519	57.204	36.839	1.00	25.06	Y	O
ATOM	7610	C	SER	64	72.947	54.763	36.675	1.00	54.48	Y	C
ATOM	7611	O	SER	64	73.000	53.632	37.154	1.00	54.48	Y	O
ATOM	7612	N	GLY	65	73.793	55.732	37.007	1.00	43.76	Y	N
ATOM	7613	CA	GLY	65	74.836	55.494	37.984	1.00	43.76	Y	C
ATOM	7614	C	GLY	65	76.218	56.023	37.637	1.00	43.76	Y	C
ATOM	7615	O	GLY	65	76.431	56.698	36.622	1.00	43.76	Y	O
ATOM	7616	N	SER	66	77.167	55.703	38.508	1.00	27.01	Y	N
ATOM	7617	CA	SER	66	78.546	56.110	38.339	1.00	27.01	Y	C
ATOM	7618	CB	SER	66	78.641	57.635	38.286	1.00	58.01	Y	C
ATOM	7619	OG	SER	66	77.927	58.229	39.355	1.00	58.01	Y	O
ATOM	7620	C	SER	66	79.367	55.563	39.498	1.00	27.01	Y	C
ATOM	7621	O	SER	66	78.817	55.039	40.464	1.00	27.01	Y	O
ATOM	7622	N	GLY	67	80.685	55.668	39.385	1.00	73.15	Y	N
ATOM	7623	CA	GLY	67	81.555	55.179	40.436	1.00	73.15	Y	C
ATOM	7624	C	GLY	67	81.312	53.733	40.822	1.00	73.15	Y	C
ATOM	7625	O	GLY	67	81.609	52.814	40.056	1.00	73.15	Y	O
ATOM	7626	N	THR	68	80.758	53.530	42.011	1.00	44.05	Y	N
ATOM	7627	CA	THR	68	80.506	52.186	42.506	1.00	44.05	Y	C
ATOM	7628	CB	THR	68	81.118	52.003	43.894	1.00	42.61	Y	C
ATOM	7629	OG1	THR	68	80.524	52.945	44.793	1.00	42.61	Y	O
ATOM	7630	CG2	THR	68	82.627	52.225	43.845	1.00	42.61	Y	C
ATOM	7631	C	THR	68	79.042	51.786	42.592	1.00	44.05	Y	C
ATOM	7632	O	THR	68	78.743	50.632	42.879	1.00	44.05	Y	O
ATOM	7633	N	ASP	69	78.128	52.720	42.352	1.00	35.15	Y	N
ATOM	7634	CA	ASP	69	76.708	52.392	42.424	1.00	35.15	Y	C
ATOM	7635	CB	ASP	69	76.066	53.103	43.617	1.00	108.02	Y	C
ATOM	7636	CG	ASP	69	76.592	52.591	44.946	1.00	108.02	Y	C
ATOM	7637	OD1	ASP	69	76.357	51.406	45.268	1.00	108.02	Y	O
ATOM	7638	OD2	ASP	69	77.249	53.370	45.667	1.00	108.02	Y	O
ATOM	7639	C	ASP	69	75.942	52.705	41.139	1.00	35.15	Y	C
ATOM	7640	O	ASP	69	75.884	53.850	40.693	1.00	35.15	Y	O
ATOM	7641	N	TYR	70	75.359	51.664	40.551	1.00	27.55	Y	N
ATOM	7642	CA	TYR	70	74.599	51.787	39.317	1.00	27.55	Y	C
ATOM	7643	CB	TYR	70	75.315	51.016	38.191	1.00	25.09	Y	C
ATOM	7644	CG	TYR	70	76.543	51.737	37.662	1.00	25.09	Y	C
ATOM	7645	CD1	TYR	70	76.447	52.637	36.596	1.00	25.09	Y	C
ATOM	7646	CE1	TYR	70	77.562	53.365	36.158	1.00	25.09	Y	C
ATOM	7647	CD2	TYR	70	77.787	51.577	38.275	1.00	25.09	Y	C
ATOM	7648	CE2	TYR	70	78.906	52.299	37.848	1.00	25.09	Y	C
ATOM	7649	CZ	TYR	70	78.785	53.194	36.790	1.00	25.09	Y	C
ATOM	7650	OH	TYR	70	79.873	53.933	36.382	1.00	25.09	Y	O
ATOM	7651	C	TYR	70	73.184	51.267	39.523	1.00	27.55	Y	C
ATOM	7652	O	TYR	70	72.920	50.545	40.488	1.00	27.55	Y	O
ATOM	7653	N	THR	71	72.270	51.635	38.627	1.00	38.36	Y	N
ATOM	7654	CA	THR	71	70.893	51.184	38.767	1.00	38.36	Y	C
ATOM	7655	CB	THR	71	70.074	52.152	39.657	1.00	44.65	Y	C
ATOM	7656	OG1	THR	71	69.921	53.403	38.978	1.00	44.65	Y	O
ATOM	7657	CG2	THR	71	70.770	52.394	40.989	1.00	44.65	Y	C
ATOM	7658	C	THR	71	70.099	50.991	37.473	1.00	38.36	Y	C
ATOM	7659	O	THR	71	70.281	51.707	36.485	1.00	38.36	Y	O
ATOM	7660	N	LEU	72	69.216	50.001	37.499	1.00	32.67	Y	N
ATOM	7661	CA	LEU	72	68.324	49.718	36.385	1.00	32.67	Y	C
ATOM	7662	CB	LEU	72	68.392	48.238	35.985	1.00	53.11	Y	C
ATOM	7663	CG	LEU	72	67.283	47.694	35.073	1.00	53.11	Y	C
ATOM	7664	CD1	LEU	72	66.871	48.731	34.059	1.00	53.11	Y	C
ATOM	7665	CD2	LEU	72	67.769	46.444	34.372	1.00	53.11	Y	C

Fig. 19: A-106

ATOM	7666	C	LEU	72	66.958	50.056	36.972	1.00	32.67	Y	C
ATOM	7667	O	LEU	72	66.688	49.738	38.129	1.00	32.67	Y	O
ATOM	7668	N	THR	73	66.106	50.715	36.195	1.00	42.60	Y	N
ATOM	7669	CA	THR	73	64.795	51.100	36.700	1.00	42.60	Y	C
ATOM	7670	CB	THR	73	64.780	52.597	37.094	1.00	57.15	Y	C
ATOM	7671	OG1	THR	73	66.018	52.943	37.730	1.00	57.15	Y	O
ATOM	7672	CG2	THR	73	63.639	52.879	38.058	1.00	57.15	Y	C
ATOM	7673	C	THR	73	63.665	50.854	35.708	1.00	42.60	Y	C
ATOM	7674	O	THR	73	63.791	51.132	34.516	1.00	42.60	Y	O
ATOM	7675	N	ILE	74	62.564	50.316	36.212	1.00	51.99	Y	N
ATOM	7676	CA	ILE	74	61.396	50.068	35.386	1.00	51.99	Y	C
ATOM	7677	CB	ILE	74	60.934	48.597	35.455	1.00	52.44	Y	C
ATOM	7678	CG2	ILE	74	60.081	48.271	34.231	1.00	52.44	Y	C
ATOM	7679	CG1	ILE	74	62.138	47.656	35.471	1.00	52.44	Y	C
ATOM	7680	CD1	ILE	74	61.757	46.182	35.513	1.00	52.44	Y	C
ATOM	7681	C	ILE	74	60.314	50.963	35.988	1.00	51.99	Y	C
ATOM	7682	O	ILE	74	59.739	50.639	37.030	1.00	51.99	Y	O
ATOM	7683	N	SER	75	60.058	52.094	35.335	1.00	41.67	Y	N
ATOM	7684	CA	SER	75	59.069	53.066	35.801	1.00	41.67	Y	C
ATOM	7685	CB	SER	75	59.090	54.291	34.889	1.00	51.63	Y	C
ATOM	7686	OG	SER	75	58.934	53.909	33.535	1.00	51.63	Y	O
ATOM	7687	C	SER	75	57.644	52.524	35.901	1.00	41.67	Y	C
ATOM	7688	O	SER	75	56.885	52.924	36.777	1.00	41.67	Y	O
ATOM	7689	N	SER	76	57.280	51.627	34.993	1.00	62.86	Y	N
ATOM	7690	CA	SER	76	55.950	51.032	34.996	1.00	62.86	Y	C
ATOM	7691	CB	SER	76	55.045	51.724	33.980	1.00	71.45	Y	C
ATOM	7692	OG	SER	76	53.779	51.086	33.932	1.00	71.45	Y	O
ATOM	7693	C	SER	76	56.056	49.558	34.649	1.00	62.86	Y	C
ATOM	7694	O	SER	76	55.970	49.176	33.480	1.00	62.86	Y	O
ATOM	7695	N	LEU	77	56.237	48.734	35.675	1.00	53.25	Y	N
ATOM	7696	CA	LEU	77	56.380	47.298	35.490	1.00	53.25	Y	C
ATOM	7697	CB	LEU	77	56.342	46.596	36.841	1.00	41.03	Y	C
ATOM	7698	CG	LEU	77	57.317	45.433	37.008	1.00	41.03	Y	C
ATOM	7699	CD1	LEU	77	56.911	44.632	38.239	1.00	41.03	Y	C
ATOM	7700	CD2	LEU	77	57.310	44.548	35.766	1.00	41.03	Y	C
ATOM	7701	C	LEU	77	55.303	46.703	34.590	1.00	53.25	Y	C
ATOM	7702	O	LEU	77	54.114	46.944	34.787	1.00	53.25	Y	O
ATOM	7703	N	GLN	78	55.723	45.921	33.602	1.00	82.27	Y	N
ATOM	7704	CA	GLN	78	54.781	45.285	32.691	1.00	82.27	Y	C
ATOM	7705	CB	GLN	78	55.094	45.667	31.243	1.00	41.92	Y	C
ATOM	7706	CG	GLN	78	54.907	47.148	30.956	1.00	41.92	Y	C
ATOM	7707	CD	GLN	78	53.508	47.627	31.288	1.00	41.92	Y	C
ATOM	7708	OE1	GLN	78	52.520	47.033	30.852	1.00	41.92	Y	O
ATOM	7709	NE2	GLN	78	53.416	48.711	32.056	1.00	41.92	Y	N
ATOM	7710	C	GLN	78	54.830	43.774	32.852	1.00	82.27	Y	C
ATOM	7711	O	GLN	78	55.851	43.213	33.244	1.00	82.27	Y	O
ATOM	7712	N	PRO	79	53.718	43.093	32.549	1.00	81.12	Y	N
ATOM	7713	CD	PRO	79	52.505	43.636	31.915	1.00	80.96	Y	C
ATOM	7714	CA	PRO	79	53.632	41.636	32.660	1.00	81.12	Y	C
ATOM	7715	CB	PRO	79	52.198	41.351	32.225	1.00	80.96	Y	C
ATOM	7716	CG	PRO	79	51.949	42.426	31.213	1.00	80.96	Y	C
ATOM	7717	C	PRO	79	54.663	40.914	31.792	1.00	81.12	Y	C
ATOM	7718	O	PRO	79	54.865	39.708	31.914	1.00	81.12	Y	O
ATOM	7719	N	GLU	80	55.316	41.670	30.921	1.00	44.20	Y	N
ATOM	7720	CA	GLU	80	56.316	41.120	30.021	1.00	44.20	Y	C
ATOM	7721	CB	GLU	80	56.117	41.729	28.636	1.00	102.65	Y	C
ATOM	7722	CG	GLU	80	55.853	43.217	28.678	1.00	102.65	Y	C
ATOM	7723	CD	GLU	80	55.814	43.833	27.301	1.00	102.65	Y	C
ATOM	7724	OE1	GLU	80	56.717	43.528	26.494	1.00	102.65	Y	O
ATOM	7725	OE2	GLU	80	54.891	44.629	27.026	1.00	102.65	Y	O
ATOM	7726	C	GLU	80	57.742	41.368	30.520	1.00	44.20	Y	C
ATOM	7727	O	GLU	80	58.672	40.652	30.145	1.00	44.20	Y	O
ATOM	7728	N	ASP	81	57.902	42.380	31.371	1.00	52.34	Y	N
ATOM	7729	CA	ASP	81	59.206	42.733	31.931	1.00	52.34	Y	C
ATOM	7730	CB	ASP	81	59.167	44.111	32.593	1.00	55.47	Y	C
ATOM	7731	CG	ASP	81	58.700	45.195	31.663	1.00	55.47	Y	C
ATOM	7732	OD1	ASP	81	58.950	45.085	30.446	1.00	55.47	Y	O
ATOM	7733	OD2	ASP	81	58.099	46.171	32.156	1.00	55.47	Y	O
ATOM	7734	C	ASP	81	59.641	41.740	32.991	1.00	52.34	Y	C
ATOM	7735	O	ASP	81	60.649	41.946	33.673	1.00	52.34	Y	O
ATOM	7736	N	PHE	82	58.884	40.664	33.138	1.00	63.15	Y	N
ATOM	7737	CA	PHE	82	59.207	39.685	34.158	1.00	63.15	Y	C
ATOM	7738	CB	PHE	82	57.917	39.041	34.647	1.00	168.46	Y	C

Fig. 19: A-107

ATOM	7739	CG	PHE	82	57.024	40.004	35.381	1.00	168.46	Y	C
ATOM	7740	CD1	PHE	82	57.371	40.454	36.650	1.00	168.46	Y	C
ATOM	7741	CD2	PHE	82	55.866	40.498	34.791	1.00	168.46	Y	C
ATOM	7742	CE1	PHE	82	56.579	41.384	37.321	1.00	168.46	Y	C
ATOM	7743	CE2	PHE	82	55.067	41.430	35.458	1.00	168.46	Y	C
ATOM	7744	CZ	PHE	82	55.425	41.872	36.724	1.00	168.46	Y	C
ATOM	7745	C	PHE	82	60.238	38.657	33.742	1.00	63.15	Y	C
ATOM	7746	O	PHE	82	59.960	37.733	32.979	1.00	63.15	Y	O
ATOM	7747	N	ALA	83	61.447	38.867	34.256	1.00	34.42	Y	N
ATOM	7748	CA	ALA	83	62.601	38.015	34.000	1.00	34.42	Y	C
ATOM	7749	CB	ALA	83	63.138	38.260	32.595	1.00	53.93	Y	C
ATOM	7750	C	ALA	83	63.669	38.353	35.036	1.00	34.42	Y	C
ATOM	7751	O	ALA	83	63.389	39.033	36.025	1.00	34.42	Y	O
ATOM	7752	N	THR	84	64.890	37.877	34.821	1.00	50.51	Y	N
ATOM	7753	CA	THR	84	65.968	38.161	35.758	1.00	50.51	Y	C
ATOM	7754	CB	THR	84	66.566	36.849	36.323	1.00	63.35	Y	C
ATOM	7755	OG1	THR	84	67.888	37.096	36.819	1.00	63.35	Y	O
ATOM	7756	CG2	THR	84	66.584	35.766	35.260	1.00	63.35	Y	C
ATOM	7757	C	THR	84	67.028	39.021	35.065	1.00	50.51	Y	C
ATOM	7758	O	THR	84	67.474	38.708	33.959	1.00	50.51	Y	O
ATOM	7759	N	TYR	85	67.401	40.119	35.723	1.00	40.66	Y	N
ATOM	7760	CA	TYR	85	68.364	41.076	35.187	1.00	40.66	Y	C
ATOM	7761	CB	TYR	85	67.819	42.503	35.330	1.00	42.00	Y	C
ATOM	7762	CG	TYR	85	66.476	42.693	34.668	1.00	42.00	Y	C
ATOM	7763	CD1	TYR	85	65.330	42.084	35.185	1.00	42.00	Y	C
ATOM	7764	CE1	TYR	85	64.110	42.163	34.521	1.00	42.00	Y	C
ATOM	7765	CD2	TYR	85	66.363	43.401	33.472	1.00	42.00	Y	C
ATOM	7766	CE2	TYR	85	65.148	43.486	32.800	1.00	42.00	Y	C
ATOM	7767	CZ	TYR	85	64.028	42.860	33.327	1.00	42.00	Y	C
ATOM	7768	OH	TYR	85	62.841	42.889	32.633	1.00	42.00	Y	O
ATOM	7769	C	TYR	85	69.746	41.012	35.816	1.00	40.66	Y	C
ATOM	7770	O	TYR	85	69.891	40.982	37.042	1.00	40.66	Y	O
ATOM	7771	N	TYR	86	70.756	41.016	34.949	1.00	43.34	Y	N
ATOM	7772	CA	TYR	86	72.159	40.970	35.349	1.00	43.34	Y	C
ATOM	7773	CB	TYR	86	72.890	39.833	34.633	1.00	34.52	Y	C
ATOM	7774	CG	TYR	86	72.406	38.441	34.941	1.00	34.52	Y	C
ATOM	7775	CD1	TYR	86	72.902	37.731	36.040	1.00	34.52	Y	C
ATOM	7776	CE1	TYR	86	72.472	36.433	36.303	1.00	34.52	Y	C
ATOM	7777	CD2	TYR	86	71.466	37.820	34.118	1.00	34.52	Y	C
ATOM	7778	CE2	TYR	86	71.031	36.530	34.375	1.00	34.52	Y	C
ATOM	7779	CZ	TYR	86	71.538	35.841	35.462	1.00	34.52	Y	C
ATOM	7780	OH	TYR	86	71.124	34.549	35.683	1.00	34.52	Y	O
ATOM	7781	C	TYR	86	72.873	42.259	34.957	1.00	43.34	Y	C
ATOM	7782	O	TYR	86	72.662	42.780	33.851	1.00	43.34	Y	O
ATOM	7783	N	CYS	87	73.706	42.773	35.862	1.00	31.05	Y	N
ATOM	7784	CA	CYS	87	74.499	43.945	35.548	1.00	31.05	Y	C
ATOM	7785	C	CYS	87	75.857	43.346	35.237	1.00	31.05	Y	C
ATOM	7786	O	CYS	87	76.171	42.248	35.707	1.00	31.05	Y	O
ATOM	7787	CB	CYS	87	74.587	44.922	36.721	1.00	63.19	Y	C
ATOM	7788	SG	CYS	87	75.151	44.318	38.354	1.00	63.19	Y	S
ATOM	7789	N	GLN	88	76.653	44.040	34.431	1.00	35.54	Y	N
ATOM	7790	CA	GLN	88	77.964	43.536	34.058	1.00	35.54	Y	C
ATOM	7791	CB	GLN	88	77.834	42.732	32.769	1.00	42.46	Y	C
ATOM	7792	CG	GLN	88	79.114	42.125	32.259	1.00	42.46	Y	C
ATOM	7793	CD	GLN	88	79.594	42.783	30.983	1.00	42.46	Y	C
ATOM	7794	OE1	GLN	88	78.834	42.928	30.019	1.00	42.46	Y	O
ATOM	7795	NE2	GLN	88	80.863	43.183	30.965	1.00	42.46	Y	N
ATOM	7796	C	GLN	88	78.930	44.691	33.873	1.00	35.54	Y	C
ATOM	7797	O	GLN	88	78.530	45.774	33.436	1.00	35.54	Y	O
ATOM	7798	N	GLN	89	80.195	44.465	34.216	1.00	24.85	Y	N
ATOM	7799	CA	GLN	89	81.208	45.502	34.082	1.00	24.85	Y	C
ATOM	7800	CB	GLN	89	81.794	45.851	35.458	1.00	29.69	Y	C
ATOM	7801	CG	GLN	89	82.481	44.722	36.182	1.00	29.69	Y	C
ATOM	7802	CD	GLN	89	83.903	44.496	35.696	1.00	29.69	Y	C
ATOM	7803	OE1	GLN	89	84.676	45.442	35.535	1.00	29.69	Y	O
ATOM	7804	NE2	GLN	89	84.261	43.238	35.476	1.00	29.69	Y	N
ATOM	7805	C	GLN	89	82.294	45.043	33.128	1.00	24.85	Y	C
ATOM	7806	O	GLN	89	82.527	43.853	32.990	1.00	24.85	Y	O
ATOM	7807	N	TRP	90	82.943	45.993	32.460	1.00	39.13	Y	N
ATOM	7808	CA	TRP	90	84.008	45.672	31.510	1.00	39.13	Y	C
ATOM	7809	CB	TRP	90	83.529	45.955	30.069	1.00	30.35	Y	C
ATOM	7810	CG	TRP	90	83.422	47.437	29.678	1.00	30.35	Y	C
ATOM	7811	CD2	TRP	90	83.088	47.967	28.385	1.00	30.35	Y	C

Fig. 19: A-108

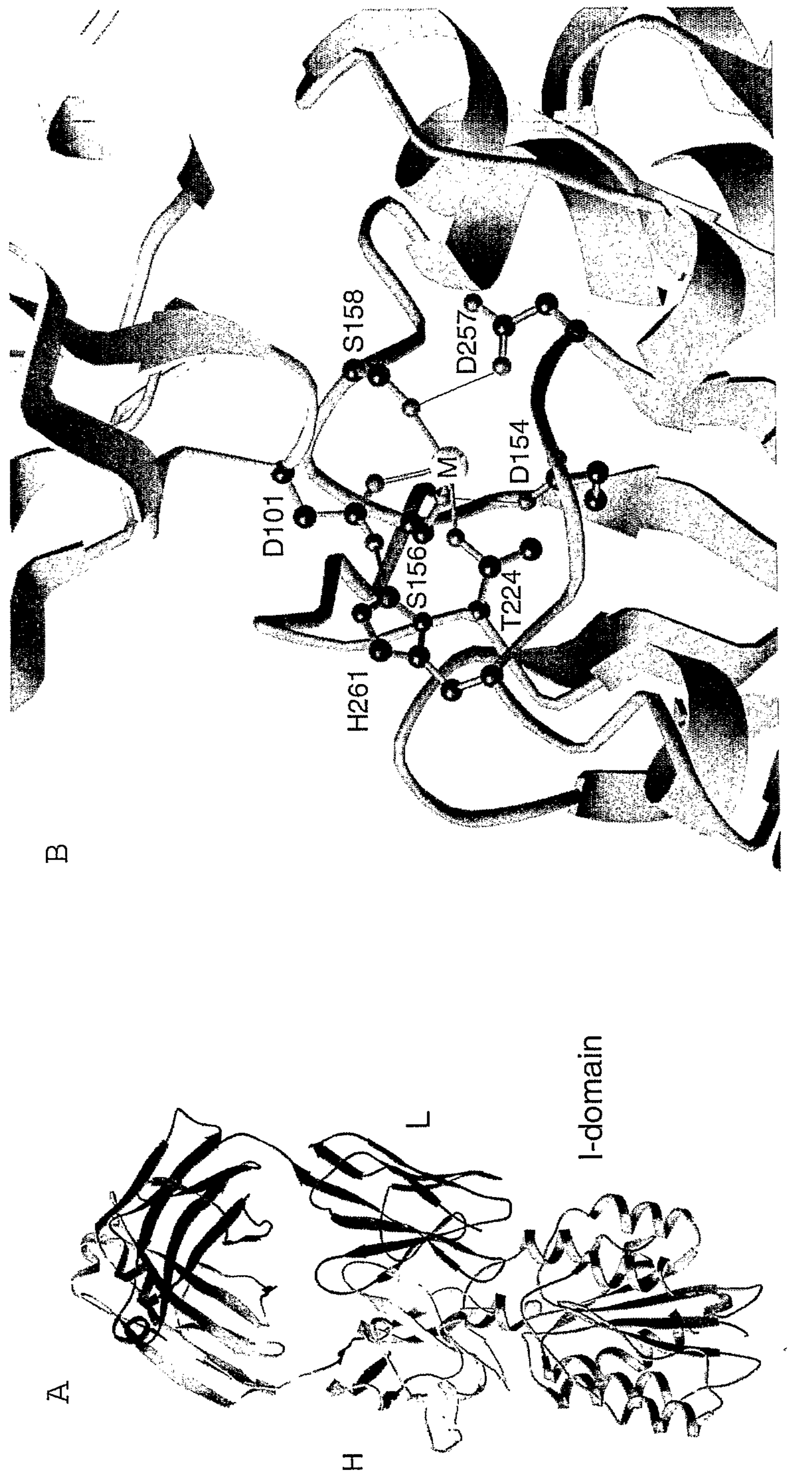
ATOM	7812	CE2	TRP	90	83.122	49.375	28.486	1.00	30.35	Y	C
ATOM	7813	CE3	TRP	90	82.762	47.389	27.152	1.00	30.35	Y	C
ATOM	7814	CD1	TRP	90	83.635	48.523	30.484	1.00	30.35	Y	C
ATOM	7815	NE1	TRP	90	83.460	49.686	29.776	1.00	30.35	Y	N
ATOM	7816	CZ2	TRP	90	82.840	50.217	27.398	1.00	30.35	Y	C
ATOM	7817	CZ3	TRP	90	82.480	48.232	26.063	1.00	30.35	Y	C
ATOM	7818	CH2	TRP	90	82.522	49.627	26.199	1.00	30.35	Y	C
ATOM	7819	C	TRP	90	85.290	46.457	31.816	1.00	39.13	Y	C
ATOM	7820	O	TRP	90	86.293	46.339	31.115	1.00	39.13	Y	O
ATOM	7821	N	SER	91	85.251	47.254	32.876	1.00	18.51	Y	N
ATOM	7822	CA	SER	91	86.395	48.067	33.257	1.00	18.51	Y	C
ATOM	7823	CB	SER	91	85.948	49.152	34.237	1.00	45.24	Y	C
ATOM	7824	OG	SER	91	84.909	49.937	33.686	1.00	45.24	Y	O
ATOM	7825	C	SER	91	87.555	47.267	33.866	1.00	18.51	Y	C
ATOM	7826	O	SER	91	88.717	47.649	33.739	1.00	18.51	Y	O
ATOM	7827	N	GLY	92	87.241	46.166	34.534	1.00	40.34	Y	N
ATOM	7828	CA	GLY	92	88.282	45.360	35.146	1.00	40.34	Y	C
ATOM	7829	C	GLY	92	88.273	43.910	34.687	1.00	40.34	Y	C
ATOM	7830	O	GLY	92	87.248	43.386	34.244	1.00	40.34	Y	O
ATOM	7831	N	ASN	93	89.420	43.249	34.801	1.00	37.36	Y	N
ATOM	7832	CA	ASN	93	89.544	41.863	34.380	1.00	37.36	Y	C
ATOM	7833	CB	ASN	93	90.765	41.702	33.492	1.00	14.59	Y	C
ATOM	7834	CG	ASN	93	90.634	42.451	32.208	1.00	14.59	Y	C
ATOM	7835	OD1	ASN	93	91.556	43.159	31.796	1.00	14.59	Y	O
ATOM	7836	ND2	ASN	93	89.482	42.305	31.552	1.00	14.59	Y	N
ATOM	7837	C	ASN	93	89.668	40.944	35.574	1.00	37.36	Y	C
ATOM	7838	O	ASN	93	90.346	41.265	36.539	1.00	37.36	Y	O
ATOM	7839	N	PRO	94	89.005	39.783	35.525	1.00	28.71	Y	N
ATOM	7840	CD	PRO	94	88.990	38.808	36.629	1.00	9.29	Y	C
ATOM	7841	CA	PRO	94	88.167	39.322	34.412	1.00	28.71	Y	C
ATOM	7842	CB	PRO	94	87.940	37.858	34.745	1.00	9.29	Y	C
ATOM	7843	CG	PRO	94	87.823	37.904	36.251	1.00	9.29	Y	C
ATOM	7844	C	PRO	94	86.845	40.076	34.372	1.00	28.71	Y	C
ATOM	7845	O	PRO	94	86.418	40.640	35.384	1.00	28.71	Y	O
ATOM	7846	N	TRP	95	86.200	40.084	33.206	1.00	37.86	Y	N
ATOM	7847	CA	TRP	95	84.910	40.743	33.082	1.00	37.86	Y	C
ATOM	7848	CB	TRP	95	84.428	40.762	31.629	1.00	24.14	Y	C
ATOM	7849	CG	TRP	95	85.220	41.665	30.744	1.00	24.14	Y	C
ATOM	7850	CD2	TRP	95	85.537	41.458	29.359	1.00	24.14	Y	C
ATOM	7851	CE2	TRP	95	86.285	42.575	28.929	1.00	24.14	Y	C
ATOM	7852	CE3	TRP	95	85.264	40.437	28.440	1.00	24.14	Y	C
ATOM	7853	CD1	TRP	95	85.770	42.867	31.085	1.00	24.14	Y	C
ATOM	7854	NE1	TRP	95	86.411	43.419	30.000	1.00	24.14	Y	N
ATOM	7855	CZ2	TRP	95	86.765	42.697	27.624	1.00	24.14	Y	C
ATOM	7856	CZ3	TRP	95	85.748	40.566	27.133	1.00	24.14	Y	C
ATOM	7857	CH2	TRP	95	86.487	41.685	26.744	1.00	24.14	Y	C
ATOM	7858	C	TRP	95	83.959	39.922	33.941	1.00	37.86	Y	C
ATOM	7859	O	TRP	95	83.997	38.688	33.920	1.00	37.86	Y	O
ATOM	7860	N	THR	96	83.105	40.605	34.695	1.00	19.88	Y	N
ATOM	7861	CA	THR	96	82.192	39.913	35.582	1.00	19.88	Y	C
ATOM	7862	CB	THR	96	82.692	40.028	37.038	1.00	22.31	Y	C
ATOM	7863	OG1	THR	96	82.747	41.408	37.404	1.00	22.31	Y	O
ATOM	7864	CG2	THR	96	84.091	39.443	37.186	1.00	22.31	Y	C
ATOM	7865	C	THR	96	80.759	40.413	35.508	1.00	19.88	Y	C
ATOM	7866	O	THR	96	80.500	41.491	34.998	1.00	19.88	Y	O
ATOM	7867	N	PHE	97	79.839	39.596	36.015	1.00	20.15	Y	N
ATOM	7868	CA	PHE	97	78.420	39.912	36.073	1.00	20.15	Y	C
ATOM	7869	CB	PHE	97	77.580	38.827	35.397	1.00	25.28	Y	C
ATOM	7870	CG	PHE	97	77.890	38.613	33.946	1.00	25.28	Y	C
ATOM	7871	CD1	PHE	97	79.062	37.994	33.554	1.00	25.28	Y	C
ATOM	7872	CD2	PHE	97	76.979	38.990	32.969	1.00	25.28	Y	C
ATOM	7873	CE1	PHE	97	79.322	37.750	32.204	1.00	25.28	Y	C
ATOM	7874	CE2	PHE	97	77.234	38.748	31.611	1.00	25.28	Y	C
ATOM	7875	CZ	PHE	97	78.404	38.128	31.233	1.00	25.28	Y	C
ATOM	7876	C	PHE	97	78.054	39.931	37.557	1.00	20.15	Y	C
ATOM	7877	O	PHE	97	78.841	39.487	38.394	1.00	20.15	Y	O
ATOM	7878	N	GLY	98	76.875	40.460	37.879	1.00	30.22	Y	N
ATOM	7879	CA	GLY	98	76.412	40.488	39.256	1.00	30.22	Y	C
ATOM	7880	C	GLY	98	75.676	39.178	39.406	1.00	30.22	Y	C
ATOM	7881	O	GLY	98	75.506	38.478	38.405	1.00	30.22	Y	O
ATOM	7882	N	GLN	99	75.235	38.819	40.608	1.00	24.51	Y	N
ATOM	7883	CA	GLN	99	74.537	37.541	40.755	1.00	24.51	Y	C
ATOM	7884	CB	GLN	99	74.350	37.163	42.231	1.00	60.71	Y	C

Fig. 19: A-109

ATOM	7885	CG	GLN	99	74.599	38.274	43.209	1.00	60.71	Y	C
ATOM	7886	CD	GLN	99	73.728	39.464	42.945	1.00	60.71	Y	C
ATOM	7887	OE1	GLN	99	72.510	39.411	43.113	1.00	60.71	Y	O
ATOM	7888	NE2	GLN	99	74.346	40.551	42.515	1.00	60.71	Y	N
ATOM	7889	C	GLN	99	73.189	37.507	40.043	1.00	24.51	Y	C
ATOM	7890	O	GLN	99	72.587	36.443	39.894	1.00	24.51	Y	O
ATOM	7891	N	GLY	100	72.730	38.666	39.586	1.00	42.40	Y	N
ATOM	7892	CA	GLY	100	71.455	38.725	38.900	1.00	42.40	Y	C
ATOM	7893	C	GLY	100	70.355	39.043	39.886	1.00	42.40	Y	C
ATOM	7894	O	GLY	100	70.483	38.749	41.074	1.00	42.40	Y	O
ATOM	7895	N	THR	101	69.283	39.662	39.399	1.00	27.30	Y	N
ATOM	7896	CA	THR	101	68.144	40.021	40.236	1.00	27.30	Y	C
ATOM	7897	CB	THR	101	68.024	41.538	40.401	1.00	28.79	Y	C
ATOM	7898	OG1	THR	101	69.008	41.995	41.336	1.00	28.79	Y	O
ATOM	7899	CG2	THR	101	66.646	41.907	40.892	1.00	28.79	Y	C
ATOM	7900	C	THR	101	66.903	39.492	39.551	1.00	27.30	Y	C
ATOM	7901	O	THR	101	66.619	39.845	38.408	1.00	27.30	Y	O
ATOM	7902	N	LYS	102	66.166	38.635	40.240	1.00	67.88	Y	N
ATOM	7903	CA	LYS	102	64.978	38.064	39.642	1.00	67.88	Y	C
ATOM	7904	CB	LYS	102	64.806	36.618	40.106	1.00	117.75	Y	C
ATOM	7905	CG	LYS	102	63.920	35.785	39.198	1.00	117.75	Y	C
ATOM	7906	CD	LYS	102	63.925	34.321	39.608	1.00	117.75	Y	C
ATOM	7907	CE	LYS	102	63.094	33.485	38.651	1.00	117.75	Y	C
ATOM	7908	NZ	LYS	102	63.586	33.621	37.250	1.00	117.75	Y	N
ATOM	7909	C	LYS	102	63.749	38.885	39.996	1.00	67.88	Y	C
ATOM	7910	O	LYS	102	63.560	39.262	41.155	1.00	67.88	Y	O
ATOM	7911	N	VAL	103	62.926	39.176	38.989	1.00	55.50	Y	N
ATOM	7912	CA	VAL	103	61.706	39.941	39.208	1.00	55.50	Y	C
ATOM	7913	CB	VAL	103	61.779	41.349	38.510	1.00	68.46	Y	C
ATOM	7914	CG1	VAL	103	63.207	41.865	38.530	1.00	68.46	Y	C
ATOM	7915	CG2	VAL	103	61.258	41.290	37.084	1.00	68.46	Y	C
ATOM	7916	C	VAL	103	60.489	39.141	38.709	1.00	55.50	Y	C
ATOM	7917	O	VAL	103	60.378	38.828	37.517	1.00	55.50	Y	O
ATOM	7918	N	GLU	104	59.597	38.779	39.633	1.00	70.95	Y	N
ATOM	7919	CA	GLU	104	58.395	38.025	39.281	1.00	70.95	Y	C
ATOM	7920	CB	GLU	104	58.243	36.764	40.145	1.00	145.77	Y	C
ATOM	7921	CG	GLU	104	57.957	37.019	41.616	1.00	145.77	Y	C
ATOM	7922	CD	GLU	104	59.215	37.263	42.418	1.00	145.77	Y	C
ATOM	7923	OE1	GLU	104	59.106	37.542	43.631	1.00	145.77	Y	O
ATOM	7924	OE2	GLU	104	60.315	37.167	41.839	1.00	145.77	Y	O
ATOM	7925	C	GLU	104	57.157	38.897	39.443	1.00	70.95	Y	C
ATOM	7926	O	GLU	104	57.197	39.939	40.108	1.00	70.95	Y	O
ATOM	7927	N	ILE	105	56.058	38.459	38.834	1.00	139.77	Y	N
ATOM	7928	CA	ILE	105	54.791	39.184	38.876	1.00	139.77	Y	C
ATOM	7929	CB	ILE	105	53.838	38.730	37.757	1.00	105.35	Y	C
ATOM	7930	CG2	ILE	105	52.923	39.875	37.373	1.00	105.35	Y	C
ATOM	7931	CG1	ILE	105	54.633	38.232	36.553	1.00	105.35	Y	C
ATOM	7932	CD1	ILE	105	53.775	37.746	35.397	1.00	105.35	Y	C
ATOM	7933	C	ILE	105	54.047	38.952	40.180	1.00	139.77	Y	C
ATOM	7934	O	ILE	105	53.763	37.810	40.533	1.00	139.77	Y	O
ATOM	7935	N	LYS	106	53.706	40.031	40.880	1.00	101.75	Y	N
ATOM	7936	CA	LYS	106	52.969	39.916	42.135	1.00	101.75	Y	C
ATOM	7937	CB	LYS	106	53.545	40.870	43.189	1.00	95.13	Y	C
ATOM	7938	CG	LYS	106	52.954	40.690	44.584	1.00	95.13	Y	C
ATOM	7939	CD	LYS	106	53.556	41.665	45.586	1.00	95.13	Y	C
ATOM	7940	CE	LYS	106	52.939	41.482	46.965	1.00	95.13	Y	C
ATOM	7941	NZ	LYS	106	53.446	42.478	47.948	1.00	95.13	Y	N
ATOM	7942	C	LYS	106	51.492	40.235	41.897	1.00	101.75	Y	C
ATOM	7943	O	LYS	106	51.148	40.637	40.765	1.00	100.80	Y	O
ATOM	7944	OXT	LYS	106	50.694	40.080	42.844	1.00	94.18	Y	O
ATOM	7945	MN	MN	400	89.864	50.249	22.621	1.00	34.24	N	

END

Fig. 20



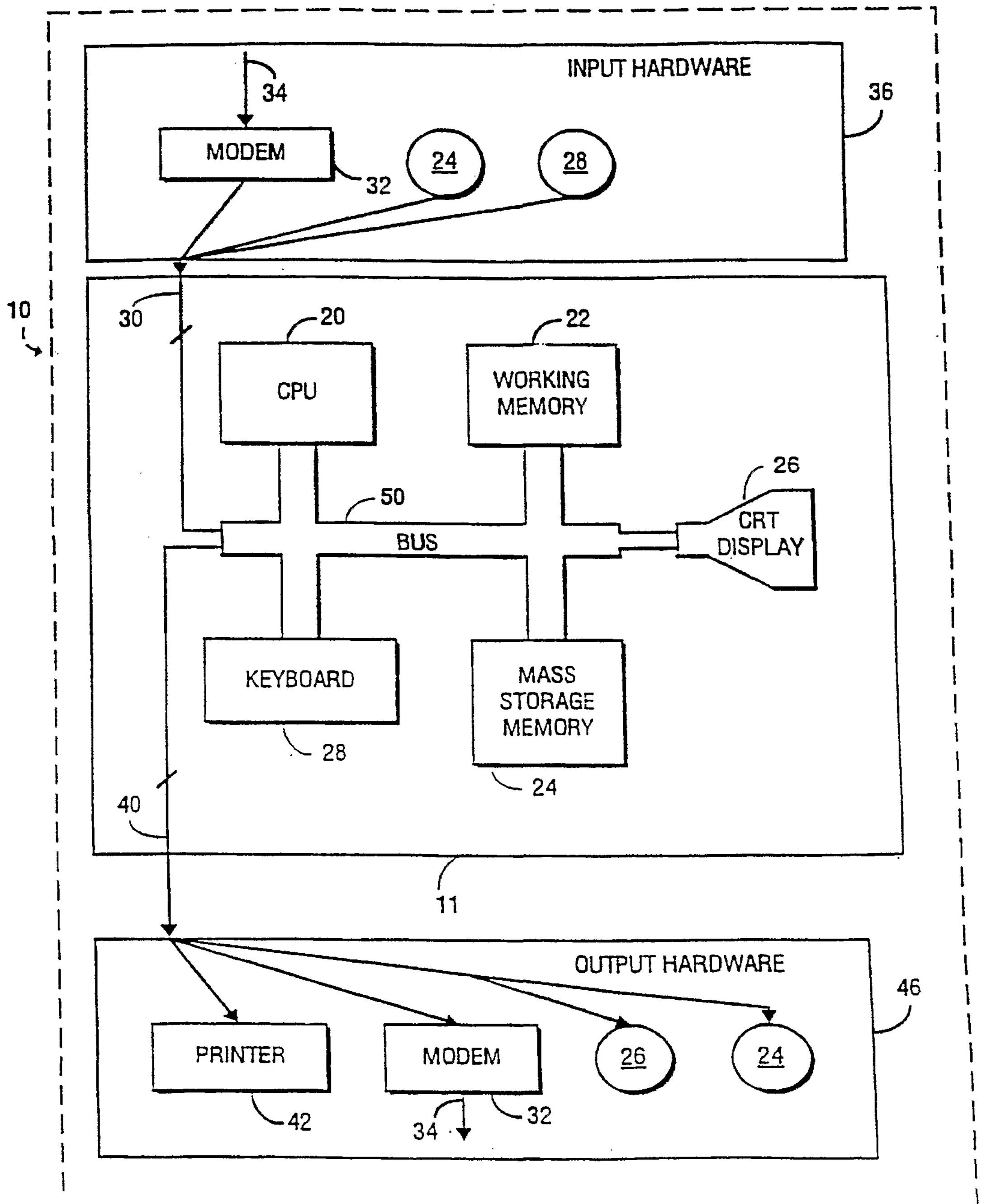

INPUT HARDWARE
34
MODEM
32
24
28
36
10
30
20
CPU
22
WORKING MEMORY
26
50
CRT DISPLAY
BUS
KEYBOARD
MASS STORAGE MEMORY
28
24
40
11
OUTPUT HARDWARE
46
PRINTER
MODEM
26
24
42
34
32

Fig. 21

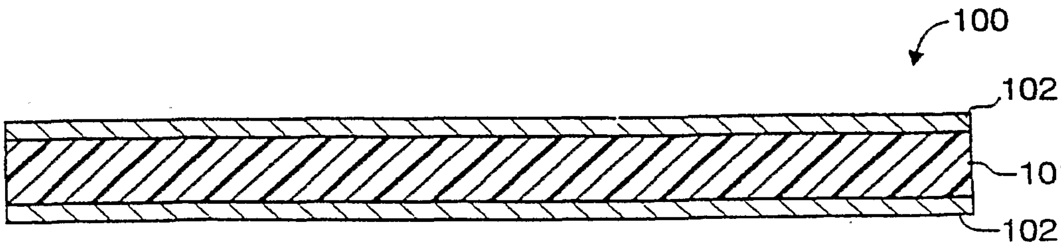


Fig. 22

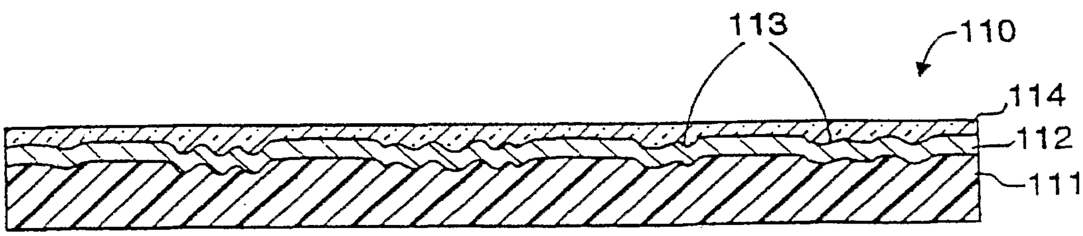


Fig. 23